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OM protein - protein search, using sw model

Run on: September 7, 2005, 19:44:24 ; Search time 16.3256 Seconds
(without alignments)
59.443 Million cell updates/sec

Title: US-10-812-238B-23

Perfect score: 73

Sequence: 1 NTRCRGDSKVQE 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A-COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73	100.0	233	4	US-09-360-376-55
2	44	60.3	705	4	US-08-311-731A-4
3	40	54.8	282	4	US-09-360-376-54
4	40	54.8	424	4	US-09-489-039A-12030
5	40	54.8	501	4	US-09-270-767-41177
6	40	54.8	501	4	US-09-270-767-56393
7	39	53.4	283	3	US-08-992-035A-3
8	39	53.4	283	4	US-09-360-376-53
9	38	52.1	120	4	US-09-513-999C-6407
10	38	52.1	136	4	US-09-690-454-131
11	37	50.7	201	3	US-09-015-734-12
12	37	50.7	201	4	US-09-515-311-12
13	37	50.7	236	3	US-09-015-734-7
14	37	50.7	236	4	US-09-515-311-7
15	37	50.7	285	3	US-09-015-734-2
16	37	50.7	255	4	US-09-515-311-2
17	37	50.7	272	4	US-09-489-039A-13748
18	37	50.7	275	4	US-09-489-039A-11789
19	37	50.7	488	4	US-09-489-039A-13164
20	36	49.3	280	4	US-09-601-478-5
21	36	49.3	280	4	US-09-401-478-8
22	36	49.3	280	4	US-09-442-013-13
23	36	49.3	280	4	US-09-513-365A-1
24	36	49.3	280	4	US-09-513-365A-6
25	36	49.3	316	4	US-09-328-352-8163
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					Sequence 56393, A
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					Sequence 7, Appli
					Sequence 2, Appli
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					Sequence 8237, Ap
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32	47.9	269	4	US-10-000-489-78	Sequence 78, Appl
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35	47.9	276	4	US-09-949-016-7261	Sequence 7261, Ap
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56	47.9	662	3	US-08-789-350-2	Sequence 2, Appli
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68	46.6	163	4	US-09-252-991A-18617	Sequence 18617, A
69	46.6	172	4	US-09-252-991A-22192	Sequence 22192, A
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77	46.6	216	4	US-09-949-016-8206	Sequence 8206, Ap
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104	34	46.6	1036	4	US-09-536-224-4	Sequence 4, Appl1	177	33	45.2	35	4	US-09-515-965A-143	Sequence 143, App
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130	33	45.2	35	3	US-09-082-279B-142	Sequence 142, App	203	33	45.2	35	4	US-09-350-841A-139	Sequence 139, App
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256	33	45.2	115	4	US-09-270-767-55504	Sequence 55504, A	329	33	45.2	850	4	US-09-107-532A-4631	Sequence 4631, Ap
257	33	45.2	130	3	US-08-329-799-37	Sequence 37, Appl	330	33	45.2	1048	4	US-09-949-016-6192	Sequence 6192, Ap
258	33	45.2	158	4	US-09-248-796A-18178	Sequence 18178, A	331	33	45.2	1149	4	US-09-949-016-7401	Sequence 7401, Ap
259	33	45.2	173	4	US-09-107-532A-4715	Sequence 4715, Ap	332	33	45.2	1436	4	US-09-578-063-78	Sequence 78, Appl
260	33	45.2	254	4	US-09-252-991A-32459	Sequence 32459, A	333	33	45.2	3200	2	US-08-477-451-8	Sequence 8, Appl
261	33	45.2	299	4	US-09-252-991A-21857	Sequence 21857, A	334	33	45.2	7	1	US-08-421-702A-17	Sequence 17, Appl
262	33	45.2	308	4	US-09-248-796A-14594	Sequence 14594, A	335	33	43.8	7	1	US-08-303-052A-17	Sequence 17, Appl
263	33	45.2	310	1	US-07-704-288C-6	Sequence 6, Appl	336	32	43.8	7	1	US-08-421-696A-17	Sequence 17, Appl
264	33	45.2	310	1	US-08-379-259-6	Sequence 6, Appl	337	32	43.8	7	1	US-08-421-697A-17	Sequence 17, Appl
265	33	45.2	310	3	US-07-791-931-6	Sequence 6, Appl	338	32	43.8	7	1	US-08-421-698A-17	Sequence 17, Appl
266	33	45.2	313	4	US-09-302-540-11218	Sequence 11218, A	339	32	43.8	7	2	US-08-421-695A-17	Sequence 17, Appl
267	33	45.2	324	1	US-08-047-413-11	Sequence 11, Appl	340	32	43.8	7	5	PCT-US95-04741-17	Sequence 17, Appl
268	33	45.2	324	3	US-08-229-050-11	Sequence 11, Appl	341	32	43.8	9	1	US-08-421-702A-26	Sequence 26, Appl
269	33	45.2	324	3	US-08-801-563-11	Sequence 11, Appl	342	32	43.8	9	1	US-08-421-696A-26	Sequence 26, Appl
270	33	45.2	346	3	US-09-034-916-2	Sequence 2, Appl	343	32	43.8	9	1	US-08-421-697A-26	Sequence 26, Appl
271	33	45.2	347	4	US-09-307-794A-148	Sequence 148, App	344	32	43.8	9	1	US-08-421-698A-26	Sequence 26, Appl
272	33	45.2	347	4	US-09-305-125A-148	Sequence 148, App	345	32	43.8	9	2	US-08-421-695A-26	Sequence 26, Appl
273	33	45.2	347	4	US-09-302-775A-148	Sequence 148, App	346	32	43.8	9	5	PCT-US95-04741-26	Sequence 26, Appl
274	33	45.2	347	4	US-09-306-700-148	Sequence 148, App	347	32	43.8	20	3	US-08-857-076-27	Sequence 27, Appl
275	33	45.2	347	4	US-09-303-603A-148	Sequence 148, App	348	32	43.8	35	3	US-08-857-076-30	Sequence 30, Appl
276	33	45.2	347	4	US-09-304-920A-148	Sequence 148, App	349	32	43.8	43	3	US-08-857-076-28	Sequence 28, Appl
277	33	45.2	347	4	US-09-309-064-148	Sequence 148, App	350	32	43.8	65	4	US-09-248-798A-27954	Sequence 27954, A
278	33	45.2	347	4	US-09-305-381A-148	Sequence 148, App	351	32	43.8	72	4	US-09-328-352-4610	Sequence 4610, Ap
279	33	45.2	347	4	US-09-306-618-148	Sequence 148, App	352	32	43.8	90	4	US-09-270-767-31781	Sequence 31781, A
280	33	45.2	359	4	US-09-372-758A-2	Sequence 2, Appl	353	32	43.8	90	4	US-09-270-767-38050	Sequence 38050, A
281	33	45.2	362	4	US-09-252-991A-24409	Sequence 24409, A	354	32	43.8	90	4	US-09-270-767-46998	Sequence 46998, A
282	33	45.2	369	4	US-09-949-016-10311	Sequence 10311, A	355	32	43.8	98	4	US-09-270-767-53267	Sequence 53267, A
283	33	45.2	383	4	US-09-248-796A-18954	Sequence 18954, A	356	32	43.8	98	4	US-09-513-999C-4239	Sequence 4239, Ap
284	33	45.2	389	4	US-09-270-767-32291	Sequence 32291, A	357	32	43.8	100	4	US-09-621-976-4269	Sequence 4269, Ap
285	33	45.2	389	4	US-09-270-767-47508	Sequence 47508, A	358	32	43.8	100	4	US-09-513-999C-5033	Sequence 5033, Ap
286	33	45.2	469	4	US-09-347-650-16	Sequence 16, Appl	359	32	43.8	107	4	US-09-107-532A-5073	Sequence 5073, Ap
287	33	45.2	503	4	US-09-302-540-11343	Sequence 11343, A	360	32	43.8	118	4	US-08-794-028B-21	Sequence 21, Appl
288	33	45.2	527	2	US-08-659-939-4	Sequence 4, Appl	361	32	43.8	118	4	US-08-794-028B-22	Sequence 22, Appl
289	33	45.2	527	2	US-08-850-041-4	Sequence 4, Appl	362	32	43.8	119	3	US-08-753-642-2	Sequence 2, Appl
290	33	45.2	527	3	US-08-896-500-4	Sequence 4, Appl	363	32	43.8	120	1	US-07-979-630-1	Sequence 1, Appl
291	33	45.2	527	3	US-08-476-397-4	Sequence 4, Appl	364	32	43.8	120	1	US-08-440-049-1	Sequence 1, Appl
292	33	45.2	527	3	US-08-373-720-4	Sequence 4, Appl	365	32	43.8	120	1	US-08-440-049-3	Sequence 3, Appl
293	33	45.2	527	3	US-08-923-558-2	Sequence 2, Appl	366	32	43.8	120	2	US-08-441-513A-1	Sequence 1, Appl
294	33	45.2	527	3	US-09-262-927-4	Sequence 4, Appl	367	32	43.8	120	2	US-08-441-513A-3	Sequence 3, Appl
295	33	45.2	527	4	US-09-486-553-2	Sequence 2, Appl	368	32	43.8	120	3	US-08-970-865-2	Sequence 2, Appl
296	33	45.2	527	4	US-09-570-383-4	Sequence 4, Appl	369	32	43.8	120	3	US-08-970-865-3	Sequence 3, Appl
297	33	45.2	527	4	US-09-395-336-4	Sequence 4, Appl	370	32	43.8	120	3	US-08-581-662-31	Sequence 31, Appl
298	33	45.2	574	6	5223254-2	Sequence 4, Appl	371	32	43.8	120	3	US-09-363-573-2	Sequence 2, Appl
299	33	45.2	574	6	5223254-2	Patent No. 5223254	372	32	43.8	120	3	US-09-363-573-3	Sequence 3, Appl
300	33	45.2	594	2	US-08-659-939-2	Sequence 2, Appl	373	32	43.8	120	3	US-08-530-340-6	Sequence 6, Appl
301	33	45.2	594	2	US-08-850-041-2	Sequence 2, Appl	374	32	43.8	120	3	US-08-845-541B-1	Sequence 1, Appl
302	33	45.2	594	2	US-08-467-963C-6	Sequence 6, Appl	375	32	43.8	120	3	US-08-845-541B-3	Sequence 3, Appl
303	33	45.2	594	2	US-08-838-189D-6	Sequence 6, Appl	376	32	43.8	120	3	US-08-845-541B-4	Sequence 4, Appl
304	33	45.2	594	3	US-08-852-344D-6	Sequence 6, Appl	377	32	43.8	120	3	US-08-845-541B-5	Sequence 5, Appl
305	33	45.2	594	3	US-08-896-500-2	Sequence 2, Appl	378	32	43.8	120	3	US-08-845-541B-6	Sequence 6, Appl
306	33	45.2	594	3	US-08-476-397-2	Sequence 2, Appl	379	32	43.8	120	3	US-08-845-541B-7	Sequence 7, Appl
307	33	45.2	594	3	US-08-373-720-2	Sequence 2, Appl	380	32	43.8	120	3	US-08-845-541B-8	Sequence 8, Appl
308	33	45.2	594	3	US-08-344-639E-6	Sequence 6, Appl	381	32	43.8	120	3	US-08-845-541B-9	Sequence 9, Appl
309	33	45.2	594	3	US-09-262-927-2	Sequence 2, Appl	382	32	43.8	120	3	US-08-845-541B-10	Sequence 10, Appl
310	33	45.2	594	3	US-08-467-969A-6	Sequence 6, Appl	383	32	43.8	120	3	US-08-845-541B-11	Sequence 11, Appl
311	33	45.2	594	3	US-08-467-961A-6	Sequence 6, Appl	384	32	43.8	120	3	US-08-845-541B-12	Sequence 12, Appl
312	33	45.2	594	3	US-08-001-554A-6	Sequence 6, Appl	385	32	43.8	120	3	US-08-845-541B-13	Sequence 13, Appl
313	33	45.2	594	4	US-09-570-383-2	Sequence 2, Appl	386	32	43.8	120	3	US-08-845-541B-17	Sequence 17, Appl
314	33	45.2	594	4	US-09-395-336-2	Sequence 2, Appl	387	32	43.8	120	3	US-08-845-541B-18	Sequence 18, Appl
315	33	45.2	681	6	5194595-19	Sequence 2, Appl	388	32	43.8	120	3	US-08-845-541B-19	Sequence 19, Appl
316	33	45.2	681	6	5194595-19	Patent No. 5194595	389	32	43.8	120	3	US-08-845-541B-20	Sequence 20, Appl
317	33	45.2	686	4	US-09-252-991A-18115	Sequence 18115, A	390	32	43.8	120	3	US-08-845-541B-21	Sequence 21, Appl
318	33	45.2	730	1	US-08-121-713D-58	Sequence 58, Appl	391	32	43.8	120	3	US-09-066-065A-1	Sequence 1, Appl
319	33	45.2	730	1	US-08-835-268-58	Sequence 58, Appl	392	32	43.8	120	3	US-09-066-065A-3	Sequence 3, Appl


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Best Local Similarity 46.2%; Pred. NO. 50;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 NYRCRGDDSKVOE 13
   |:|:|:|:|
Db 150 NFVCQGNQKQVRE 162

RESULT 4
US-09-489-039A-12030
; Sequence 12030, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12030
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12030

Query Match 54.8%; Score 40; DB 4; Length 424;
Best Local Similarity 85.7%; Pred. NO. 76;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
   :|:|:|:|
Db 63 FRCRGDD 69

RESULT 5
US-09-270-767-41177
; Sequence 41177, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41177
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41177

Query Match 54.8%; Score 40; DB 4; Length 501;
Best Local Similarity 60.0%; Pred. NO. 90;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 YRCRGDDSKV 11
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Db 485 YRCRGDSSLI 494

RESULT 6
US-09-270-767-56393
; Sequence 56393, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

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FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 56393
LENGTH: 501
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-56393

Query Match 54.8%; Score 40; DB 4; Length 501;
Best Local Similarity 60.0%; Pred. No. 90;
Matches 6; Conservative 2; Mismatches 2; Indels 2; Gaps 0;

QY 2 YRCRGDSDSV 11
DB 485 YRCKGDSLI 494

RESULT 7
US-08-992-035A-3
Sequence 3, Application US/08992035A
Patent No. 6242179
GENERAL INFORMATION:
APPLICANT: Shah, Purvi
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: HUMAN PHOSPHATASES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/992,035A
FILING DATE: December 17, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0433 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 283 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 1487873
US-08-992-035A-3

Query Match 53.4%; Score 39; DB 3; Length 283;
Best Local Similarity 46.2%; Pred. No. 74;
Matches 6; Conservative 5; Mismatches 2; Indels 2; Gaps 0;

QY 1 NYRCRGDDSKVQE 13
DB 150 DYICQGNKEVKKE 162
RESULT 8
US-09-360-376-53
Sequence 53, Application US/09360376
Patent No. 6495739
GENERAL INFORMATION:
APPLICANT: Lassner, Michael
APPLICANT: Ruezinsky, Diane
TITLE OF INVENTION: PLANT PHOSPHATIDIC ACID PHOSPHATASES
FILE REFERENCE: 17026/01/US
CURRENT APPLICATION NUMBER: US/09/360,376
CURRENT FILING DATE: 1999-07-23
PRIOR APPLICATION NUMBER: US 09/122,315
PRIOR FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn version 3.0
SEQ ID NO 53
LENGTH: 283
TYPE: PRT
ORGANISM: Mus musculus
US-09-360-376-53

Query Match 53.4%; Score 39; DB 4; Length 283;
Best Local Similarity 46.2%; Pred. No. 74;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 NYRCRGDDSKVQE 13
DB 150 DYICQGNKEVKKE 162

RESULT 9
US-09-513-999C-6407
Sequence 6407, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59 US2,REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 6407
LENGTH: 120
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: 67
OTHER INFORMATION: Xaa=Arg or Ser
FEATURE:
NAME/KEY: UNSURE
LOCATION: 70
OTHER INFORMATION: Xaa=Lys or Asn or Thr
FEATURE:
NAME/KEY: UNSURE
LOCATION: 94
OTHER INFORMATION: Xaa= * or Ala or Glu or Gly or Lys or Leu or Met or Pro or Gln or

Query Match 52.1%; Score 38; DB 4; Length 120;
Best Local Similarity 54.5%; Pred. No. 46;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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QY      2 YRCRGDSKVQ 12
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Db     101 YRCCKGNRVQ 111

RESULT 10
US-09-690-454-131
; Sequence 131, Application US/09690454
; Patent No. 6531447
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; FILE REFERENCE: PZ006P1
; CURRENT APPLICATION NUMBER: US/09/690,454
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: 09/189,144
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,190
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/050,935
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,101
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/056,250
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,296
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,293
; PRIOR FILING DATE: August 29, 1997
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 131
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-690-454-131

Query Match      52.1%; Score 38; DB 4; Length 136;
Best Local Similarity 54.5%; Pred. No. 52;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      2 YRCRGDSKVQ 12
      |||:| :||
Db     61 YRCCKGNRVQ 71

RESULT 11
US-09-015-734-12
; Sequence 12, Application US/09015734
; Patent No. 6057127
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL EQUINE Fc EPSILON RECEPTOR ALPHA
; TITLE OF INVENTION: CHAIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heeka Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/515,311
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/015,734
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 201 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; COMPUTER: IBM PC compatible

QY      2 YRCRGDSKVQ 13
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Db     91 YRCNRNDLNLSE 102

RESULT 12
US-09-515-311-12
; Sequence 12, Application US/09515311
; Patent No. 6582701
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL EQUINE Fc EPSILON RECEPTOR ALPHA
; TITLE OF INVENTION: CHAIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heeka Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/515,311
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/015,734
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 201 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; COMPUTER: IBM PC compatible
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Query Match          50.7%; Score 37; DB 4; Length 201;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 YRCRGDDSKVQE 13
   |||| :| :|
Db 91 YRCRNDLNLSE 102

RESULT 13
US-09-015-734-7
; Sequence 7, Application US/09015734
; Patent No. 6057127
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL EQUINE FC EPSILON RECEPTOR ALPHA
; TITLE OF INVENTION: CHAIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,734
; FILING DATE: 29-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/494-9505
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-09-015-734-7

Query Match          50.7%; Score 37; DB 3; Length 236;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 YRCRGDDSKVQE 13
   |||| :| :|
Db 72 YRCRNDLNLSE 83

RESULT 14
US-09-515-311-7
; Sequence 7, Application US/09515311
; Patent No. 6582701
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL EQUINE FC EPSILON RECEPTOR ALPHA
; TITLE OF INVENTION: CHAIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,734
; FILING DATE: 29-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/494-9505
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-09-015-734-7
```

```
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/515,311
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/015,734
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-09-515-311-7

Query Match          50.7%; Score 37; DB 4; Length 236;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 YRCRGDDSKVQE 13
   |||| :| :|
Db 72 YRCRNDLNLSE 83

RESULT 15
US-09-015-734-2
; Sequence 2, Application US/09015734
; Patent No. 6057127
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL EQUINE FC EPSILON RECEPTOR ALPHA
; TITLE OF INVENTION: CHAIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,734
; FILING DATE: 29-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
```

```
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 255 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: Protein
US-09-015-734-2

Query Match      50.7%; Score 37; DB 3; Length 255;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 YRCRGDDSKVQE 13
Db      91 YRCRNDNLNLS 102

RESULT 16
US-09-515-311-2
; Sequence 2, Application US/09515311
; Patent No. 6582701
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL EQUINE Pepsilon Receptor Alpha
; TITLE OF INVENTION: CHAIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/515,311
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/015,734
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 255 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: Protein
US-09-515-311-2

Query Match      50.7%; Score 37; DB 4; Length 255;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 YRCRGDDSKVQE 13
Db      91 YRCRNDNLNLS 102

RESULT 17
US-09-489-039A-13748
; Sequence 13748, Application US/09489039A
```

```
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13748
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13748

Query Match      50.7%; Score 37; DB 4; Length 272;
Best Local Similarity 46.2%; Pred. No. 1.5e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      1 NYRCRGDDSKVQE 13
Db      210 NVRFKGGDDAKAEK 222

RESULT 18
US-09-489-039A-11789
; Sequence 11789, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11789
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11789

Query Match      50.7%; Score 37; DB 4; Length 275;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 NYRCRGDDSD 9
Db      32 NWRCGGDSD 40

RESULT 19
US-09-489-039A-13164
; Sequence 13164, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13164
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
```



```
US-09-489-039A-13164
Query Match          50.7%; Score 37; DB 4; Length 488;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 RCRGDD 8
DB      102 RCRGDD 107

RESULT 20
US-09-601-478-5
; Sequence 5, Application US/09601478
; Patent No. 6403785
; GENERAL INFORMATION:
; APPLICANT: Oetuka Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: Human TSC403 gene and human INGIL gene
; FILE REFERENCE: Q60193
; CURRENT APPLICATION NUMBER: US/09/601,478
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP H10-134679
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: JP H10-73234
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: JP H10-38133
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human embryonic brain cDNA library
US-09-601-478-5

Query Match          49.3%; Score 36; DB 4; Length 280;
Best Local Similarity 45.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      3 RCRGDSKVQE 13
DB      257 KCRGDNEXTMD 267

RESULT 21
US-09-601-478-8
; Sequence 8, Application US/09601478
; Patent No. 6403785
; GENERAL INFORMATION:
; APPLICANT: Oetuka Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: Human TSC403 gene and human INGIL gene
; FILE REFERENCE: Q60193
; CURRENT APPLICATION NUMBER: US/09/601,478
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP H10-134679
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: JP H10-73234
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: JP H10-38133
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: human embryonic brain cDNA library
US-09-601-478-8

Query Match          49.3%; Score 36; DB 4; Length 280;
Best Local Similarity 45.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

US-09-489-039A-13164
Query Match          50.7%; Score 37; DB 4; Length 488;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 RCRGDD 8
DB      102 RCRGDD 107

RESULT 20
US-09-601-478-5
; Sequence 5, Application US/09601478
; Patent No. 6403785
; GENERAL INFORMATION:
; APPLICANT: Oetuka Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: Human TSC403 gene and human INGIL gene
; FILE REFERENCE: Q60193
; CURRENT APPLICATION NUMBER: US/09/601,478
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP H10-134679
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: JP H10-73234
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: JP H10-38133
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human embryonic brain cDNA library
US-09-601-478-5

Query Match          49.3%; Score 36; DB 4; Length 280;
Best Local Similarity 45.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      3 RCRGDSKVQE 13
DB      257 KCRGDNEXTMD 267

RESULT 21
US-09-601-478-8
; Sequence 8, Application US/09601478
; Patent No. 6403785
; GENERAL INFORMATION:
; APPLICANT: Oetuka Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: Human TSC403 gene and human INGIL gene
; FILE REFERENCE: Q60193
; CURRENT APPLICATION NUMBER: US/09/601,478
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP H10-134679
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: JP H10-73234
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: JP H10-38133
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: human embryonic brain cDNA library
US-09-601-478-8

Query Match          49.3%; Score 36; DB 4; Length 280;
Best Local Similarity 45.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

US-09-442-013-13
; Sequence 13, Application US/09442013
; Patent No. 6737232
; GENERAL INFORMATION:
; APPLICANT: Lou, Ying
; APPLICANT: Xu, Xiang
; APPLICANT: Leo, Cindy
; APPLICANT: Huang, Betty
; APPLICANT: Shen, Mary
; TITLE OF INVENTION: NOVEL IAPS ASSOCIATED CELL CYCLE PROTEINS, COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: A-68289/DJB/RMS/DAV
; CURRENT APPLICATION NUMBER: US/09/442,013
; CURRENT FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-09-442-013-13

Query Match          49.3%; Score 36; DB 4; Length 280;
Best Local Similarity 45.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      3 RCRGDSKVQE 13
DB      257 KCRGDNEXTMD 267

RESULT 23
US-09-513-365A-1
; Sequence 1, Application US/09513365A
; Patent No. 6790948
; GENERAL INFORMATION:
; APPLICANT: Harris, Curtis C
; APPLICANT: Nagashima, Makoto
; APPLICANT: Government of United States as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: New Tumor Suppressor Gene P33ING2
; FILE REFERENCE: 015280-376100US
; CURRENT APPLICATION NUMBER: US/09/513,365A
; CURRENT FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: US 60/121,891
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: p33ING2
; OTHER INFORMATION: polypeptide sequence
US-09-513-365A-1

Query Match          49.3%; Score 36; DB 4; Length 280;
Best Local Similarity 45.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      3 RCRGDSKVQE 13
DB      257 KCRGDNEXTMD 267
```

```
RESULT 24
US-09-513-365A-6
; Sequence 6, Application US/09513365A
; Patent No. 6790948
; GENERAL INFORMATION:
; APPLICANT: Harris, Curtis C
; APPLICANT: Nagashima, Makoto
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: New Tumor Suppressor Gene P33ING2
; FILE REFERENCE: 015280-376100US
; CURRENT APPLICATION NUMBER: US/09/513,365A
; CURRENT FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: US 60/121,891
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: missense
; OTHER INFORMATION: p33ING2 sequence - Arg 153 to Ser
US-09-513-365A-6

Query Match          49.3%; Score 36; DB 4; Length 280;
Best Local Similarity 45.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      3 RCRGDDSKVQ 13
DB      257 KCRGDNKTKMD 267

RESULT 25
US-09-328-352-8163
; Sequence 8163, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 8163
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-8163

Query Match          49.3%; Score 36; DB 4; Length 316;
Best Local Similarity 63.6%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 YRCRGDDSKVQ 12
DB      175 YRCRGTYYKAQ 185

RESULT 26
US-09-949-016-8237
; Sequence 8237, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
```

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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8237
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8237

Query Match          49.3%; Score 36; DB 4; Length 416;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 NYRCRGDDSK 10
DB      400 NWRCPGTDSE 409

RESULT 27
US-09-786-240-1
; Sequence 1, Application US/09786240
; Patent No. 6558935
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: TANG, Y. Tom
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: AZIMZAI, Yalda
; TITLE OF INVENTION: HUMAN TRANSFERASE PROTEINS
; FILE REFERENCE: PF-0592 PCT
; CURRENT APPLICATION NUMBER: US/09/786,240
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/150,657; unassigned; 09/186,779; unassigned; 60/133,642
; PRIOR FILING DATE: 1998-09-10; 1998-09-10; 1998-11-04; 1998-11-04; 1999-05-11
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6558935 1632930CD1
US-09-786-240-1

Query Match          49.3%; Score 36; DB 4; Length 498;
Best Local Similarity 60.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 NYRCRGDDSK 10
DB      482 NWRCPGTDSE 491

RESULT 28
US-09-198-452A-1290
; Sequence 1290, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffois, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevent
; TITLE OF INVENTION: and treatment of infection
```

FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1290
LENGTH: 94
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1290

Query Match 47.9%; Score 35; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NVRCRGD 7
| | | | |
DB 13 NRRCRGD 19

RESULT 29
US-08-473-981A-12
Sequence 12, Application US/08473981A
Patent No. 5629162
GENERAL INFORMATION:
APPLICANT: deFougerolles, Antonin R
APPLICANT: Springer, Timothy A
TITLE OF INVENTION: METHODS OF IDENTIFYING AGENTS WHICH MODULATE
TITLE OF INVENTION: ICAM-3 BINDING TO LFA-1 (AS AMENDED)
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W. SUITE 600
CITY: WASHINGTON
STATE: D. C.
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,981A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
REGISTRATION NUMBER: 34,395
NAME: MILLONIG, ROBERT C
REFERENCE/DOCKET NUMBER: 1011.0560004
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-473-981A-12

Query Match 47.9%; Score 35; DB 1; Length 99;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 CRGDDSKVOE 13
| | | | |
DB 19 CPGSDKVEE 28

RESULT 30
US-08-474-087-12
Sequence 12, Application US/08474087

Patent No. 5891841
GENERAL INFORMATION:
APPLICANT: de Fougerolles, Antonin R
APPLICANT: Springer, Timothy A
TITLE OF INVENTION: METHODS OF USING INTERCELLULAR ADHESION MOLECULE-
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W. SUITE 600
CITY: WASHINGTON
STATE: D. C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,087
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/038,990
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/712,879
FILING DATE: 11-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MILLONIG, ROBERT C
REGISTRATION NUMBER: 34,395
REFERENCE/DOCKET NUMBER: 1011.0560003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-474-087-12

Query Match 47.9%; Score 35; DB 2; Length 99;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 CRGDDSKVOE 13
| | | | |
DB 19 CPGSDKVEE 28

RESULT 31
US-09-252-991A-22600
Sequence 22600, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22600
LENGTH: 213
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-22600

Query Match 47.9%; Score 35; DB 4; Length 213;
Best Local Similarity 46.2%; Pred. No. 2.6e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 NYRCRGDDSKVQE 13
DB 84 DYTQGRGDKVED 96

RESULT 32

US-10-000-489-78

; Sequence 78, Application US/10000489
; Patent No. 6794363
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US6.DIV
; CURRENT APPLICATION NUMBER: US/10/000,489
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Jpatent
; SEQ ID NO 78
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..21
US-10-000-489-78

Query Match 47.9%; Score 35; DB 4; Length 269;
Best Local Similarity 66.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YRCRGDDSK 10
DB 183 YRCNGTSSK 191

RESULT 33

US-09-949-016-6121
; Sequence 6121, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6121

; LENGTH: 269

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-6121

Query Match 47.9%; Score 35; DB 4; Length 269;
Best Local Similarity 66.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YRCRGDDSK 10
DB 183 YRCNGTSSK 191

RESULT 34

US-08-282-951-6
; Sequence 6, Application US/08282951
; Patent No. 5685590
; GENERAL INFORMATION:
; APPLICANT: YANG, ZHI
; TITLE OF INVENTION: METHOD FOR ISOLATING AND DIRECTLY
; TITLE OF INVENTION: CLONING GENES WHICH ENCODE CELL-SURFACE AND SECRETED
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/282,951
; FILING DATE: 29-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 20296-20012.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 272 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-282-951-6

Query Match 47.9%; Score 35; DB 1; Length 272;
Best Local Similarity 54.5%; Pred. No. 3.3e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 YRCRGDDSKVQ 12
DB 91 YRCQATDAKQ 101

RESULT 35

US-09-949-016-7261
; Sequence 7261, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

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/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 7261
/ LENGTH: 276
/ TYPE: PRT
/ ORGANISM: Human
/ US-09-949-016-7261

Query Match 47.9%; Score 35; DB 4; Length 276;
Best Local Similarity 66.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YRCRGDSSK 10
Db 190 YRCNGTSSK 198

RESULT 36
US-08-992-035A-1
/ Sequence 1, Application US/08992035A
/ Patent No. 6242179
/ GENERAL INFORMATION:
/ APPLICANT: Shah, Purvi
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Corley, Neil C.
/ APPLICANT: Lal, Preeti
/ TITLE OF INVENTION: HUMAN PHOSPHATASES
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Dr.
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/992,035A
/ FILING DATE: December 17, 1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0433 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-855-0555
/ TELEFAX: 650-845-4166
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 285 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: BLADNOT06
/ CLONE: 1719418
/ US-08-992-035A-1
```

```
Query Match 47.9%; Score 35; DB 3; Length 285;
Best Local Similarity 50.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 YRCRGDSSKVQE 13
Db 152 YICRGNARVKE 163

RESULT 37
US-09-506-286B-92
/ Sequence 92, Application US/09506286B
/ Patent No. 6482414
/ GENERAL INFORMATION:
/ APPLICANT: Dowling, Patricia W.
/ APPLICANT: Youngner, Julius S.
/ APPLICANT: The University of Pittsburgh, of the Commonwealth
/ TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
/ FILE REFERENCE: EQ-1-C2
/ CURRENT APPLICATION NUMBER: US/09/506,286B
/ CURRENT FILING DATE: 2000-02-16
/ PRIOR APPLICATION NUMBER: 09/133,921
/ PRIOR FILING DATE: 1998-08-13
/ PRIOR APPLICATION NUMBER: PCT/US99/18583
/ PRIOR FILING DATE: 1999-08-12
/ NUMBER OF SEQ ID NOS: 108
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 92
/ LENGTH: 396
/ TYPE: PRT
/ ORGANISM: Equine influenza virus H3N8
/ US-09-506-286B-92

Query Match 47.9%; Score 35; DB 4; Length 396;
Best Local Similarity 45.5%; Pred. No. 4.8e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 YRCRGDSSKVQ 12
Db 198 YRCQRGDTQIQ 208

RESULT 38
US-09-506-286B-95
/ Sequence 95, Application US/09506286B
/ Patent No. 6482414
/ GENERAL INFORMATION:
/ APPLICANT: Dowling, Patricia W.
/ APPLICANT: Youngner, Julius S.
/ APPLICANT: The University of Pittsburgh, of the Commonwealth
/ TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
/ FILE REFERENCE: EQ-1-C2
/ CURRENT APPLICATION NUMBER: US/09/506,286B
/ CURRENT FILING DATE: 2000-02-16
/ PRIOR APPLICATION NUMBER: 09/133,921
/ PRIOR FILING DATE: 1998-08-13
/ PRIOR APPLICATION NUMBER: PCT/US99/18583
/ PRIOR FILING DATE: 1999-08-12
/ NUMBER OF SEQ ID NOS: 108
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 95
/ LENGTH: 396
/ TYPE: PRT
/ ORGANISM: Equine influenza virus H3N8
/ US-09-506-286B-95

Query Match 47.9%; Score 35; DB 4; Length 396;
Best Local Similarity 45.5%; Pred. No. 4.8e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 YRCRGDSSKVQ 12
```

```
Db      198 YRCRGDTQIQ 208

RESULT 39
US-10-065-133A-92
; Sequence 92, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-92

Query Match      47.9%; Score 35; DB 4; Length 396;
Best Local Similarity 45.5%; Pred. No. 4.8e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      2 YRCRGDSKVQ 12
      |||: |||:
Db      198 YRCRGDTQIQ 208

RESULT 40
US-10-065-133A-95
; Sequence 95, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-95

Query Match      47.9%; Score 35; DB 4; Length 396;
Best Local Similarity 45.5%; Pred. No. 4.8e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      2 YRCRGDSKVQ 12
      |||: |||:
Db      198 YRCRGDTQIQ 208

TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,950
FILING DATE: 05-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,279
FILING DATE: 21-MARCH-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,181
FILING DATE: 16-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,252
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0670K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1204
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 439 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-985-950-12

Query Match      47.9%; Score 35; DB 3; Length 439;
Best Local Similarity 60.0%; Pred. No. 5.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 NYRCRGDSK 10
      :|||: |||:
Db      194 SYRCGYDSR 203

RESULT 42
US-09-310-463-8
; Sequence 8, Application US/09310463A
; Patent No. 6384203
; GENERAL INFORMATION:
; APPLICANT: Cosman, David J.
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Borges, Luis
; TITLE OF INVENTION: Family of Immunoregulators Designated Leukocyte Immunoglobulin-
; TITLE OF INVENTION: Like Receptors (LIR)
; FILE REFERENCE: 2624-A
; CURRENT APPLICATION NUMBER: US/09/310,463A
; CURRENT FILING DATE: 1999-05-12
; EARLIER APPLICATION NUMBER: 08/842,248
; EARLIER FILING DATE: 1997-04-24
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 439
; TYPE: PRT
; ORGANISM: human
US-09-310-463-8
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```

Query Match      47.9%; Score 35; DB 3; Length 439;
Best Local Similarity 60.0%; Pred. No. 5.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
DB 194 SYRCGYDSR 203

RESULT 43
US-08-842-248A-8
; Sequence 8, Application US/08842248A
; Patent No. 6448035
; GENERAL INFORMATION:
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Family of Immunoregulators Designated
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM/PC Compatible
; OPERATING SYSTEM: Microsoft Word 7.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842,248A
; FILING DATE: April 24, 1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C.
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2624
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 439 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-842-248A-8

Query Match      47.9%; Score 35; DB 4; Length 439;
Best Local Similarity 60.0%; Pred. No. 5.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
DB 194 SYRCGYDSR 203

RESULT 44
US-09-546-049-12
; Sequence 12, Application US/09546049
; Patent No. 6479638
; GENERAL INFORMATION:
; APPLICANT: Adema, Gosse Jan
; Meyaard, Linde
; Gorman, Daniel M.
; McClanahan, Terrill K.
; Zurawski, Sandra M.
; Zurawski, Gerard
; Lanier, Lewis L.
; Phillips Jr., Joseph H.

```

```

; TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/546,049
; FILING DATE: 10-Apr-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,950
; FILING DATE: 05-DEC-1997
; APPLICATION NUMBER: US 60/041,279
; FILING DATE: 21-MARCH-1997
; APPLICATION NUMBER: US 60/033,181
; FILING DATE: 16-DEC-1996
; APPLICATION NUMBER: US 60/032,252
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0670K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1204
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 439 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-546-049-12

Query Match      47.9%; Score 35; DB 4; Length 439;
Best Local Similarity 60.0%; Pred. No. 5.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
DB 194 SYRCGYDSR 203

RESULT 45
US-09-627-376-10
; Sequence 10, Application US/09627376
; Patent No. 6342385
; GENERAL INFORMATION:
; APPLICANT: Qi, Fengxia
; TITLE OF INVENTION: MUTACIN I BIOSYNTHESIS GENES AND PROTEINS
; FILE REFERENCE: UAB-17402/22
; CURRENT APPLICATION NUMBER: US/09/627,376
; CURRENT FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-09-627-376-10

Query Match      47.9%; Score 35; DB 3; Length 447;
Best Local Similarity 50.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```


QY 1 NYRCRGDSSKVQ 12
|||:|||||:
Db 410 NYHLOGDSSSKAR 421

RESULT 46
US-10-047-676B-10
; Sequence 10, Application US/10047676B
; Patent No. 6699970
; GENERAL INFORMATION:
; APPLICANT: Qi, Fengxia
; APPLICANT: Caulfield, Page W.
; APPLICANT: Chen, Ping
; TITLE OF INVENTION: MUTACIN I BIOSYNTHESIS GENES AND PROTEINS
; FILE REFERENCE: UAB-17403/22
; CURRENT APPLICATION NUMBER: US/10/047,676B
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 09/627,376
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 10
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-047-676B-10

Query Match 47.9%; Score 35; DB 4; Length 447;
Best Local Similarity 50.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 NYRCRGDSSKVQ 12
|||:|||||:
Db 410 NYHLOGDSSSKAR 421

RESULT 47
US-09-248-796A-17110
; Sequence 17110, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17110
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-17110

Query Match 47.9%; Score 35; DB 4; Length 503;
Best Local Similarity 66.7%; Pred. No. 6.1e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YRCRGDSSK 10
|||:|||||:
Db 288 YRCFSDDDK 296

RESULT 48
US-08-419-652-4
; Sequence 4, Application US/08419652
; Patent No. 5831007
; GENERAL INFORMATION:

; APPLICANT: Chua, Anne O
; APPLICANT: Gubler, Ulrich A
; TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: PC compatible
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; FILING DATE: 11-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
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; FILING DATE: 31-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/094,713
; FILING DATE: 19-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kass, Alan P
; REGISTRATION NUMBER: 32142
; REFERENCE/DOCKET NUMBER: CD 9174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-4205
; TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 4:
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; LENGTH: 621 amino acids
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; Patent No. 5536657
; GENERAL INFORMATION:
; APPLICANT: Chua, Anne O
; APPLICANT: Gubler, Ulrich A
; TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
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; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/094,713
; FILING DATE: 19-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kass, Alan P
; REGISTRATION NUMBER: 32142
; REFERENCE/DOCKET NUMBER: CD 8973
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-4205
; TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
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; TOPOLOGY: linear
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; APPLICANT: Chua, Anne O
; APPLICANT: Gubler, Ulrich A
; TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07110-1199
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; FILING DATE: 31-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/094,713
; FILING DATE: 19-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kass, Alan P
; REGISTRATION NUMBER: 32142
; REFERENCE/DOCKET NUMBER: CD 9174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-4205
; TELEFAX: (201) 235-3500
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-419-652-3
; Query Match 47.9%; Score 35; DB 2; Length 660;
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; Job time : 17.3256 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 7, 2005, 19:48:00 ; Search time 86.1628 Seconds
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Title: US-10-812-238B-23

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Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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381	36	49.3	225	14	US-10-199-884-358	Sequence 358, App	454	36	49.3	225	14	US-10-199-459-358	Sequence 358, App
382	36	49.3	225	14	US-10-196-744-358	Sequence 358, App	455	36	49.3	225	14	US-10-199-460-358	Sequence 358, App
383	36	49.3	225	14	US-10-196-755-358	Sequence 358, App	456	36	49.3	225	14	US-10-199-461-358	Sequence 358, App
384	36	49.3	225	14	US-10-197-704-358	Sequence 358, App	457	36	49.3	225	14	US-10-199-667-358	Sequence 358, App
385	36	49.3	225	14	US-10-197-710-358	Sequence 358, App	458	36	49.3	225	14	US-10-199-673-358	Sequence 358, App
386	36	49.3	225	14	US-10-198-758-358	Sequence 358, App	459	36	49.3	225	14	US-10-201-321-358	Sequence 358, App
387	36	49.3	225	14	US-10-198-766-358	Sequence 358, App	460	36	49.3	225	14	US-10-201-322-358	Sequence 358, App
388	36	49.3	225	14	US-10-199-304-358	Sequence 358, App	461	36	49.3	225	14	US-10-201-326-358	Sequence 358, App
389	36	49.3	225	14	US-10-199-309-358	Sequence 358, App	462	36	49.3	225	14	US-10-201-532-358	Sequence 358, App
390	36	49.3	225	14	US-10-199-313-358	Sequence 358, App	463	36	49.3	225	14	US-10-201-533-358	Sequence 358, App
391	36	49.3	225	14	US-10-199-456-358	Sequence 358, App	464	36	49.3	225	14	US-10-201-535-358	Sequence 358, App
392	36	49.3	225	14	US-10-201-329-358	Sequence 358, App	465	36	49.3	225	14	US-10-201-769-358	Sequence 358, App
393	36	49.3	225	14	US-10-202-412-358	Sequence 358, App	466	36	49.3	225	14	US-10-201-771-358	Sequence 358, App
394	36	49.3	225	14	US-10-206-919-358	Sequence 358, App	467	36	49.3	225	14	US-10-201-854-358	Sequence 358, App
395	36	49.3	225	14	US-10-206-922-358	Sequence 358, App	468	36	49.3	225	14	US-10-202-410-358	Sequence 358, App
396	36	49.3	225	14	US-10-206-924-358	Sequence 358, App	469	36	49.3	225	14	US-10-202-473-358	Sequence 358, App
397	36	49.3	225	14	US-10-206-928-358	Sequence 358, App	470	36	49.3	225	14	US-10-202-474-358	Sequence 358, App
398	36	49.3	225	14	US-10-207-914-358	Sequence 358, App	471	36	49.3	225	14	US-10-205-503-358	Sequence 358, App
399	36	49.3	225	14	US-10-207-921-358	Sequence 358, App	472	36	49.3	225	14	US-10-205-512-358	Sequence 358, App
400	36	49.3	225	14	US-10-207-922-358	Sequence 358, App	473	36	49.3	225	14	US-10-205-892-358	Sequence 358, App
401	36	49.3	225	14	US-10-208-027-358	Sequence 358, App	474	36	49.3	225	14	US-10-205-894-358	Sequence 358, App
402	36	49.3	225	14	US-10-013-907A-328	Sequence 328, App	475	36	49.3	225	14	US-10-205-896-358	Sequence 358, App
403	36	49.3	225	14	US-10-015-499A-328	Sequence 328, App	476	36	49.3	225	14	US-10-205-898-358	Sequence 358, App
404	36	49.3	225	14	US-10-063-555-120	Sequence 120, App	477	36	49.3	225	14	US-10-205-901-358	Sequence 358, App
405	36	49.3	225	14	US-10-196-757-358	Sequence 358, App	478	36	49.3	225	14	US-10-205-903-358	Sequence 358, App
406	36	49.3	225	14	US-10-196-759-120	Sequence 120, App	479	36	49.3	225	14	US-10-206-909-358	Sequence 358, App
407	36	49.3	225	14	US-10-196-754-358	Sequence 358, App	480	36	49.3	225	14	US-10-206-910-358	Sequence 358, App
408	36	49.3	225	14	US-10-174-571-358	Sequence 358, App	481	36	49.3	225	14	US-10-206-911-358	Sequence 358, App
409	36	49.3	225	14	US-10-176-746-358	Sequence 358, App	482	36	49.3	225	14	US-10-206-912-358	Sequence 358, App
410	36	49.3	225	14	US-10-176-923-358	Sequence 358, App	483	36	49.3	225	14	US-10-206-913-358	Sequence 358, App
411	36	49.3	225	14	US-10-183-011-358	Sequence 358, App	484	36	49.3	225	14	US-10-206-914-358	Sequence 358, App
412	36	49.3	225	14	US-10-184-633-358	Sequence 358, App	485	36	49.3	225	14	US-10-206-920-358	Sequence 358, App
413	36	49.3	225	14	US-10-184-639-358	Sequence 358, App	486	36	49.3	225	14	US-10-206-921-358	Sequence 358, App
414	36	49.3	225	14	US-10-187-742-358	Sequence 358, App	487	36	49.3	225	14	US-10-206-923-358	Sequence 358, App
415	36	49.3	225	14	US-10-187-748-358	Sequence 358, App	488	36	49.3	225	14	US-10-206-925-358	Sequence 358, App
416	36	49.3	225	14	US-10-188-766-358	Sequence 358, App	489	36	49.3	225	14	US-10-206-926-358	Sequence 358, App
417	36	49.3	225	14	US-10-188-771-358	Sequence 358, App	490	36	49.3	225	14	US-10-206-927-358	Sequence 358, App
418	36	49.3	225	14	US-10-192-006-358	Sequence 358, App	491	36	49.3	225	14	US-10-207-916-358	Sequence 358, App
419	36	49.3	225	14	US-10-192-008-358	Sequence 358, App	492	36	49.3	225	14	US-10-207-917-358	Sequence 358, App
420	36	49.3	225	14	US-10-192-009-358	Sequence 358, App	493	36	49.3	225	14	US-10-207-918-358	Sequence 358, App
421	36	49.3	225	14	US-10-192-012-358	Sequence 358, App	494	36	49.3	225	14	US-10-207-919-358	Sequence 358, App
422	36	49.3	225	14	US-10-192-014-358	Sequence 358, App	495	36	49.3	225	14	US-10-207-920-358	Sequence 358, App
423	36	49.3	225	14	US-10-192-016-358	Sequence 358, App	496	36	49.3	225	14	US-10-207-925-358	Sequence 358, App
424	36	49.3	225	14	US-10-194-364-358	Sequence 358, App	497	36	49.3	225	14	US-10-208-021-358	Sequence 358, App
425	36	49.3	225	14	US-10-194-364-358	Sequence 358, App	498	36	49.3	225	14	US-10-208-022-358	Sequence 358, App
426	36	49.3	225	14	US-10-194-395-358	Sequence 358, App	499	36	49.3	225	14	US-10-208-023-358	Sequence 358, App
427	36	49.3	225	14	US-10-194-424-358	Sequence 358, App	500	36	49.3	225	14	US-10-208-026-358	Sequence 358, App
428	36	49.3	225	14	US-10-194-458-358	Sequence 358, App							
429	36	49.3	225	14	US-10-194-459-358	Sequence 358, App							
430	36	49.3	225	14	US-10-194-488-358	Sequence 358, App							
431	36	49.3	225	14	US-10-195-886-358	Sequence 358, App							
432	36	49.3	225	14	US-10-195-891-358	Sequence 358, App							
433	36	49.3	225	14	US-10-196-746-358	Sequence 358, App							
434	36	49.3	225	14	US-10-196-752-358	Sequence 358, App							
435	36	49.3	225	14	US-10-196-753-358	Sequence 358, App							
436	36	49.3	225	14	US-10-196-761-358	Sequence 358, App							
437	36	49.3	225	14	US-10-197-692-358	Sequence 358, App							
438	36	49.3	225	14	US-10-197-693-358	Sequence 358, App							
439	36	49.3	225	14	US-10-197-696-358	Sequence 358, App							
440	36	49.3	225	14	US-10-197-698-358	Sequence 358, App							
441	36	49.3	225	14	US-10-197-703-358	Sequence 358, App							
442	36	49.3	225	14	US-10-197-711-358	Sequence 358, App							
443	36	49.3	225	14	US-10-198-757-358	Sequence 358, App							
444	36	49.3	225	14	US-10-198-761-358	Sequence 358, App							
445	36	49.3	225	14	US-10-198-762-358	Sequence 358, App							
446	36	49.3	225	14	US-10-198-763-358	Sequence 358, App							
447	36	49.3	225	14	US-10-198-767-358	Sequence 358, App							
448	36	49.3	225	14	US-10-199-301-358	Sequence 358, App							
449	36	49.3	225	14	US-10-199-307-358	Sequence 358, App							

ALIGNMENTS

RESULT 1

US-10-812-238A-23
; Sequence 23, Application US/10812238A
; Publication No. US20050002904A1
; GENERAL INFORMATION:
; APPLICANT: Wary, Kishore, K.
; APPLICANT: Huntsoe, Joseph O.
; TITLE OF INVENTION: Uses of Vascular Endothelial Growth Factor
; TITLE OF INVENTION: and Type I Collagen Inducible Protein (VCIP)
; FILE REFERENCE: D6563
; CURRENT FILING DATE: 2004-03-29
; CURRENT APPLICATION NUMBER: US 60/458,164
; PRIOR FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 23
; LENGTH: 13

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Db      178 NYRCRGDDSKVQE 190
|||||
RESULT 4
US-10-812-238A-13
; Sequence 13, Application US/10812238A
; Publication No. US20050002904A1
; GENERAL INFORMATION:
; APPLICANT: Wary, Kishore, K.
; APPLICANT: Humtsoe, Joseph O.
; TITLE OF INVENTION: Uses of Vascular Endothelial Growth Factor
; TITLE OF INVENTION: and Type I Collagen Inducible Protein (VCIP)
; FILE REFERENCE: D6563
; CURRENT APPLICATION NUMBER: US/10/812,238A
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,164
; PRIOR FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 13
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: human VCIP
US-10-812-238A-13
Query Match      100.0%; Score 73; DB 17; Length 311;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NYRCRGDDSKVQE 13
|||||
Db      178 NYRCRGDDSKVQE 190
|||||
RESULT 5
US-10-812-238A-20
; Sequence 20, Application US/10812238A
; Publication No. US20050002904A1
; GENERAL INFORMATION:
; APPLICANT: Wary, Kishore, K.
; APPLICANT: Humtsoe, Joseph O.
; TITLE OF INVENTION: Uses of Vascular Endothelial Growth Factor
; TITLE OF INVENTION: and Type I Collagen Inducible Protein (VCIP)
; FILE REFERENCE: D6563
; CURRENT APPLICATION NUMBER: US/10/812,238A
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,164
; PRIOR FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: a peptide containing RGD sequence
US-10-812-238A-20
Query Match      80.8%; Score 59; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NYRCRGDDSK 10
|||||
Db      1 NYRCRGDDSK 10
|||||
RESULT 6
US-10-812-238A-22
; Sequence 22, Application US/10812238A

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; Publication No. US20050002904A1
; GENERAL INFORMATION:
; APPLICANT: Wary, Kishore, K.
; APPLICANT: Humtsoe, Joseph O.
; TITLE OF INVENTION: Uses of Vascular Endothelial Growth Factor
; TITLE OF INVENTION: and Type I Collagen Inducible Protein (VCIP)
; FILE REFERENCE: D6563
; CURRENT APPLICATION NUMBER: US/10/812,238A
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,164
; PRIOR FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: a peptide containing a mutated RGD sequence
US-10-812-238A-22

Query Match 75.1%; Score 55; DB 17; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.021; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
: |||||: |||
Db 1 NYRCRGEDSK 10

RESULT 7
US-10-812-238A-21
; Sequence 21, Application US/10812238A
; Publication No. US20050002904A1
; GENERAL INFORMATION:
; APPLICANT: Wary, Kishore, K.
; APPLICANT: Humtsoe, Joseph O.
; TITLE OF INVENTION: Uses of Vascular Endothelial Growth Factor
; TITLE OF INVENTION: and Type I Collagen Inducible Protein (VCIP)
; FILE REFERENCE: D6563
; CURRENT APPLICATION NUMBER: US/10/812,238A
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,164
; PRIOR FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: a peptide containing a mutated RGD sequence
US-10-812-238A-21

Query Match 72.6%; Score 53; DB 17; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.046; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
: |||||: |||
Db 1 NYRCRADDSK 10

RESULT 8
US-10-425-115-262985
; Sequence 262985, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 262985
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_171454C.1.pep
US-10-425-115-262985

Query Match 63.0%; Score 46; DB 16; Length 74;
Best Local Similarity 58.3%; Pred. No. 4.9; Mismatches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 YRCRGDDSKVQE 13
: |||||: |||
Db 42 FLCRGDDSEMQD 53

RESULT 9
US-10-437-963-135805
; Sequence 135805, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 135805
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(208)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_37445C.1.pep
US-10-437-963-135805

Query Match 56.2%; Score 41; DB 16; Length 208;
Best Local Similarity 53.8%; Pred. No. 92; Mismatches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 NYRCRGDDSKVQE 13
: |||||: |||
Db 96 DYSCGDDSGTEE 108

RESULT 10
US-10-291-172-610
; Sequence 610, Application US/10291172
; Publication No. US20030228584A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20030228584A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/291,172
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 09/693,267

; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 610
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-172-610

Query Match 56.2%; Score 41; DB 15; Length 237;
Best Local Similarity 70.0%; Pred. No. 1e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
|:|||||:
Db 5 NHRCRGDLTK 14

RESULT 11
US-10-221-278-610
; Sequence 610, Application US/10221278
; Publication No. US20040034208A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20040034208A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/221,278
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 610
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-221-278-610

Query Match 56.2%; Score 41; DB 15; Length 237;
Best Local Similarity 70.0%; Pred. No. 1e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
|:|||||:
Db 5 NHRCRGDLTK 14

RESULT 12
US-10-210-281-12
; Sequence 12, Application US/10210281
; Publication No. US20040030096A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Padigar, Muralidhara
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Zhong, Mei
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Sciore, Paul
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J., Jr.
; APPLICANT: Casman, Stacie
; APPLICANT: Rothenberg, Mark B.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc L.
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
; FILE REFERENCE: 21402-416D
; CURRENT APPLICATION NUMBER: US/10/210,281
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: 60/309,501
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/310,291
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/361,775
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 60/310,951
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/361,832
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/312,203
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/313,201
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/313,702
; PRIOR FILING DATE: 2001-08-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 12
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-210-281-12

Query Match 56.2%; Score 41; DB 15; Length 421;
Best Local Similarity 70.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
|:|||||:
Db 197 NHRCRGDLTK 206

RESULT 13
US-10-210-281-10
; Sequence 10, Application US/10210281
; Publication No. US20040030096A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Zhong, Mei
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles E.

```
/ APPLICANT: Ji, Weizhen
/ APPLICANT: Pena, Carol E.A.
/ APPLICANT: Burgess, Catherine E.
/ APPLICANT: Sciore, Paul
/ APPLICANT: Stone, David J.
/ APPLICANT: Taupier, Raymond J., Jr.
/ APPLICANT: Casman, Stacie
/ APPLICANT: Rothenberg, Mark E.
/ APPLICANT: Malyankar, Uriel M.
/ APPLICANT: Boldog, Ferenc L.
/ TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS
/ TITLE OF INVENTION: THE SAME
/ FILE REFERENCE: 21402-416D
/ CURRENT APPLICATION NUMBER: US/10/210,281
/ CURRENT FILING DATE: 2003-02-05
/ PRIOR APPLICATION NUMBER: 60/309,501
/ PRIOR FILING DATE: 2001-08-02
/ PRIOR APPLICATION NUMBER: 60/310,291
/ PRIOR FILING DATE: 2001-08-03
/ PRIOR APPLICATION NUMBER: 60/361,775
/ PRIOR FILING DATE: 2002-03-05
/ PRIOR APPLICATION NUMBER: 60/310,951
/ PRIOR FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: 60/361,832
/ PRIOR FILING DATE: 2002-03-05
/ PRIOR APPLICATION NUMBER: 60/311,292
/ PRIOR FILING DATE: 2001-08-09
/ PRIOR APPLICATION NUMBER: 60/311,979
/ PRIOR FILING DATE: 2001-08-13
/ PRIOR APPLICATION NUMBER: 60/312,203
/ PRIOR FILING DATE: 2001-08-14
/ PRIOR APPLICATION NUMBER: 60/313,201
/ PRIOR FILING DATE: 2001-08-17
/ PRIOR APPLICATION NUMBER: 60/313,702
/ PRIOR FILING DATE: 2001-08-20
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ SOFTWARE: CuraseqList version 0.1
/ SEQ ID NO 10
/ LENGTH: 424
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-210-281-10

Query Match 56.2%; Score 41; DB 15; Length 424;
Best Local Similarity 70.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
Db 198 NHRCRGDLTK 207

RESULT 14
US-10-157-031-139
/ Sequence 139, Application US/10157031
/ Publication No. US20030108890A1
/ GENERAL INFORMATION:
/ APPLICANT: Baranova, A. V.
/ APPLICANT: Yankovsky, N. K.
/ APPLICANT: Kozlov, A. P.
/ APPLICANT: Lobashev, A. V.
/ APPLICANT: Krukovskaya, L. L.
/ TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
/ FILE REFERENCE: 2760-103
/ CURRENT APPLICATION NUMBER: US/10/157,031
/ CURRENT FILING DATE: 2002-05-30
/ NUMBER OF SEQ ID NOS: 415
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 139
/ LENGTH: 428
/ TYPE: PRT
/ ORGANISM: Homo sapiens

US-10-157-031-139
Query Match 56.2%; Score 41; DB 14; Length 428;
Best Local Similarity 70.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
Db 197 NHRCRGDLTK 206

RESULT 15
US-10-437-963-135808
/ Sequence 135808, Application US/10437963
/ Publication No. US20040123343A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Barbazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ CURRENT FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 135808
/ LENGTH: 473
/ TYPE: PRT
/ ORGANISM: Oryza sativa
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)..(473)
/ OTHER INFORMATION: unsure at all xaa locations
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MET4530_37448C.1.pcp
US-10-437-963-135808

Query Match 56.2%; Score 41; DB 16; Length 473;
Best Local Similarity 53.8%; Pred. No. 2.1e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 NYRCGDDSKVQE 13
Db 153 DYSCGDDSGTEE 165

RESULT 16
US-10-108-260A-2988
/ Sequence 2988, Application US/10108260A
/ Publication No. US20040005560A1
/ GENERAL INFORMATION:
/ APPLICANT: HELIX RESEARCH INSTITUTE
/ TITLE OF INVENTION: No. US20040005560A1el full length cDNA
/ FILE REFERENCE: H1-A0106
/ CURRENT APPLICATION NUMBER: US/10/108,260A
/ CURRENT FILING DATE: 2002-03-27
/ NUMBER OF SEQ ID NOS: 5458
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2988
/ LENGTH: 489
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-108-260A-2988

Query Match 56.2%; Score 41; DB 15; Length 489;
Best Local Similarity 70.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY      1 NYRCRGDSK 10
      |||||||:
Db      258 NHRCRGDLTK 267

RESULT 17
US-09-147-947-6
; Sequence 6, Application US/09147947A
; Patent No. US20020160490A1
; GENERAL INFORMATION:
; APPLICANT: TSURUOKA, No. US20020160490A1uo
; APPLICANT: YAMASHIRO, Kyoto
; APPLICANT: YAMAGUCHI, No. US20020160490A1el Serine Protease
; TITLE OF INVENTION: No. US20020160490A1el
; FILE REFERENCE: 001560-349
; CURRENT APPLICATION NUMBER: US/09/147,947A
; CURRENT FILING DATE: 1997-03-24
; EARLIER APPLICATION NUMBER: PCT/JP98/03324
; EARLIER FILING DATE: 1998-07-24
; EARLIER APPLICATION NUMBER: JP 9/213969
; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; OTHER INFORMATION:
US-09-147-947-6

Query Match      56.2%; Score 41; DB 9; Length 822;
Best Local Similarity 54.5%; Pred. No. 3.5e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 NYRCRGDSK 11
      |||||||:
Db      183 NVRCRGEENI 193

RESULT 18
US-10-757-262-34
; Sequence 34, Application US/10757262
; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; FILE REFERENCE: MPI03-007PIRNMNM
; CURRENT APPLICATION NUMBER: US/10/757,262
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16

QY      1 NYRCRGDSK 11
      |||||||:
Db      183 NVRCRGEENI 193

RESULT 19
US-10-723-860-4046
; Sequence 4046, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4046
; LENGTH: 875
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-4046

Query Match      56.2%; Score 41; DB 16; Length 875;
Best Local Similarity 54.5%; Pred. No. 3.8e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 NYRCRGDSK 11
      |||||||:
Db      236 NVRCRGEENI 246

RESULT 20
US-10-843-299-2
; Sequence 2, Application US/10843299
; Publication No. US20050032694A1
; GENERAL INFORMATION:
; APPLICANT: SONDEREGGER, Peter
; TITLE OF INVENTION: NEUOTRYPsin
; FILE REFERENCE: 030708-035
; CURRENT APPLICATION NUMBER: US/10/843,299
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/403,724
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/IB98/00625
; PRIOR FILING DATE: 1998-04-24
; PRIOR APPLICATION NUMBER: CH 0966/97
; PRIOR FILING DATE: 1997-04-26
```

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; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 875
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-843-299-2

Query Match          56.2%; Score 41; DB 17; Length 875;
Best Local Similarity 54.5%; Pred. No. 3.8e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 NVRCRGDDSKV 11
   |||||:
Db 236 NVRCRGDENI 246

RESULT 21
US-10-424-599-260014
; Sequence 260014, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 260014
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(102)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_76817C.1.pep
US-10-424-599-260014

Query Match          54.8%; Score 40; DB 15; Length 102;
Best Local Similarity 70.0%; Pred. No. 67;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YRCRGDDSKV 11
   |||||:
Db 4 YRCRIDDXRV 13

RESULT 22
US-10-424-599-254922
; Sequence 254922, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 254922
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:

; NAME/KEY: unsure
; LOCATION: (1)-(111)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_72217C.1.pep
US-10-424-599-254922

Query Match          54.8%; Score 40; DB 15; Length 111;
Best Local Similarity 60.0%; Pred. No. 72;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 YRCRGDDSKV 11
   |||||:
Db 66 YXCKGNDTKV 75

RESULT 23
US-10-369-493-15738
; Sequence 15738, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 15738
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Xanthomonas campestris
US-10-369-493-15738

Query Match          54.8%; Score 40; DB 15; Length 301;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 CRGDSKVQE 13
   |||||:
Db 200 CRGDDARIHD 209

RESULT 24
US-10-369-493-16124
; Sequence 16124, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 16124
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Xanthomonas campestris
US-10-369-493-16124
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Query Match      54.8%; Score 40; DB 15; Length 301;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      4 CRGDDSKVOE 13
      |||||...:
Db      200 CRGDDARIHD 209

RESULT 25
US-10-369-493-15371
; Sequence 15371, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 15371
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Xanthomonas campestris
US-10-369-493-15371

Query Match      54.8%; Score 40; DB 15; Length 302;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      4 CRGDDSKVOE 13
      |||||...:
Db      203 CRGDDARIHD 212

RESULT 26
US-10-282-122A-43293
; Sequence 43293, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangou
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59506
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; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43293
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-282-122A-43293

Query Match      54.8%; Score 40; DB 15; Length 400;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 YRCRGDD 8
      :|||||
Db      39 FRCRGDD 45

RESULT 27
US-10-282-122A-59506
; Sequence 59506, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangou
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59506
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```
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-10-282-122A-59506

Query Match      54.8%; Score 40; DB 15; Length 400;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 YRCRGDD 8
       :|||||
Db      39 FRCRGDD 45

RESULT 28
US-10-282-122A-73186
; Sequence 73186, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73186
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Salmonella paratyphi A
US-10-282-122A-73186

Query Match      54.8%; Score 40; DB 15; Length 400;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 YRCRGDD 8
       :|||||
Db      39 FRCRGDD 45

RESULT 29
US-10-282-122A-75975
; Sequence 75975, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75975
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Salmonella typhi
US-10-282-122A-75975

Query Match      54.8%; Score 40; DB 15; Length 400;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 YRCRGDD 8
       :|||||
Db      39 FRCRGDD 45

RESULT 30
US-10-425-115-215599
; Sequence 215599, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
```


Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 RCRGDDSKVQE 13
||:| ||:| ||
Db 23 RCGRDSRSQE 33

RESULT 34
US-10-437-963-170560
; Sequence 170560, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 170560
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_68875C.1.pap
US-10-437-963-170560

Query Match 53.4%; Score 39; DB 16; Length 77;
Best Local Similarity 85.7%; Pred. No. 74;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
:|||||
Db 34 HRCRGDD 40

RESULT 35
US-10-898-775-28
; Sequence 28, Application US/10898775
; Publication No. US20050142647A1
; GENERAL INFORMATION:
; APPLICANT: WASSSELL, PAUL
; APPLICANT: SOE, JORN BORCH
; APPLICANT: MIKKELSON, JORN DALGAARD
; APPLICANT: KRISTENSEN, ANNA CECILIE JENTOF
; TITLE OF INVENTION: METHOD
; FILE REFERENCE: 674509-2058
; CURRENT APPLICATION NUMBER: US/10/898,775
; CURRENT FILING DATE: 2004-07-26
; PRIOR APPLICATION NUMBER: GB 0416023.0
; PRIOR FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: PCT/IB04/00655
; PRIOR FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: GB 0330016.7
; PRIOR FILING DATE: 2003-12-24
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 28
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Streptomyces coelicolor
US-10-898-775-28

Query Match 53.4%; Score 39; DB 18; Length 305;
Best Local Similarity 63.6%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 RCRGDDSKVQE 13
||| ||| |||
Db 258 RCRSDDGAVHE 268

RESULT 36
US-10-417-700A-21
; Sequence 21, Application US/10417700A
; Publication No. US20040033581A1
; GENERAL INFORMATION:
; APPLICANT: ECOPIA BIOSCIENCES INC.
; APPLICANT: ZAZOPOULOS, Emmanuel
; APPLICANT: STAFFA, Alfredo
; APPLICANT: FARNET, Chris
; TITLE OF INVENTION: Specialized dual condensation/epimerization domain in non-ribosome
; TITLE OF INVENTION: Peptide synthetase systems
; FILE REFERENCE: 3002-14US
; CURRENT APPLICATION NUMBER: US/10/417,700A
; CURRENT FILING DATE: 2003-04-17
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Pseudomonas syringae pv. syringae strain B301D
US-10-417-700A-21

Query Match 53.4%; Score 39; DB 15; Length 461;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDDSKVQ 12
||| :||:|
Db 341 NYRHOGEDNRLQ 352

RESULT 37
US-10-369-493-22730
; Sequence 22730, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 22730
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(690)
; OTHER INFORMATION: unsure at all xaa locations
US-10-369-493-22730

Query Match 53.4%; Score 39; DB 15; Length 690;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 RCRGDDSKVQ 12
||| ||| |||
Db 561 RVRGDDSDVQ 570

```
RESULT 38
US-10-062-831-131
; Sequence 131, Application US/10062831
; Publication No. US20030105297A1
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; FILE REFERENCE: P2006P1
; CURRENT APPLICATION NUMBER: US/10/062,831
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/690,454
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: PCT/US98/10868
; PRIOR FILING DATE: May 28, 1998
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,190
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/050,935
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,101
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/056,250
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,296
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,293
; PRIOR FILING DATE: August 29, 1997
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 131
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-831-131

Query Match      52.1%; Score 38; DB 14; Length 136;
Best Local Similarity 54.5%; Pred. No. 1.9e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      2 YRCRGDSDKVQ 12
      |||:|:|:|
Db      61 YRCKGKNVRVQ 71

RESULT 39
US-10-062-599-131
; Sequence 131, Application US/10062599
; Publication No. US20030195346A1
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; FILE REFERENCE: P2006P1
; CURRENT APPLICATION NUMBER: US/10/062,599
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/690,454
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: 09/189,144
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,190
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/050,935
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,101
```

```
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/056,250
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,296
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,293
; PRIOR FILING DATE: August 29, 1997
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 131
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-599-131

Query Match      52.1%; Score 38; DB 14; Length 136;
Best Local Similarity 54.5%; Pred. No. 1.9e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      2 YRCRGDSDKVQ 12
      |||:|:|:|
Db      61 YRCKGKNVRVQ 71

RESULT 40
US-10-425-115-269918
; Sequence 269918, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(S3222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 269918
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(151)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MPT4577_177763C.1.pap
US-10-425-115-269918

Query Match      52.1%; Score 38; DB 16; Length 151;
Best Local Similarity 54.5%; Pred. No. 2.1e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 NYRCRGDSDKV 11
      |:|:|:|:|
Db      132 NHRCKGRDIKL 142

RESULT 41
US-10-282-122A-54254
; Sequence 54254, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
```

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; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 2000-07-27
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-03-35
; PRIOR FILING DATE: 2000-09-06
; PRIOR FILING DATE: 2000-03-347
; PRIOR FILING DATE: 2000-09-09
; PRIOR FILING DATE: 2000-12-578
; PRIOR FILING DATE: 2000-10-23
; PRIOR FILING DATE: 2001-02-625
; PRIOR FILING DATE: 2000-11-27
; PRIOR FILING DATE: 2000-12-931
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2001-02-636
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54254
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
US-10-282-122A-54254
```

```
Query Match 52.1%; Score 38; DB 15; Length 172;
Best Local Similarity 77.8%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 3 RCRGDDSKV 11
DB 19 RCVGDDGV 27

RESULT 42
US-10-087-192-1548
; Sequence 1548, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 52945200122
; CURRENT FILING DATE: 2002-03-01
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1548
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(206)
```

```
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-087-192-1548

Query Match 52.1%; Score 38; DB 13; Length 206;
Best Local Similarity 54.5%; Pred. No. 2.9e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 YRCRGDDSKVQ 12
DB 103 YRCRGKVRVQ 113

RESULT 43
US-10-322-281-322
; Sequence 322, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 322
; LENGTH: 537
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-281-322
```

```
Query Match 52.1%; Score 38; DB 16; Length 537;
Best Local Similarity 54.5%; Pred. No. 7.4e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 YRCRGDDSKVQ 12
DB 99 YRCRGKVRVQ 109
```

```
RESULT 44
US-10-264-049-2872
; Sequence 2872, Application US/10264049
; Publication No. US2004000579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133PI
; CURRENT FILING DATE: 2002-10-04
; PRIOR FILING DATE: 2001-06-07
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2872
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-2872
```

```
Query Match 52.1%; Score 38; DB 15; Length 545;
Best Local Similarity 54.5%; Pred. No. 7.5e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 YRCRGDDSKVQ 12
DB 103 YRCRGKVRVQ 113
```

```
RESULT 45
US-10-264-049-3870
```

; Sequence 3870, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:

; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3870

; LENGTH: 77

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: MISC_FEATURE

; LOCATION: (1)

; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-3870

Query Match 50.7%; Score 37; DB 15; Length 77;
Best Local Similarity 60.8%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NYRCRGDGSK 10

Db 41 NPFCKGPDSK 50

RESULT 46

US-09-764-855-84

; Sequence 84, Application US/09764855

; Patent No. US20020119919A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PA110

; CURRENT APPLICATION NUMBER: US/09/764,855

; CURRENT FILING DATE: 2001-01-17

; Prior application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 334

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 84

; LENGTH: 113

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-764-855-84

Query Match 50.7%; Score 37; DB 9; Length 113;
Best Local Similarity 62.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8

Db 10 NYQCEGED 17

RESULT 47

US-10-072-349-84

; Sequence 84, Application US/10072349

; Publication No. US20030054420A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PA110C1

; CURRENT APPLICATION NUMBER: US/10/072,349

; CURRENT FILING DATE: 2002-02-11

; Prior Application removed - See file Wrapper or Palm

; NUMBER OF SEQ ID NOS: 334

; SOFTWARE: PatentIn Ver. 3.1

; SEQ ID NO 84

; LENGTH: 113

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-072-349-84

Query Match 50.7%; Score 37; DB 14; Length 113;
Best Local Similarity 62.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8

Db 10 NYQCEGED 17

RESULT 48

US-10-424-599-165388

; Sequence 165388, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 165388

; LENGTH: 115

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_120361C.1.pep

US-10-424-599-165388

Query Match 50.7%; Score 37; DB 15; Length 115;
Best Local Similarity 54.5%; Pred. No. 2.4e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 YRCRGDSKVQ 12

Db 24 FRCRATNSKIQ 34

RESULT 49

US-10-425-115-283941

; Sequence 283941, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 283941

; LENGTH: 133

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(133)

; OTHER INFORMATION: unsure at all Xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_22053C.1.pep

US-10-425-115-283941

Query Match 50.7%; Score 37; DB 16; Length 133;
Best Local Similarity 55.6%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 CRGDDSKVQ 12
| | | | |
Db 48 CRGDDEKIE 56

RESULT 50

US-10-276-774-1857
; Sequence 1857, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: No. US20040053245A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 1857
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(140)
; OTHER INFORMATION: xaa = any amino acid or nothing
US-10-276-774-1857

Query Match 50.7%; Score 37; DB 15; Length 140;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 CRGDDSK 10
| | | | |
Db 80 CRGEDSK 86

Search completed: September 7, 2005, 20:03:13
Job time : 94.1628 secs

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OM protein - protein search, using sw model

Run on: September 7, 2005, 19:48:00 ; Search time 66.2791 Seconds
(without alignments)
59.419 Million cell updates/sec

Title: US-10-812-238B-20
Perfect score: 59
Sequence: 1 NTRCRGDDSK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1774312 seqs, 393823214 residues

Total number of hits satisfying chosen parameters: 1774312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	59	100.0	13	17 US-10-812-238A-23	Sequence 23, Appl
3	59	100.0	20	17 US-10-812-238A-2	Sequence 2, Appl
4	59	100.0	311	16 US-10-655-601-2	Sequence 2, Appl
5	59	100.0	311	17 US-10-812-238A-13	Sequence 13, Appl
6	55	93.2	10	17 US-10-812-238A-22	Sequence 22, Appl
7	53	89.8	10	17 US-10-812-238A-21	Sequence 21, Appl
8	41	69.5	237	15 US-10-291-172-610	Sequence 610, App
9	41	69.5	237	15 US-10-221-278-610	Sequence 610, App
10	41	69.5	421	15 US-10-210-281-12	Sequence 12, Appl
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41	69.5	428	14	US-10-157-031-139	Sequence 139, App
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ALIGNMENTS

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US-10-812-238A-20

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; Publication No. US20050002904A1
; GENERAL INFORMATION:
; APPLICANT: Wary, Kishore, K.
; APPLICANT: Humtsoe, Joseph O.
; TITLE OF INVENTION: Uses of Vascular Endothelial Growth Factor
; TITLE OF INVENTION: and Type I Collagen Inducible Protein (VCIP)
; FILE REFERENCE: D6563
; CURRENT APPLICATION NUMBER: US/10/812,238A
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,164
; PRIOR FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 20
; LENGTH: 10

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; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: a peptide containing RGD sequence
US-10-812-238A-20

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; Publication No. US20050002904A1
; GENERAL INFORMATION:
; APPLICANT: Wary, Kishore, K.
; APPLICANT: Humtsoe, Joseph O.
; TITLE OF INVENTION: Uses of Vascular Endothelial Growth Factor
; TITLE OF INVENTION: and Type I Collagen Inducible Protein (VCIP)
; FILE REFERENCE: D6563
; CURRENT APPLICATION NUMBER: US/10/812,238A
; PRIOR FILING DATE: 2004-03-29
; PRIOR FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 23
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: a peptide containing RGD sequence
US-10-812-238A-23

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; Publication No. US20050002904A1
; GENERAL INFORMATION:
; APPLICANT: Wary, Kishore, K.
; APPLICANT: Humtsoe, Joseph O.
; TITLE OF INVENTION: Uses of Vascular Endothelial Growth Factor
; TITLE OF INVENTION: and Type I Collagen Inducible Protein (VCIP)
; FILE REFERENCE: D6563
; CURRENT APPLICATION NUMBER: US/10/812,238A
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,164
; PRIOR FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 2
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: peptide used to raise anti-VCIP-RGD antibody
US-10-812-238A-2
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Best Local Similarity 100.0%; Pred. No. 0.0067;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 6 NYRCRGDSDK 15

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; Sequence 2, Application US/10655601
; Publication No. US20040137522A1
; GENERAL INFORMATION:
; APPLICANT: Feany, Mel B.
; APPLICANT: Shulman, Joshua M.
; TITLE OF INVENTION: Genes and Proteins Altering Tau-Related Neuropathy
; FILE REFERENCE: 7570/73251
; CURRENT APPLICATION NUMBER: US/10/655,601
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
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; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-10-655-601-2

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Best Local Similarity 100.0%; Pred. No. 0.089;
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QY 1 NYRCRGDSDK 10
Db 178 NYRCRGDSDK 187

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; Sequence 13, Application US/10812238A
; Publication No. US20050002904A1
; GENERAL INFORMATION:
; APPLICANT: Wary, Kishore, K.
; APPLICANT: Humtsoe, Joseph O.
; TITLE OF INVENTION: Uses of Vascular Endothelial Growth Factor
; TITLE OF INVENTION: and Type I Collagen Inducible Protein (VCIP)
; FILE REFERENCE: D6563
; CURRENT APPLICATION NUMBER: US/10/812,238A
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,164
; PRIOR FILING DATE: 2003-03-27
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US-10-812-238A-13

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; Publication No. US20050002904A1
; GENERAL INFORMATION:
; APPLICANT: Wary, Kishore, K.
; APPLICANT: Humtsoe, Joseph O.
; TITLE OF INVENTION: Uses of Vascular Endothelial Growth Factor
; TITLE OF INVENTION: and Type I Collagen Inducible Protein (VCIP)
; FILE REFERENCE: D6563
; CURRENT APPLICATION NUMBER: US/10/812,238A
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,164
; PRIOR FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: a peptide containing a mutated RGD sequence
US-10-812-238A-22

Query Match 93.2%; Score 55; DB 17; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.016;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
|||||
Db 1 NYRCRGEDSK 10

RESULT 7
US-10-812-238A-21
; Sequence 21, Application US/10812238A
; Publication No. US20050002904A1
; GENERAL INFORMATION:
; APPLICANT: Wary, Kishore, K.
; APPLICANT: Humtsoe, Joseph O.
; TITLE OF INVENTION: Uses of Vascular Endothelial Growth Factor
; TITLE OF INVENTION: and Type I Collagen Inducible Protein (VCIP)
; FILE REFERENCE: D6563
; CURRENT APPLICATION NUMBER: US/10/812,238A
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,164
; PRIOR FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: a peptide containing a mutated RGD sequence
US-10-812-238A-21

Query Match 89.8%; Score 53; DB 17; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.035;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
|||||
Db 1 NYRCRADDSK 10

RESULT 8
US-10-291-172-610
; Sequence 610, Application US/10291172
; Publication No. US20030228584A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20030228584A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/291,172
; CURRENT FILING DATE: 2000-11-08

; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 610
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-172-610

Query Match 69.5%; Score 41; DB 15; Length 237;
Best Local Similarity 70.0%; Pred. No. 69;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
|:|||||:|
Db 5 NHRRCRGLTK 14

RESULT 9
US-10-221-278-610
; Sequence 610, Application US/10221278
; Publication No. US20040034208A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20040034208A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/221,278
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 610
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-221-278-610

Query Match 69.5%; Score 41; DB 15; Length 237;
Best Local Similarity 70.0%; Pred. No. 69;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
|:|||||:|
Db 5 NHRRCRGLTK 14

RESULT 10
US-10-210-281-12
; Sequence 12, Application US/10210281
; Publication No. US20040030096A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Linda
; APPLICANT: Zetthusen, Bryan D.

```

; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Zhong, Mei
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Sciore, David J.
; APPLICANT: Taupier, Raymond J., Jr.
; APPLICANT: Casman, Stacie
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc L.
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS
; FILE REFERENCE: 21402-416D
; CURRENT APPLICATION NUMBER: US/10/210,281
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: 60/309,501
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/310,291
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/361,775
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 60/310,951
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/361,832
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/312,203
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/313,201
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/313,702
; PRIOR FILING DATE: 2001-08-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 12
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-210-281-12

```

```

Query Match      69.5%; Score 41; DB 15; Length 421;
Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 NYRCRGDDSK 10
      |:|||||:|
DB      197 NHRCRGDLTK 206

```

```

RESULT 11
US-10-210-281-10
; Sequence 10, Application US/10210281
; Publication No. US20040030096A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Zhong, Mei
; APPLICANT: Patturajan, Meera

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; APPLICANT: Miller, Charles E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Sciore, Paul
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J., Jr.
; APPLICANT: Casman, Stacie
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc L.
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS
; FILE REFERENCE: 21402-416D
; CURRENT APPLICATION NUMBER: US/10/210,281
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: 60/309,501
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/310,291
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/361,775
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 60/310,951
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/361,832
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/312,203
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/313,201
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/313,702
; PRIOR FILING DATE: 2001-08-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 10
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-210-281-10

```

```

Query Match      69.5%; Score 41; DB 15; Length 424;
Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 NYRCRGDDSK 10
      |:|||||:|
DB      198 NHRCRGDLTK 207

```

```

RESULT 12
US-10-157-031-139
; Sequence 139, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 139
; LENGTH: 428
; TYPE: PRT

```

; ORGANISM: Homo sapiens
US-10-157-031-139

Query Match 69.5%; Score 41; DB 14; Length 428;
Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
|:|||||:
Db 197 NHRCRGDLTK 206

RESULT 13

US-10-108-260A-2988
; Sequence 2988, Application US/10108260A
; Publication No. US20040005560A1

; GENERAL INFORMATION:

; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2988
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-108-260A-2988

Query Match 69.5%; Score 41; DB 15; Length 489;
Best Local Similarity 70.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
|:|||||:
Db 258 NHRCRGDLTK 267

RESULT 14

US-10-282-122A-43293
; Sequence 43293, Application US/10282122A
; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43293
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-282-122A-43293

Query Match 67.8%; Score 40; DB 15; Length 400;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
|:|||||:
Db 39 FRCRGDD 45

RESULT 15

US-10-282-122A-59506

; Sequence 59506, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 59506

; LENGTH: 400

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

US-10-282-122A-59506

Query Match 67.8%; Score 40; DB 15; Length 400;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
:|||||
Db 39 FRCRGDD 45

RESULT 16

US-10-282-122A-73186

; Sequence 73186, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zyskind, Judith

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John

; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.

; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 73186

; LENGTH: 400

; TYPE: PRT

; ORGANISM: Salmonella paratyphi A

US-10-282-122A-73186

Query Match 67.8%; Score 40; DB 15; Length 400;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
:|||||
Db 39 FRCRGDD 45

RESULT 17

US-10-282-122A-75975

; Sequence 75975, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zyskind, Judith

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John

; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.

; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 75975

; LENGTH: 400

; TYPE: PRT

; ORGANISM: Salmonella typhi

US-10-282-122A-75975

Query Match 67.8%; Score 40; DB 15; Length 400;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
:|||||
Db 39 FRCRGDD 45

RESULT 18

US-10-425-115-215599

; Sequence 215599, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 215599

; LENGTH: 669

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/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)..(669)
/ OTHER INFORMATION: unsure at all Xaa locations
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_128224C.1.pep
US-10-425-115-215599

Query Match          67.8%; Score 40; DB 16; Length 669;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YRCRGDDSK 10
   |:|||||
Db 379 YKXGDDKK 387

RESULT 19
US-10-437-963-170560
/ Sequence 170560, Application US/10437963
/ Publication No. US20040123343A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Barbazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ CURRENT FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 170560
/ LENGTH: 77
/ TYPE: PRT
/ ORGANISM: Oryza sativa
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_68875C.1.pep
US-10-437-963-170560

Query Match          66.1%; Score 39; DB 16; Length 77;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
   |:|||||
Db 34 HRCRGDD 40

RESULT 20
US-10-437-963-157113
/ Sequence 157113, Application US/10437963
/ Publication No. US20040123343A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Barbazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ CURRENT FILING DATE: 2003-05-14
```

```
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 157113
/ LENGTH: 43
/ TYPE: PRT
/ ORGANISM: Oryza sativa
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)..(43)
/ OTHER INFORMATION: unsure at all Xaa locations
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_56716C.1.pep
US-10-437-963-157113

Query Match          64.4%; Score 38; DB 16; Length 43;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 RCRGDDSK 10
   |:|||||
Db 29 RCRGDDXE 36

RESULT 21
US-10-425-115-262985
/ Sequence 262985, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 262985
/ LENGTH: 74
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_171454C.1.pep
US-10-425-115-262985

Query Match          64.4%; Score 38; DB 16; Length 74;
Best Local Similarity 66.7%; Pred. No. 73;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YRCRGDDSK 10
   |:|||||
Db 42 FLCRGDDSE 50

RESULT 22
US-09-147-947-6
/ Sequence 6, Application US/09147947A
/ Patent No. US20020160490A1
/ GENERAL INFORMATION:
/ APPLICANT: TSURUOKA, No. US20020160490A1uo
/ APPLICANT: YAMASHIRO, Kyoto
/ APPLICANT: YAMAGUCHI, No. US20020160490A1omi
/ TITLE OF INVENTION: No. US20020160490A1el Serine Protease
/ FILE REFERENCE: 001560-349
/ CURRENT APPLICATION NUMBER: US/09/147,947A
/ CURRENT FILING DATE: 1997-03-24
/ EARLIER APPLICATION NUMBER: PCT/JP98/03324
/ EARLIER FILING DATE: 1998-07-24
/ EARLIER APPLICATION NUMBER: JP 9/213969
/ EARLIER FILING DATE: 1997-07-24
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 6
```



```
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; OTHER INFORMATION:
US-09-147-947-6

Query Match          64.4%; Score 38; DB 9; Length 822;
Best Local Similarity 75.0%; Pred. No. 7.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NVRCRGDD 8
    |||||:
Db 183 NVRCRGDE 190

RESULT 23
US-10-757-262-34
; Sequence 34, Application US/10757262
; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 15816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8283, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; TITLE OF INVENTION: 55053
; FILE REFERENCE: MPI03-007PIRNMNMIM
; CURRENT APPLICATION NUMBER: US/10/757,262
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 875
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-757-262-34

Query Match          64.4%; Score 38; DB 16; Length 875;
Best Local Similarity 75.0%; Pred. No. 7.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NVRCRGDD 8
    |||||:
Db 236 NVRCRGDE 243

us-10-723-860-4046
; Sequence 4046, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4046
; LENGTH: 875
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-4046

Query Match          64.4%; Score 38; DB 16; Length 875;
Best Local Similarity 75.0%; Pred. No. 7.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NVRCRGDD 8
    |||||:
Db 236 NVRCRGDE 243

RESULT 24
US-10-723-860-4046
; Sequence 4046, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4046
; LENGTH: 875
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-4046

Query Match          64.4%; Score 38; DB 16; Length 875;
Best Local Similarity 75.0%; Pred. No. 7.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NVRCRGDD 8
    |||||:
Db 236 NVRCRGDE 243

RESULT 25
US-10-843-299-2
; Sequence 2, Application US/10843299
; Publication No. US20050032694A1
; GENERAL INFORMATION:
; APPLICANT: SONDEREGGER, Peter
; TITLE OF INVENTION: NEUROTRYP SIN
; FILE REFERENCE: 030708-035
; CURRENT APPLICATION NUMBER: US/10/843,299
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/403,724
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/IB98/00625
; PRIOR FILING DATE: 1998-04-24
; PRIOR APPLICATION NUMBER: CH 0966/97
; PRIOR FILING DATE: 1997-04-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 875
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-843-299-2

Query Match          64.4%; Score 38; DB 17; Length 875;
Best Local Similarity 75.0%; Pred. No. 7.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NVRCRGDD 8
    |||||:
Db 236 NVRCRGDE 243

RESULT 26
US-10-264-049-3870
; Sequence 3870, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
```

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; FILE REFERENCE: PA133PI
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3870
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-3870

Query Match          62.7%; Score 37; DB 15; Length 77;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
   |:|:|
Db 41 NFFCKGPD SK 50

RESULT 27
US-09-764-855-84
; Sequence 84, Application US/09764855
; Patent No. US20020119919A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA110
; CURRENT APPLICATION NUMBER: US/09/764,855
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-855-84

Query Match          62.7%; Score 37; DB 9; Length 113;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
   ||:|:|
Db 10 NYQCEGED 17

RESULT 28
US-10-072-349-84
; Sequence 84, Application US/10072349
; Publication No. US20030054420A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA110C1
; CURRENT APPLICATION NUMBER: US/10/072,349
; CURRENT FILING DATE: 2002-02-11
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 84
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```
US-10-072-349-84

Query Match          62.7%; Score 37; DB 14; Length 113;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
   ||:|:|
Db 10 NYQCEGED 17

RESULT 29
US-10-276-774-1857
; Sequence 1857, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: NO. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 1857
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(140)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-276-774-1857

Query Match          62.7%; Score 37; DB 15; Length 140;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 CRGDDSK 10
   ||:|:|
Db 80 CRGEDSK 86

RESULT 30
US-10-425-115-269918
; Sequence 269918, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 269918
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(151)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: MRT4577_177763C.1.pep
US-10-425-115-269918
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Query Match      62.7%; Score 37; DB 16; Length 151;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 NVRCRGDDSK 10
Db      132 NHRCKGRDIK 141

RESULT 31
US-10-425-115-296818
; Sequence 296818, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 296818
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_33771C.1.pap
US-10-425-115-296818

Query Match      62.7%; Score 37; DB 16; Length 184;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 RCRGDDS 9
Db      93 RCRGDS 99

RESULT 32
US-10-425-115-324709
; Sequence 324709, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 324709
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(286)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_59205C.1.pap
US-10-425-115-324709

Query Match      62.7%; Score 37; DB 16; Length 286;
Best Local Similarity 66.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 NVRCRGDDSK 10
Db      132 NHRCKGRDIK 141

RESULT 33
US-10-156-761-9249
; Sequence 9249, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9249
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9249

Query Match      62.7%; Score 37; DB 14; Length 330;
Best Local Similarity 60.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 NVRCRGDDSK 10
Db      191 SYKCPGDTSK 200

RESULT 34
US-10-739-930-8397
; Sequence 8397, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 8397
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: ZEAWA-23APR03-C6211_2.p
US-10-739-930-8397

Query Match      62.7%; Score 37; DB 16; Length 348;
Best Local Similarity 85.7%; Pred. No. 4.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 RCRGDDS 9
Db      253 RCRGDS 259

RESULT 35
US-10-812-238A-32
; Sequence 32, Application US/10812238A
```

; Publication No. US20050002904A1

; GENERAL INFORMATION:

; APPLICANT: Mary, Kishore, K.

; APPLICANT: Humtsoe, Joseph O.

; TITLE OF INVENTION: Uses of Vascular Endothelial Growth Factor

; FILE REFERENCE: D6563 and Type I Collagen Inducible Protein (VCIP)

; CURRENT APPLICATION NUMBER: US/10/812,238A

; CURRENT FILING DATE: 2004-03-29

; PRIOR APPLICATION NUMBER: US 60/458,164

; PRIOR FILING DATE: 2003-03-27

; NUMBER OF SEQ ID NOS: 36

; SEQ ID NO 32

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Unknown

; FEATURE:

; NAME/KEY: CHAIN

; OTHER INFORMATION: a peptide containing a RGD sequence

US-10-812-238A-32

Query Match

Best Local Similarity 61.0%; Score 36; DB 17; Length 6;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CRGDDS 9

Db 1 CRGDDS 6

RESULT 36

US-10-424-599-260014

; Sequence 260014, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 260014

; LENGTH: 102

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(102)

; OTHER INFORMATION: unsure at all Xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_76817C.1.pap

US-10-424-599-260014

Query Match

Best Local Similarity 61.0%; Score 36; DB 15; Length 102;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YRCRGDDSK 10

Db 4 YRCRIDDXR 12

RESULT 37

US-10-424-599-254922

; Sequence 254922, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 254922

; LENGTH: 111

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(111)

; OTHER INFORMATION: unsure at all Xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_72217C.1.pap

US-10-424-599-254922

Query Match

Best Local Similarity 61.0%; Score 36; DB 15; Length 111;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 YRCRGDDSK 10

Db 66 YXCKGNDTK 74

RESULT 38

US-10-437-963-126010

; Sequence 126010, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 126010

; LENGTH: 159

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_28599C.1.pap

US-10-437-963-126010

Query Match

Best Local Similarity 61.0%; Score 36; DB 16; Length 159;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 CRGDDSK 10

Db 144 CRGDNSK 150

RESULT 39

US-10-437-963-135805

; Sequence 135805, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 135805
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(208)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_37445C.1.pap
US-10-437-963-135805

Query Match 61.0%; Score 36; DB 16; Length 208;
Best Local Similarity 66.7%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NYRCRGDD 9
:| | | | |
Db 96 DYSCGGDD 104

RESULT 40
US-10-425-115-214055
; Sequence 214055, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 214055
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_126814C.1.pap
US-10-425-115-214055

Query Match 61.0%; Score 36; DB 16; Length 438;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CRGDD 9
| | | | |
Db 281 CRGDD 286

RESULT 41
US-10-767-701-41046
; Sequence 41046, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 41046
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C16361_1.pap
US-10-767-701-41046

Query Match 61.0%; Score 36; DB 16; Length 445;
Best Local Similarity 66.7%; Pred. No. 8.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 9
:| | | | |
Db 372 NDQCRGDES 380

RESULT 42
US-10-369-493-2996
; Sequence 2996, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2996
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Thermotoga maritima
US-10-369-493-2996

Query Match 61.0%; Score 36; DB 15; Length 466;
Best Local Similarity 71.4%; Pred. No. 9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
:| | | | |
Db 214 FRCRGED 220

RESULT 43
US-10-369-493-2942
; Sequence 2942, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374

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; SEQ ID NO 2942
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Thermotoga maritima
US-10-369-493-2942

Query Match      61.0%; Score 36; DB 15; Length 470;
Best Local Similarity 71.4%; Pred. No. 96+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 YRCRGDD 8
DB      214 FRCRGD 220

RESULT 44
US-10-437-963-135808
; Sequence 135808, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 135808
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; LOCATION: (1)..(473)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_37448C.1.pap
US-10-437-963-135808

Query Match      61.0%; Score 36; DB 16; Length 473;
Best Local Similarity 66.7%; Pred. No. 91e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 NYRCRGDD 9
DB      153 DYSCGGDD 161

RESULT 45
US-10-108-260A-2858
; Sequence 2858, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2858
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-2858
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Query Match      61.0%; Score 36; DB 15; Length 485;
Best Local Similarity 60.0%; Pred. No. 9.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 NYRCRGDDSK 10
DB      469 NWRCPGTDSE 478

RESULT 46
US-10-427-631-1
; Sequence 1, Application US/10427631
; Publication No. US20030175923A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; TANG, Y. Tom;
; APPLICANT: CORLEY, Neil C.; GUEGLER, Karl J.;
; APPLICANT: BAUGHN, Mariah R.; LAL, Preeti G.;
; APPLICANT: YUE, Henry; HILLMAN, Jennifer L.;
; APPLICANT: AZIMZAI, Yalda
; TITLE OF INVENTION: HUMAN TRANSFERASE PROTEINS
; FILE REFERENCE: PF-0592-1 DIV
; CURRENT APPLICATION NUMBER: US/10/427,631
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US 09/786,240
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: PCT/US99/20989
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: US 60/172,220
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: US 60/155,248
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 60/133,642
; PRIOR FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030175923A1 1632930CD1
US-10-427-631-1

Query Match      61.0%; Score 36; DB 14; Length 498;
Best Local Similarity 60.0%; Pred. No. 9.5e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 NYRCRGDDSK 10
DB      482 NWRCPGTDSE 491

RESULT 47
US-10-425-115-274886
; Sequence 274886, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 274886
; LENGTH: 1075
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
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; NAME/KEY: unsure
; LOCATION: (1)..(1075)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_182286C.1.pep
US-10-425-115-27486

Query Match      61.0%; Score 36; DB 16; Length 1075;
Best Local Similarity 66.7%; Pred. No. 2e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NVRCRGDGS 9
Db 751 NGQCRGDES 759

RESULT 48
US-10-424-599-161655
; Sequence 161655, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 161655
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_116993C.1.pep
US-10-424-599-161655

Query Match      59.3%; Score 35; DB 15; Length 48;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NVRCRGDGS 10
Db 6 NRCRCGQDLK 15

RESULT 49
US-10-425-115-320012
; Sequence 320012, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 320012
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_54919C.1.pep
US-10-425-115-320012

Query Match      59.3%; Score 35; DB 16; Length 49;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
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Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YRCRGDGS 10
Db 28 YRCSGSQSK 36

RESULT 50
US-10-425-115-249920
; Sequence 249920, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 249920
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_159510C.1.pep
US-10-425-115-249920
```

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Query Match      59.3%; Score 35; DB 16; Length 57;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 2 YRCRGD 7
Db 45 YKCRGD 50
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Search completed: September 7, 2005, 20:03:05
Job time : 73.2791 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 7, 2005, 19:37:54 ; Search time 93.7209 Seconds
(without alignments)
53.647 Million cell updates/sec

Title: US-10-812-238B-23

Perfect score: 73

Sequence: 1 NYRCRGDDSKVQE 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

- 1: Genesecp16Dec04:*
- 2: Genesecp1980s:*
- 3: Genesecp2000s:*
- 4: Genesecp2001s:*
- 5: Genesecp2002s:*
- 6: Genesecp2003as:*
- 7: Genesecp2003bs:*
- 8: Genesecp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73	100.0	311	2 AAW79286	Human pho
2	73	100.0	311	7 ADE60703	Human pro
3	73	100.0	311	8 ADM72103	Human tau
4	73	100.0	311	8 ADN04415	Antipsori
5	73	100.0	311	8 ADP24274	PRO polyP
6	69	94.5	312	5 ABB99112	Rat phosph
7	69	94.5	312	7 ADE60701	Rat Prote
8	44	60.3	705	7 ADB74255	Mycobacte
9	42	57.5	1304	6 ABP72189	Plasmodiu
10	41	56.2	152	4 ABG23434	Novel hum
11	41	56.2	237	4 AAU28253	Novel hum
12	41	56.2	237	8 ADS12199	Human the
13	41	56.2	421	8 ADJ50947	Human nov
14	41	56.2	424	8 ADJ50945	Human nov
15	41	56.2	428	6 ADA83857	Human POM
16	41	56.2	451	4 ABB67864	Drosophil
17	41	56.2	481	8 ADR09234	Human pro
18	41	56.2	481	8 ADS10966	Human the
19	41	56.2	489	7 ADM04303	Human pro
20	41	56.2	822	2 AAW99087	Human ser
21	41	56.2	875	2 AAW83361	Human neu
22	41	56.2	875	8 ADQ21226	Human sof
23	41	56.2	875	8 ADQ89082	Human uro
24	41	56.2	20	5 ABP56183	Chimeric
25	40	54.8	282	5 ABB99111	Rat phosph

26	40	54.8	282	7 ADE58904	Rat Prote
27	40	54.8	282	7 ADE58900	Rat Prote
28	40	54.8	282	7 ADD45532	Rat Prote
29	40	54.8	301	8 ADS26705	Bacterial
30	40	54.8	301	8 ADS27091	Bacterial
31	40	54.8	302	8 ADS26338	Bacterial
32	40	54.8	400	6 ABU31582	Protein e
33	40	54.8	400	6 ABU45262	Protein e
34	40	54.8	400	6 ABU48051	Protein e
35	40	54.8	400	6 ABU15369	Protein e
36	40	54.8	424	7 ABO65513	Klebsiell
37	40	54.8	1299	6 ABP72191	Plasmodiu
38	39	53.4	74	4 ABB04096	Human mus
39	39	53.4	74	6 ABU13390	Novel hum
40	39	53.4	74	8 ADJ29416	Human mus
41	39	53.4	283	7 ADE61256	Rat Prote
42	39	53.4	305	8 ADR41635	Lipid acy
43	39	53.4	305	8 ADR41585	Lipid acy
44	39	53.4	393	8 ADN48160	Thermococ
45	39	53.4	461	7 ADG33762	Actinomyc
46	39	53.4	690	8 ADS44300	Bacterial
47	38.5	52.7	1269	7 ADD46237	Rat Prote
48	38.5	52.7	1272	7 ADP46239	Human Pro
49	38	52.1	84	4 AAU60236	Propionib
50	38	52.1	84	6 AEM56755	Propionib
51	38	52.1	120	3 AAG02326	Human sec
52	38	52.1	136	2 AAW73460	Human sec
53	38	52.1	172	6 ABU26330	Protein e
54	38	52.1	206	7 AEM85711	Human pro
55	38	52.1	543	8 ABB61306	Human tra
56	38	52.1	543	8 ABO84861	Human can
57	38	52.1	545	5 ABP41740	Human ova
58	38	52.1	798	4 ABG24175	Novel hum
59	38	52.1	1307	6 ABP72192	Plasmodiu
60	38	52.1	1365	6 ABP72194	Plasmodiu
61	38	52.1	2647	8 ADP25446	Plasmodiu
62	37	50.7	59	4 AAU49621	Propionib
63	37	50.7	59	6 AEM46140	Propionib
64	37	50.7	64	4 AAU58627	Propionib
65	37	50.7	60	6 AEM55146	Propionib
66	37	50.7	77	5 ABP42738	Human ova
67	37	50.7	92	4 AAU61299	Propionib
68	37	50.7	92	6 AEM57818	Propionib
69	37	50.7	113	4 AAM91935	Human dig
70	37	50.7	113	4 AAM38569	Human col
71	37	50.7	113	5 ABG97621	Human col
72	37	50.7	113	7 ADB92877	Human col
73	37	50.7	140	4 ABB11487	Human sec
74	37	50.7	185	6 ABU35961	Protein e
75	37	50.7	190	5 AAE18631	Equine hi
76	37	50.7	201	2 AAY27061	Recombina
77	37	50.7	236	2 AAY27060	Equine FC
78	37	50.7	255	2 AAY27058	Equine FC
79	37	50.7	272	7 ABO67231	Klebsiell
80	37	50.7	275	7 ABO65272	Klebsiell
81	37	50.7	324	5 ABB90953	Herbicida
82	37	50.7	349	4 AAM42035	Human pol
83	37	50.7	409	5 ABP73846	Candida a
84	37	50.7	488	7 ABO66647	Klebsiell
85	37	50.7	801	4 AAU34022	Staphyloc
86	37	50.7	801	4 AAU36926	Staphyloc
87	37	50.7	801	6 ABU16301	Protein e
88	37	50.7	801	6 AEM70889	Staphyloc
89	36	49.3	15	8 ABO32557	Secreted
90	36	49.3	15	8 ADO10180	Human pol
91	36	49.3	134	6 ABB58494	Human sec
92	36	49.3	135	8 ADP29987	Human sec
93	36	49.3	162	4 AAG89271	Human sec
94	36	49.3	191	6 ABO32566	Secreted
95	36	49.3	191	6 ABU54593	Human NOV
96	36	49.3	191	8 ADO10191	Human pol
97	36	49.3	215	4 AAU00678	Human INT
98	36	49.3	215	6 ABO32553	Secreted

245	36	49.3	225	6	ABR74106	Human sec	318	49.3	225	6	ADA19982	Novel hum
246	36	49.3	225	6	ABR95698	Human sec	319	49.3	225	6	Abo23799	Human sec
247	36	49.3	225	6	ABR80995	Human sec	320	49.3	225	6	ADB17365	Human tra
248	36	49.3	225	6	ABR81300	Human sec	321	49.3	225	6	ABR97285	Human sec
249	36	49.3	225	6	ABM00996	Human sec	322	49.3	225	6	ABR87073	Human sec
250	36	49.3	225	6	ABR88598	Human sec	323	49.3	225	6	ABM11115	Human sec
251	36	49.3	225	6	ABM77419	Human sec	324	49.3	225	6	ABM28259	Human sec
252	36	49.3	225	6	ABO28903	Human sec	325	49.3	225	6	Abo32258	Human sec
253	36	49.3	225	6	ABO31648	Human sec	326	49.3	225	6	ABM15385	Human sec
254	36	49.3	225	6	ABM08065	Human sec	327	49.3	225	6	ABM06540	Human sec
255	36	49.3	225	6	ABO40545	Human sec	328	49.3	225	6	ABM04351	Human sec
256	36	49.3	225	6	ABO35970	Human PRO	329	49.3	225	6	ABM22464	Human sec
257	36	49.3	225	6	ABO44109	Human PRO	330	49.3	225	6	ABM07760	Human sec
258	36	49.3	225	6	ADA78110	Human sec	331	49.3	225	6	Abo40850	Human sec
259	36	49.3	225	6	ABM24904	Human sec	332	49.3	225	6	ABM35497	Human sec
260	36	49.3	225	6	ABO03172	Human sec	333	49.3	225	6	ABM33260	Human sec
261	36	49.3	225	6	ABR90428	Human sec	334	49.3	225	6	Abo52786	Human PRO
262	36	49.3	225	6	ABM17342	Human sec	335	49.3	225	6	Abo50346	Human sec
263	36	49.3	225	6	ABR95088	Human sec	336	49.3	225	6	ABU99340	Human sec
264	36	49.3	225	6	ABR95393	Human sec	337	49.3	225	6	Abo04392	Human sec
265	36	49.3	225	6	ADB17177	Human tra	338	49.3	225	6	ABO06022	Human sec
266	36	49.3	225	6	Abo21631	Human sec	339	49.3	225	6	ABM18562	Human sec
267	36	49.3	225	6	ABR97895	Human sec	340	49.3	225	6	ABR97590	Human sec
268	36	49.3	225	6	ABR87683	Human sec	341	49.3	225	6	ABR80690	Human sec
269	36	49.3	225	6	ABM77724	Human sec	342	49.3	225	6	ABM01301	Human sec
270	36	49.3	225	6	ABM27954	Human sec	343	49.3	225	6	ABR88903	Human sec
271	36	49.3	225	6	ABM06235	Human sec	344	49.3	225	6	ABM13555	Human sec
272	36	49.3	225	6	ABM03741	Human sec	345	49.3	225	6	ABM20939	Human sec
273	36	49.3	225	6	ABM35192	Human sec	346	49.3	225	6	Abo42070	Human sec
274	36	49.3	225	6	ABM26429	Human sec	347	49.3	225	6	Abo42680	Human sec
275	36	49.3	225	6	ABO48211	Human sec	348	49.3	225	6	ABM10200	Human sec
276	36	49.3	225	6	ABR92953	Human sec	349	49.3	225	6	ABO38715	Human sec
277	36	49.3	225	6	ABO24714	Human sec	350	49.3	225	6	ABM32955	Human sec
278	36	49.3	225	6	ABM11725	Human sec	351	49.3	225	6	ABM22769	Human sec
279	36	49.3	225	6	ABM02826	Human sec	352	49.3	225	6	ABM74980	Human sec
280	36	49.3	225	6	ABM16122	Human sec	353	49.3	225	6	ADA79902	Human sec
281	36	49.3	225	6	ABO27683	Human sec	354	49.3	225	6	ABR96370	Human sec
282	36	49.3	225	6	ABM29174	Human sec	355	49.3	225	6	ABM02521	Human sec
283	36	49.3	225	6	ABM07150	Human sec	356	49.3	225	6	ABR86463	Human sec
284	36	49.3	225	6	ABM21244	Human sec	357	49.3	225	6	ABR86768	Human sec
285	36	49.3	225	6	ABM09590	Human sec	358	49.3	225	6	ABM16732	Human sec
286	36	49.3	225	6	ABO41460	Human sec	359	49.3	225	6	ABM29784	Human sec
287	36	49.3	225	6	ABO36275	Human PRO	360	49.3	225	6	ABM29208	Human sec
288	36	49.3	225	6	ABO43804	Human PRO	361	49.3	225	6	ABM23379	Human sec
289	36	49.3	225	6	ABM76504	Human sec	362	49.3	225	6	ABM22159	Human sec
290	36	49.3	225	6	ABM76200	Human sec	363	49.3	225	6	ABM22159	Human sec
291	36	49.3	225	6	ABM25819	Human sec	364	49.3	225	6	ABO37800	Human sec
292	36	49.3	225	6	ABM26124	Human sec	365	49.3	225	6	ABM28564	Human sec
293	36	49.3	225	6	ABO03477	Human sec	366	49.3	225	6	ABM28869	Human sec
294	36	49.3	225	6	ABO02562	Human sec	367	49.3	225	6	ABM66513	Human sec
295	36	49.3	225	6	ABO44298	Human sec	368	49.3	225	6	ABM75895	Human sec
296	36	49.3	225	6	ABR90733	Human sec	369	49.3	225	6	ABM34175	Human sec
297	36	49.3	225	6	ABR73801	Human sec	370	49.3	225	6	ABM34480	Human sec
298	36	49.3	225	6	ABO17053	Human sec	371	49.3	225	6	Abo20411	Human sec
299	36	49.3	225	6	ABR94478	Human sec	372	49.3	225	6	ABO21326	Human sec
300	36	49.3	225	6	ABR75985	Human sec	373	49.3	225	6	ABO22241	Human sec
301	36	49.3	225	6	ABR71361	Human sec	374	49.3	225	6	ADA20154	Novel hum
302	36	49.3	225	6	ABR93258	Human sec	375	49.3	225	6	Abo34226	Human sec
303	36	49.3	225	6	ABR93563	Human sec	376	49.3	225	6	ABR96675	Human sec
304	36	49.3	225	6	ABR87988	Human sec	377	49.3	225	6	ABR85853	Human sec
305	36	49.3	225	6	ABO33675	Novel hum	378	49.3	225	6	ABR99835	Human sec
306	36	49.3	225	6	Abo27988	Human sec	379	49.3	225	6	ABM00691	Human sec
307	36	49.3	225	6	Abo30123	Human sec	380	49.3	225	6	ABM00386	Human sec
308	36	49.3	225	6	Abo33332	Human PRO	381	49.3	225	6	Abo29818	Human sec
309	36	49.3	225	6	ABM05020	Human sec	382	49.3	225	6	ABM23684	Human sec
310	36	49.3	225	6	ABM08980	Human sec	383	49.3	225	6	ABM29479	Human sec
311	36	49.3	225	6	ABO36580	Human sec	384	49.3	225	6	Abo38410	Human sec
312	36	49.3	225	6	ABO35665	Human PRO	385	49.3	225	6	Abo45710	Human PRO
313	36	49.3	225	6	Abo39630	Human sec	386	49.3	225	6	ABM20634	Human sec
314	36	49.3	225	6	ABM10505	Human sec	387	49.3	225	6	ADA81629	Human sec
315	36	49.3	225	6	ABM12030	Human sec	388	49.3	225	6	Abo16748	Human sec
316	36	49.3	225	6	Abo52176	Human PRO	389	49.3	225	6	Abo18374	Human sec
317	36	49.3	225	6	ABO52481	Human PRO	390	49.3	225	6	Abo22801	Human PRO

391	36	49.3	225	6	ABO23106	Human PRO	464	36	49.3	225	6	ADA00451	Human sec
392	36	49.3	225	6	ABR92648	Human sec	465	36	49.3	225	6	ABM27039	Human sec
393	36	49.3	225	6	ABR81605	Human sec	466	36	49.3	225	6	ABM03436	Human sec
394	36	49.3	225	6	ABM78029	Human sec	467	36	49.3	225	6	ABO39935	Human sec
395	36	49.3	225	6	ABR89818	Human sec	468	36	49.3	225	6	ABO50041	Human sec
396	36	49.3	225	6	ABM26734	Human sec	469	36	49.3	225	7	ABO50956	Human sec
397	36	49.3	225	6	ABM13860	Human sec	470	36	49.3	225	7	ABO05412	Human sec
398	36	49.3	225	6	ABO28598	Human sec	471	36	49.3	225	7	ABR74716	Human sec
399	36	49.3	225	6	ABO30428	Human sec	472	36	49.3	225	7	ABO44528	Human sec
400	36	49.3	225	6	ABM07455	Human sec	473	36	49.3	225	7	ABR77195	Human sec
401	36	49.3	225	6	ABM04046	Human sec	474	36	49.3	225	7	ABM17952	Human sec
402	36	49.3	225	6	ABO37190	Human sec	475	36	49.3	225	7	ABR96003	Human sec
403	36	49.3	225	6	ABO41765	Human sec	476	36	49.3	225	7	ABO21936	Human sec
404	36	49.3	225	6	ABO35360	Human PRO	477	36	49.3	225	7	ABO20106	Human sec
405	36	49.3	225	6	ABM25209	Human sec	478	36	49.3	225	7	ABO24409	Human sec
406	36	49.3	225	6	ABO47601	Human sec	479	36	49.3	225	7	ABR86158	Human sec
407	36	49.3	225	6	ABO47906	Human sec	480	36	49.3	225	7	ABM10810	Human sec
408	36	49.3	225	6	ABO48516	Human sec	481	36	49.3	225	7	ABM76809	Human sec
409	36	49.3	225	6	ABO51566	Human PRO	482	36	49.3	225	7	ABR89513	Human sec
410	36	49.3	225	6	ABO51871	Human PRO	483	36	49.3	225	7	ABM12640	Human sec
411	36	49.3	225	6	ABO50651	Human sec	484	36	49.3	225	7	ABM05930	Human sec
412	36	49.3	225	6	ABR79775	Human sec	485	36	49.3	225	7	ABO35055	Human PRO
413	36	49.3	225	6	ABM17037	Human sec	486	36	49.3	225	7	ABM03131	Human sec
414	36	49.3	225	6	ABO18069	Human sec	487	36	49.3	225	7	ABM19109	Human sec
415	36	49.3	225	6	ABO21021	Human sec	488	36	49.3	225	7	ABM19414	Human sec
416	36	49.3	225	6	ABR96980	Human sec	489	36	49.3	225	7	ABO46625	Human PRO
417	36	49.3	225	6	ABM12335	Human sec	490	36	49.3	225	7	ABO49126	Human sec
418	36	49.3	225	6	ABM16427	Human sec	491	36	49.3	225	7	ABR69169	Human sec
419	36	49.3	225	6	ABM24294	Human sec	492	36	49.3	225	7	ABR89208	Human sec
420	36	49.3	225	6	ABM14775	Human sec	493	36	49.3	225	7	ABR72581	Human sec
421	36	49.3	225	6	ABM04656	Human sec	494	36	49.3	225	7	ABR74411	Human sec
422	36	49.3	225	6	ABM06845	Human sec	495	36	49.3	225	7	ABO18679	Human sec
423	36	49.3	225	6	ABM09285	Human sec	496	36	49.3	225	7	ABR80385	Human sec
424	36	49.3	225	6	ABO39325	Human sec	497	36	49.3	225	7	ABM01606	Human sec
425	36	49.3	225	6	ABM75590	Human sec	498	36	49.3	225	7	ABM02216	Human sec
426	36	49.3	225	6	ABM25514	Human sec	499	36	49.3	225	7	ABR87378	Human sec
427	36	49.3	225	6	ABM20024	Human sec	500	36	49.3	225	7	ABM12945	Human sec
428	36	49.3	225	6	ABO46930	Human PRO							
429	36	49.3	225	6	ABO47235	Human PRO							
430	36	49.3	225	6	ADA83427	Human sec							
431	36	49.3	225	6	ABR71666	Human sec							
432	36	49.3	225	6	ABR72276	Human sec							
433	36	49.3	225	6	ABR98615	Human sec							
434	36	49.3	225	6	ABO06985	Human sec							
435	36	49.3	225	6	ABR84938	Human sec							
436	36	49.3	225	6	ABR73496	Human sec							
437	36	49.3	225	6	ABR76590	Human sec							
438	36	49.3	225	6	ABR73191	Human sec							
439	36	49.3	225	6	ABM18257	Human sec							
440	36	49.3	225	6	ABO20716	Human sec							
441	36	49.3	225	6	ABO25459	Human PRO							
442	36	49.3	225	6	ABO25764	Human PRO							
443	36	49.3	225	6	ABR94173	Human sec							
444	36	49.3	225	6	ABR80080	Human sec							
445	36	49.3	225	6	ABM11420	Human sec							
446	36	49.3	225	6	ABO33027	Human PRO							
447	36	49.3	225	6	ABO30733	Human sec							
448	36	49.3	225	6	ABM31038	Human sec							
449	36	49.3	225	6	ABM27344	Human sec							
450	36	49.3	225	6	ABM30089	Human sec							
451	36	49.3	225	6	ABM05625	Human sec							
452	36	49.3	225	6	ABM15690	Human sec							
453	36	49.3	225	6	ABM08675	Human sec							
454	36	49.3	225	6	ABO42375	Human sec							
455	36	49.3	225	6	ABO42375	Human sec							
456	36	49.3	225	6	ABO38105	Human sec							
457	36	49.3	225	6	ABO46015	Human PRO							
458	36	49.3	225	6	ABM66818	Human sec							
459	36	49.3	225	6	ADB20470	Human sec							
460	36	49.3	225	6	ABM19719	Human sec							
461	36	49.3	225	6	ABO49431	Human sec							
462	36	49.3	225	6	ABO49736	Human sec							
463	36	49.3	225	6	ADA78722	Human sec							
					ABR88293	Human sec							

ALIGNMENTS

RESULT 1

AAW79286	
ID AAW79286 standard; protein; 311 AA.	
XX	
AC AAW79286;	
XX	
DT 15-FEB-1999 (first entry)	
DE Human phosphatidic acid phosphatase beta.	
XX	
DE Phosphatidic acid phosphatase beta; PAP-beta; human; dephosphorylation;	
KW tumour suppressor; cancer; gene therapy.	
XX	
OS Homo sapiens.	
PN WO9846730-A1.	
XX	
PD 22-OCT-1998.	
XX	
PF 16-APR-1998; 98WO-US007928.	
XX	
PR 17-APR-1997; 97US-00842827.	
XX	
PA (CELL-) CELL THERAPEUTICS INC.	
XX	
PI Leung DW, Tompkins CK;	
XX	
DR WPI; 1998-594568/50.	
XX	
DR N-PSDB; AAV69088.	
XX	
PT New nucleic acid encoding human phosphatidic acid phosphatases - used to	

PT regulate levels of lipid cellular mediators and in gene therapy of e.g.
PT cancer.
XX
XX Claim 8; Fig 3A-B; 62pp; English.
XX This is the amino acid sequence of human mature phosphatidic acid
CC phosphatase-beta (PAP-beta), an enzyme that catalyses the conversion of
CC phosphatidic acid into diacylglycerol. 3 Variants of human PAP, i.e. PAP-
CC alpha 1 and 2 (see AAW79284-85), PAP-beta (see AAW79286) and PAP-gamma
CC (see AAW79287) have been identified. The invention provides PAP
CC polynucleotides (see AAV69086-89) and polypeptides, a method of preparing
CC PAP in a transformed host cell, and a method of using PAP to
CC dephosphorylate a substrate, especially lysophosphatidic acid, ceramide 1
CC -phosphate or sphingosine 1-phosphate, particularly for production of
CC diacylglycerol, but also monoacylglycerol, ceramide and sphingosine. PAP
CC is able to control the balance of lipid mediators of cellular activation
CC and signal transduction. Sequences that encode PAP are potentially
CC useful, in gene therapy, for treatment of cancer (PAP may be tumour
CC suppressors, PAP-alpha is expressed at lower levels in cancer cells than
CC in normal cells of same tissue type), inflammatory disease and diabetes-
CC associated obesity
XX
SQ Sequence 311 AA;
Query Match 100.0%; Score 73; DB 2; Length 311;
Best Local Similarity 100.0%; Pred. No. 0.00083;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYRCRGDDSKVQE 13
Db 178 NYRCRGDDSKVQE 190
RESULT 2
ADBE60703
ID ADE60703 standard; protein; 311 AA.
XX
XX ADE60703;
XX
XX 29-JAN-2004 (first entry)
XX Human Protein NP_003704, SEQ ID NO 6615.
XX
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
XX Homo sapiens.
XX
XX WO2003016475-A2.
PN
XX 27-FEB-2003.
PD
XX 14-AUG-2002; 2002WO-US025765.
PF
XX 14-AUG-2001; 2001US-0312147P.
PR
XX 01-NOV-2001; 2001US-0346382P.
PR
XX 26-NOV-2001; 2001US-0333347P.
XX
XX (GEO) GEN HOSPITAL CORP.
PA
XX (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
DR
XX GENBANK; NP_003704.
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat

CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 311 AA;
Query Match 100.0%; Score 73; DB 7; Length 311;
Best Local Similarity 100.0%; Pred. No. 0.00083;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYRCRGDDSKVQE 13
Db 178 NYRCRGDDSKVQE 190
RESULT 3
ADM72103
ID ADM72103 standard; protein; 311 AA.
XX
XX ADM72103;
XX
XX 03-JUN-2004 (first entry)
XX Human tau-related polypeptide PPAP2B.
XX
XX Tau; PPAP2A; PPAP2B; IHPK1; IHPK2; IHPK3; FLJ20530; DJ434014.5; E2F1;
KW Loc127424; Loc113179; KIAA0826; neuroprotective; neurotropic;
KW antiparkinsonian; tau-protein kinase; human.
XX
XX Homo sapiens.
XX
XX WO2004022708-A2.
PN
XX 18-MAR-2004.
PD
XX 04-SEP-2003; 2003WO-US027590.
PF
XX 09-SEP-2002; 2002US-0408877P.
PR
XX (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
XX
XX Feany MB, Shulman JM;
XX
XX WPI; 2004-248456/23.
XX
XX New substantially pure Tau-related polypeptides and polynucleotides,
PT useful for diagnosing and/or treating neurological conditions with
PT aberrant expression of the Tau-related polypeptide, such as Alzheimer's
PT disease.
XX

PS Claim 1; SEQ ID NO 2; 62pp; English.

XX The invention relates to tau-related polypeptide consisting essentially
 CC of an amino acid sequence selected from PPAP2A, PPAP2B, IHPK1, IHPK3,
 CC IHPK2, ELJ20530, DJ434014.5, EZF1, LOC127424, LOC113179 and KIAA0826
 CC (ADM72102-ADM72112 respectively). The methods and compositions of the
 CC present invention are useful for the diagnosis and/or treatment of
 CC neurological diseases or conditions associated with aberrant expression
 CC or activity of the Tau-related polypeptide, such as Alzheimer's disease
 CC and Parkinson's disease. The present sequence represents a human tau-
 CC related polypeptide homologue PPAP2B.

XX Sequence 311 AA;

Query Match 100.0%; Score 73; DB 8; Length 311;

Best Local Similarity 100.0%; Pred. No. 0.00083;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYRCRGDDSKVQE 13

|||||

DB 178 NYRCRGDDSKVQE 190

RESULT 4

ADN04415

ID ADN04415 standard; protein; 311 AA.

AC ADN04415;

XX 01-JUL-2004 (first entry)

DE Antipsoriatic protein sequence #401.

XX antipsoriatic; gene therapy; psoriasis; diagnosis.

OS Homo sapiens.

PN WO2004028479-A2.

PD 08-APR-2004.

PF 25-SEP-2003; 2003WO-US030907.

PR 25-SEP-2002; 2002US-0414006P.

PA (GETH) GENENTECH INC.

XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;

PI Wu TD;

XX WPI; 2004-305105/28.

DR N-PSDB; ADN04414.

XX New PRO nucleic acid or polypeptide, useful for preparing a
 PT pharmaceutical composition for diagnosing or treating psoriasis in a
 PT mammal.

PS Claim 9; SEQ ID NO 809; 3069pp; English.

XX The invention relates to novel polynucleotide and polypeptides for
 CC treating psoriasis or a sequence having at least 80% identity to the
 CC above sequences. The nucleic acid is useful for preparing a composition
 CC for diagnosing or treating psoriasis in a mammal. This sequence
 CC corresponds to one of the polypeptides of the invention.

XX Sequence 311 AA;

Query Match

Best Local Similarity 100.0%; Score 73; DB 8; Length 311;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYRCRGDDSKVQE 13

|||||

DB 178 NYRCRGDDSKVQE 190

RESULT 5

ADP24274

ID ADP24274 standard; protein; 311 AA.

XX ADP24274;

DT 18-NOV-2004 (first entry)

XX PRO polypeptide SEQ ID NO:1452.

XX PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
 KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
 KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.

OS Unidentified.

PN WO2004041170-A2.

PD 21-MAY-2004.

PF 30-OCT-2003; 2003WO-US034312.

PR 01-NOV-2002; 2002US-0423394P.

PA (GETH) GENENTECH INC.

XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;

PI Wu TD;

DR WPI; 2004-419628/39.

DR N-PSDB; ADP24273.

XX New PRO polypeptides and polynucleotides, useful for treating e.g.
 PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
 PT renal disease, or demyelinating diseases of the central or peripheral
 PT nervous system.

XX Claim 7; SEQ ID NO 1452; 2940pp; English.

XX The invention relates to a novel isolated nucleic acid and the PRO
 CC polypeptide encoded by it. A protein of the invention has
 CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
 CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
 CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its
 CC agonist, antagonist, or antibody that specifically binds to the
 CC polypeptide is useful for treating an immune related disorder such as
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein
 CC of the invention.

XX Sequence 311 AA;

Query Match 100.0%; Score 73; DB 8; Length 311;

Best Local Similarity 100.0%; Pred. No. 0.00083; Mismatches 0; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYRCRGDDSKVQE 13
 |||||
 Db 178 NYRCRGDDSKVQE 190

RESULT 6
 ABB99112
 ID ABB99112 standard; protein; 312 AA.
 XX
 AC ABB99112;
 XX
 DT 29-OCT-2002 (first entry)
 XX
 DE Rat phosphatase #2.
 XX
 KW Phosphatase; prenilyphosphoric acid; prenily alcohol; rat.
 XX
 OS Rattus norvegicus.
 XX
 PN WO200253751-A1.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-JP011223.
 XX
 PR 28-DEC-2000; 2000JP-00401515.
 PR 28-DEC-2000; 2000JP-00401806.
 XX
 PA (TOYW) TOYOTA CHUO KENKUSHO KK.
 PA (TOYT) TOYOTA JIDOSHA KK.
 XX
 PI Tokuhiko K, Muramoto N, Yamada Y, Asami O, Hirai M, Ohto C;
 PI Obata S, Muramatsu M;
 XX
 XX WPI; 2002-643303/69.
 DR N-PSDB; ABQ78948.
 XX
 PT Phosphatase polypeptides and encoded polynucleotides with substrate-
 PT specificity for prenilyphosphoric acid, applicable in mass-production of
 PT all-trans-prenily alcohols by culturing transformants.
 XX
 PS Claim 1; Page 67-68; 93pp; Japanese.
 XX
 CC The invention relates to a novel phosphatase polypeptide, exhibiting
 CC substrate-specificity for not less than 15C prenilyphosphoric acid. The
 CC polynucleotides and encoded polypeptides are applicable in mass-
 CC production of all-trans-prenily alcohols. The sequence represents a rat
 CC phosphatase polypeptide of the invention
 XX
 SQ Sequence 312 AA;

Query Match 94.5%; Score 69; DB 5; Length 312;
 Best Local Similarity 92.3%; Pred. No. 0.0039;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYRCRGDDSKVQE 13
 |||||
 Db 179 NYRCRGDDSKVQE 191

RESULT 7
 ADE60701
 ID ADE60701 standard; protein; 312 AA.
 XX
 AC ADE60701;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Rat Protein CAA69106, SEQ ID NO 6613.
 XX

KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX
 OS Rattus norvegicus.
 XX
 PN WO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX
 DR WPI; 2003-268312/26.
 DR GENBANK; CAA69106.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method of identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 312 AA;

Query Match 94.5%; Score 69; DB 7; Length 312;
 Best Local Similarity 92.3%; Pred. No. 0.0039;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYRCRGDDSKVQE 13
 |||||
 Db 179 NYRCRGDDSKVQE 191

RESULT 8
 ADB74255
 ID ADB74255 standard; protein; 705 AA.
 XX
 AC ADB74255;
 XX

KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

XX WO200175067-A2.

PD 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR N-PSDB; AAS87621.

XX New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

XX Claim 20; SEQ ID NO 53793; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 152 AA;

Query Match 56.2%; Score 41; DB 4; Length 152;
Best Local Similarity 70.0%; Pred. No. 85;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NTRCRGDDSK 10

Db 68 NTRCRGDLTK 77

RESULT 11

AAU28253

ID AAU28253 standard; protein; 237 AA.

XX AAU28253;

XX 18-DEC-2001 (first entry)

XX Novel human secretory protein, Seq ID No 610.

XX Human, secreted protein; arthritis; Crohn's disease; sepsis; shock;
KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;

KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
KW gut protection; lung; liver fibrosis; immune deficiency; infection;
KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
KW fertility; analgesic; pain; antigen.

XX Homo sapiens.

XX WO200166689-A2.

XX 13-SEP-2001.

XX 05-MAR-2001; 2001WO-US004942.

XX 07-MAR-2000; 2000US-00519705.

PR 19-MAY-2000; 2000US-00574454.

PR 17-JUN-2000; 2000US-00596193.

PR 14-JUL-2000; 2000US-00616847.

PR 19-SEP-2000; 2000US-00665363.

PR 20-OCT-2000; 2000US-00693267.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;

PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;

XX WPI; 2001-589934/66.

DR N-PSDB; AAS45153.

XX Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders.

XX Example 2; SEQ ID NO 610; 107pp; English.

CC The invention relates to novel isolated human secreted polypeptides (I) and polynucleotides (II). (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses, and is involved in increasing haematopoiesis, stem cell survival, bone growth and remodeling. (I), (II) and modulators of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, and amyotrophic lateral sclerosis. In addition, (I) is involved in chemotactic or chemokinetic activity, regulation of haematopoiesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease. Furthermore, (I) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. In addition, (I) affects biorhythms or circadian cycles of rhythms, fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAU28020-AAU28395 represent novel human secreted protein amino acid sequences of the invention

XX Sequence 237 AA;

Query Match 56.2%; Score 41; DB 4; Length 237;

Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NYRCRGDSK 10
Db 5 NHRCRGDLTK 14

RESULT 12

ADSI212199
ID ADSI212199 standard; protein; 237 AA.

XX AC
XX AC
XX ADSI212199;

DT 16-DEC-2004 (first entry)

DE Human therapeutic contig protein - SEQ ID 2436.

XX antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
KW aplastic anaemia; cancer; wound healing; gene therapy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 1..237
FT /label= Unknown, OTHER
FT /note= "OTHER = In-frame STOP codon"

XX WO2004080148-A2.

XX 23-SEP-2004.

XX 30-SEP-2003; 2003WO-US030720.

XX 02-OCT-2002; 2002US-0416186P.

XX (NUVE-) NUVELO INC.

XX Tang YT, Auendi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y,
PI Wang D, Chen R, Zhao QX, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
XX N-PSDB; ADSI1601.

XX New polynucleotide, useful in preparing a composition for diagnosing or
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
PT aplastic anemia or cancer for promoting wound healing.

XX Example 2; SEQ ID NO 2436; 718pp; English.

XX The invention relates to a novel isolated polynucleotide and the encoded
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
CC be useful in preparing a composition for diagnosing or treating
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
CC disorders, such as aplastic anaemia or cancer, as well as for promoting
CC wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic contig
CC protein of the invention.

XX SQ Sequence 237 AA;

Query Match 56.2%; Score 41; DB 8; Length 237;

Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NYRCRGDSK 10
Db 5 NHRCRGDLTK 14

RESULT 13

ADJ50947

ID ADJ50947 standard; protein; 421 AA.

XX AC
XX ADJ50947;

DT 06-MAY-2004 (first entry)

DE Human novel protein NOV4b.

XX Human; NOVX; autoimmune disease; Alzheimer's disease; stroke; allergy;
KW Parkinson's disease; Huntington's disease; multiple sclerosis; anxiety;
KW pain; diabetes; graft versus host disease; pancreatitis; obesity; ulcer;
KW anaemia; cancer; viral infection; bacterial infection;
KW parasitic infection.

XX OS Homo sapiens.

XX PN US2004030096-A1.

XX PD 12-FEB-2004.

XX PF 01-AUG-2002; 2002US-00210281.

XX 02-AUG-2001; 2001US-0309501P.

XX 03-AUG-2001; 2001US-0310291P.

XX 08-AUG-2001; 2001US-0310951P.

XX 09-AUG-2001; 2001US-0311292P.

XX 13-AUG-2001; 2001US-0311979P.

XX 14-AUG-2001; 2001US-0312203P.

XX 17-AUG-2001; 2001US-0313201P.

XX 20-AUG-2001; 2001US-0313643P.

XX 21-AUG-2001; 2001US-0313702P.

XX 23-AUG-2001; 2001US-0314031P.

XX 28-AUG-2001; 2001US-0315403P.

XX 29-AUG-2001; 2001US-0315853P.

XX 05-MAR-2002; 2002US-0361775P.

XX 05-MAR-2002; 2002US-0361832P.

XX (GORM/) GORMAN L.

XX (ZERH/) ZERHUSEN B D.

XX (EDIN/) EDINGER S R.

XX (PADI/) PADIGARU M.

XX (GUOX/) GUO X.

XX (KEKU/) KEKUDA R.

XX (ZHON/) ZHONG M.

XX (PATT/) PATTURAJAN M.

XX (MILL/) MILLER C E.

XX (JIWW/) JI W.

XX (PENA/) PENNA C E A.

XX (BURG/) BURGESS C E.

XX (SCIO/) SCIORE P.

XX (STON/) STONE D J.

XX (TAUP/) TAUPIER R J.

XX (CASM/) CASMAN S J.

XX (ROTH/) ROTHENBERG M E.

XX (MALY/) MALYANKAR U M.

XX (BOLD/) BOLDG F L.

XX Gorman L, Zerhusen BD, Edinger SR, Padigaru M, Guo X, Kekuda R;
PI Zhong M, Patturajan M, Miller CE, Ji W, Pena CEA, Burgess CE;
PI Sciore P, Stone DJ, Taupier RJ, Casman SJ, Rothenberg ME;
PI Malyankar UM, Boldog FL;
XX WPI; 2004-168942/16.
DR N-PSDB; ADJ50946.

XX New NOVX polypeptides and polynucleotides, useful in diagnosing, treating
PT or preventing diseases or conditions, e.g. autoimmune disease,
PT Alzheimer's disease, diabetes, graft versus host disease, cancer or viral
PT or bacterial infections.

XX Claim 2; SEQ ID NO 12; 342pp; English.

XX The invention relates to an isolated NOVX polypeptide (of 44 disclosed)
CC comprising its mature form, a sequence having at least 95% sequence
CC identity to NOVX or a sequence comprising one or more conservative
CC substitutions in the amino acid sequence of NOVX. Also included are a
CC composition comprising NOVX and a carrier, a kit comprising, in one or
CC more containers, the composition, a method of identifying an agent that
CC binds to NOVX, a method for identifying a potential therapeutic agent for
CC use in treatment of a pathology related to aberrant expression or
CC aberrant physiological interactions of NOVX, a method for screening for a
CC modulator of activity of or of latency or predisposition to a pathology
CC associated with NOVX, a method for modulating the activity of NOVX, a
CC method of treating or preventing a pathology associated with NOVX or a
CC pathological state in a mammal, an isolated nucleic acid molecule
CC encoding a NOVX protein, a vector comprising the nucleic acid molecule,
CC a cell comprising the vector, an antibody that immunospecifically binds
CC to NOVX, a method for determining the presence or amount of NOVX or the
CC nucleic acid molecule in a sample, a method for determining the presence
CC of or predisposition to a disease associated with altered levels of
CC expression of NOVX or the nucleic acid molecule in a first mammalian
CC subject and a method of producing NOVX (comprising culturing the cell
CC under conditions that lead to expression of the polypeptide). NOVX is
CC useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease associated with NOVX. The polypeptides
CC and nucleic acid molecules are useful in diagnosing, treating or
CC preventing diseases or conditions, e.g. autoimmune disease, Alzheimer's
CC disease, stroke, allergies, Parkinson's disease, Huntington's disease,
CC multiple sclerosis, anxiety, pain, diabetes, graft versus host disease,
CC pancreatitis, obesity, ulcers, anaemia, cancer, viral or bacterial and
CC parasitic infections (many more diseases and disorders are listed in the
CC specification). The present sequence represents a NOVX protein.

XX SQ Sequence 421 AA;

Query Match 56.2%; Score 41; DB 8; Length 421;
Best Local Similarity 70.0%; Pred. No. 2.4e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 NVCRCGDDSK 10
Db 197 NHCRCGDLTK 206
|:|||||:

RESULT 14
ADJ50945
ID ADJ50945 standard; protein; 424 AA.

XX AC ADJ50945;

XX DT 06-MAY-2004 (first entry)

XX DE Human novel protein NOV4a.

XX Human; NOVX; autoimmune disease; Alzheimer's disease; stroke; allergy;
KW Parkinson's disease; Huntington's disease; multiple sclerosis; anxiety;
KW pain; diabetes; graft versus host disease; pancreatitis; obesity; ulcer;
KW anaemia; cancer; viral infection; bacterial infection;
KW parasitic infection.

XX OS Homo sapiens.

XX FN US2004030096-A1.

XX PD 12-FEB-2004.

XX PF 01-AUG-2002; 2002US-00210281.

XX PR 02-AUG-2001; 2001US-0309501P.

PR 03-AUG-2001; 2001US-0310291P.

PR 08-AUG-2001; 2001US-0310951P.

PR 09-AUG-2001; 2001US-0311292P.

PR 13-AUG-2001; 2001US-0311979P.

PR 14-AUG-2001; 2001US-0312203P.

PR 17-AUG-2001; 2001US-0313201P.
PR 20-AUG-2001; 2001US-0313643P.
PR 20-AUG-2001; 2001US-0313702P.
PR 21-AUG-2001; 2001US-0314031P.
PR 23-AUG-2001; 2001US-0314466P.
PR 28-AUG-2001; 2001US-0315403P.
PR 29-AUG-2001; 2001US-0315853P.
PR 05-MAR-2002; 2002US-0361775P.
PR 05-MAR-2002; 2002US-0361832P.

XX (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (EDIN/) EDINGER S R.
PA (PADI/) PADIGARU M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
PA (ZHON/) ZHONG M.
PA (PATT/) PATTURAJAN M.
PA (MILL/) MILLER C E.
PA (JIWV/) JI W.
PA (PENA/) PENA C E A.
PA (BURG/) BURGESS C E.
PA (SCIO/) SCIORE P.
PA (STON/) STONE D J.
PA (TAUP/) TAUPIER R J.
PA (CASM/) CASMAN S J.
PA (ROTH/) ROTHENBERG M E.
PA (MALY/) MALYANKAR U M.
PA (BOLD/) BOLDOG F L.

XX Gorman L, Zerhuseen BD, Edinger SR, Padigaru M, Guo X, Kekuda R;
PI Zhong M, Patturajan M, Miller CE, Ji W, Pena CE, Burgess CS;
PI Sciore P, Stone DJ, Taupier RJ, Casman SJ, Rothenberg ME;
PI Malyankar UM, Boldog FL;

XX WPI: 2004-168942/16.
DR N-PSDB; ADJ50944.

XX New NOVX polypeptides and polynucleotides, useful in diagnosing, treating
PT or preventing diseases or conditions, e.g. autoimmune disease,
PT Alzheimer's disease, diabetes, graft versus host disease, cancer or viral
PT or bacterial infections.

PS Claim 2; SEQ ID NO 10; 342pp; English.

XX The invention relates to an isolated NOVX polypeptide (of 44 disclosed)
CC comprising its mature form, a sequence having at least 95% sequence
CC identity to NOVX or a sequence comprising one or more conservative
CC substitutions in the amino acid sequence of NOVX. Also included are a
CC composition comprising NOVX and a carrier, a kit comprising, in one or
CC more containers, the composition, a method of identifying an agent that
CC binds to NOVX, a method for identifying a potential therapeutic agent for
CC use in treatment of a pathology related to aberrant expression or
CC aberrant physiological interactions of NOVX, a method for screening for a
CC modulator of activity of or of latency or predisposition to a pathology
CC associated with NOVX, a method for modulating the activity of NOVX, a
CC method of treating or preventing a pathology associated with NOVX or a
CC pathological state in a mammal, an isolated nucleic acid molecule
CC encoding a NOVX protein, a vector comprising the nucleic acid molecule,
CC a cell comprising the vector, an antibody that immunospecifically binds
CC to NOVX, a method for determining the presence or amount of NOVX or the
CC nucleic acid molecule in a sample, a method for determining the presence
CC of or predisposition to a disease associated with altered levels of
CC expression of NOVX or the nucleic acid molecule in a first mammalian
CC subject and a method of producing NOVX (comprising culturing the cell
CC under conditions that lead to expression of the polypeptide). NOVX is
CC useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease associated with NOVX. The polypeptides
CC and nucleic acid molecules are useful in diagnosing, treating or
CC preventing diseases or conditions, e.g. autoimmune disease, Alzheimer's
CC disease, stroke, allergies, Parkinson's disease, Huntington's disease,
CC multiple sclerosis, anxiety, pain, diabetes, graft versus host disease,
CC pancreatitis, obesity, ulcers, anaemia, cancer, viral or bacterial and

CC parasitic infections (many more diseases and disorders are listed in the
CC specification). The present sequence represents a NOVX protein.
XX
SQ Sequence 424 AA;
Query Match 56.2%; Score 41; DB 8; Length 424;
Best Local Similarity 70.0%; Pred. No. 2.4e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 NVRCRGDDSK 10
Db 198 NHRCRGDLTK 207
RESULT 15
ADA83857
ID ADA83857 standard; protein; 428 AA.
XX
AC ADA83857;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human POM18 protein.
XX
KW human; marker; expressed sequence tag; EST; arabidopsis; tumour;
KW stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;
KW vaccine.
XX
OS Homo sapiens.
XX
PN WO2002103028-A2.
PD 27-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-IB004189.
XX
PR 30-MAY-2001; 2001US-0293999P.
PR 22-OCT-2001; 2001US-0330457P.
PR 19-FEB-2002; 2002US-0357144P.
XX
PA (BIOM-) BIOMEDICAL CENT.
XX
PI Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LL;
DR WPI; 2003-175241/17.
DR N-PSDB; ADA83856.
XX
PT Determining if a nucleic acid is a marker for a phenotype/cell type of
PT interest, by global comparison of expressed sequence tags known to be
PT expressed in the phenotype/cell type with all ESTs expressed in normal
PT tissue.
XX
PS Claim 29; Page 269-271; 516pp; English.
XX
CC The invention relates to a novel method for determining if a nucleic acid
CC is a marker for a predetermined phenotype/cell type of interest from a
CC biological species. The method comprises performing a global comparison
CC of a group of expressed sequence tags (ESTs) known to be expressed in the
CC phenotype/cell type of interest with all ESTs expressed in normal tissue
CC in order to identify ESTs that are preferentially expressed in the
CC phenotype/cell of interest. A method of the invention is useful for
CC determining whether a nucleic acid is a marker for a predetermined
CC phenotype or cell type of interest from a biological species, preferably
CC Arabidopsis or human. The cell type of interest is an abnormal cell such
CC as a tumour cell, and the predetermined phenotype is a stress-induced
CC phenotype such as hyperosmotic stress or high salt conditions. A method
CC of the invention is also useful for determining the progression of colon
CC cancer in a human, for detecting a tumour cell, and for regulating or
CC preventing the growth of a tumour cell. An antibody of the invention is
CC useful for detecting the absence or presence of peptides encoded by
CC tumour-associated markers. A polypeptide of the invention is useful as an
CC immunogen for vaccinating an animal. The present sequence represents a
CC tumour-associated antigen of the invention.

XX
SQ Sequence 428 AA;
Query Match 56.2%; Score 41; DB 6; Length 428;
Best Local Similarity 70.0%; Pred. No. 2.5e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 NVRCRGDDSK 10
Db 197 NHRCRGDLTK 206
RESULT 16
ABB67864
ID ABB67864 standard; protein; 451 AA.
XX
AC ABB67864;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 30384.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-658860/75.
DR N-PSDB; ABL11967.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Disclosure; SEQ ID NO 30384; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 451 AA;
Query Match 56.2%; Score 41; DB 4; Length 451;
Best Local Similarity 63.6%; Pred. No. 2.6e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 YRCRGDDSKVQ 12
Db 3 YRCRGNESSDQ 13
RESULT 17
ADR09234

ID ADR09234 standard; protein; 481 AA.
AC ADR09234;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human protein useful for treating neurological disease Seq 2740.
XX
KW human; oligo-capping method; diagnostic marker; gene therapy;
KW osteoporosis; neurological disease; Alzheimer's disease;
KW Parkinson's disease; dementia; short memory; cancer;
KW sense or motor function; emotional reaction; fear response; panic;
KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cyostatic;
KW tranquiliser.
XX
OS Homo sapiens.
XX
PN EP1447413-A2.
XX
PD 18-AUG-2004.
XX
PF 12-FEB-2004; 2004EP-00003145.
XX
PR 14-FEB-2003; 2003JP-00102207.
PR 09-MAY-2003; 2003JP-00131452.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;
PI Wakamatsu A, Ishii S, Nagai K, Irie R;
XX
DR WPI; 2004-593285/57.
XX
DR N-PSDB; ADR07278.
XX
XX New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
PS Claim 1; SEQ ID NO 2740; 2686pp; English.
XX
CC This invention relates to novel, isolated full length human cDNA
CC molecules and the encoded proteins thereof. Specifically, it refers to
CC cDNA clones obtained by an oligo-capping method, where none of these
CC clones are identical to any known human mRNAs. The present invention
CC describes an immunoassay to identify agonists and antagonists, as well as
CC antibodies, antisense molecules and siRNAs that can all be used to bind
CC to and modulate expression of the cDNA molecules. As such, these
CC molecules are useful for diagnostic markers or therapeutic targets for
CC the various diseases or morbid states. In particular, they are useful in
CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's
CC disease, Parkinson's disease, dementia, short memory and various cancers,
CC as well as for maintaining equilibrium of sense or motor function, and
CC for treating emotional reaction, fear response and panic. Accordingly,
CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,
CC cyostatic and tranquiliser activities. This polypeptide is a protein
CC encoded by a full length human cDNA sequence of the invention. NOTE: This
CC sequence is not given in the sequence listing of the specification but
CC can be obtained on CD-ROM from the European Patent Office, Vienna Sub-
CC office.
XX
SQ Sequence 481 AA;

Query Match 56.2%; Score 41; DB 8; Length 481;
Best Local Similarity 70.0%; Pred. No. 2.8e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDSDK 10
|:|||||:
Db 250 NHRCRGDLTK 259

RESULT 18
ADSI0966
ID ADSI0966 standard; protein; 481 AA.

XX ADSI0966;
AC
XX
DT 16-DEC-2004 (first entry)
XX
DE Human therapeutic protein - SEQ ID 1203.
XX
KW antinflammatory; neuroprotective; antianaemic; cyostatic; vulnerary;
KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
KW aplastic anaemia; cancer; wound healing; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2004080148-A2.
XX
XX
PD 23-SEP-2004.
XX
XX 30-SEP-2003; 2003WO-US030720.
XX
XX 02-OCT-2002; 2002US-0416186P.
XX
XX (NUVE-) NUVELO INC.
XX
XX Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
XX Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
XX
XX WPI; 2004-668857/65.
XX
XX N-PSDB; ADSI0282.
XX
XX New polynucleotide, useful in preparing a composition for diagnosing or
XX treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
XX aplastic anemia or cancer for promoting wound healing.
XX
XX Claim 20; SEQ ID NO 1203; 718pp; English.
XX
XX The invention relates to a novel isolated polynucleotide and the encoded
XX polypeptide. The molecules of the invention demonstrate antiinflammatory,
XX neuroprotective, antianaemic, cyostatic and vulnerary activities and may
XX be useful in preparing a composition for diagnosing or treating
XX inflammatory, haematopoietic, immune, neurodegenerative or stem cell
XX disorders, such as aplastic anaemia or cancer, as well as for promoting
XX wound healing. The molecules may also be utilised during gene therapy
XX procedures. The current sequence is that of a human therapeutic protein
XX of the invention. The current sequence is not shown explicitly within the
XX specification but can be accessed from the WIPO web-site.
XX
SQ Sequence 481 AA;

Query Match 56.2%; Score 41; DB 8; Length 481;
Best Local Similarity 70.0%; Pred. No. 2.8e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDSDK 10
|:|||||:
Db 250 NHRCRGDLTK 259

RESULT 19
ADM04303
ID ADM04303 standard; protein; 489 AA.
XX
XX ADM04303;
AC
XX
XX 20-MAY-2004 (first entry)
DT
XX
XX Human protein of the invention SEQ ID NO:2988.
DE
XX human; gene therapy; diagnostic marker; pharmaceutical.
KW
XX Homo sapiens.
OS
XX
XX EP1347046-A1.
PN
XX

PD 24-SEP-2003.
 XX
 PF 12-APR-2002; 2002EP-00008400.
 XX
 PR 22-MAR-2002; 2002JP-00137785.
 XX
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
 XX
 DR WPI; 2003-723558/69.
 DR N-PSDB; ADM01860.
 XX
 XX New polynucleotides and polypeptides are useful in gene therapy, for
 PT developing a diagnostic marker or medicines for regulating their
 PT expression and activity, or as a target of gene therapy.
 XX
 PS Claim 1; SEQ ID NO 2988; 305pp; English.
 XX
 CC The invention relates to a novel human polynucleotide and the encoded
 CC polypeptide. A polynucleotide of the invention may have a use in gene
 CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
 CC as a primer for synthesizing the polynucleotide or as a probe for
 CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
 CC useful in gene therapy, for developing a diagnostic marker or medicines
 CC for regulating their expression and activity, or as a target of gene
 CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
 CC are useful as pharmaceutical agents. The present sequence represents a
 CC protein sequence of the invention.
 XX
 SQ Sequence 489 AA;
 Query Match 56.2%; Score 41; DB 7; Length 489;
 Best Local Similarity 70.0%; Pred. NO. 2.8e+02;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NVRCRGDSSK 10
 DB 258 NHRCGDLTK 267
 ||:|||||+|
 RESULT 20
 AAW99087
 ID AAW99087 standard; protein; 822 AA.
 XX
 AC AAW99087;
 XX
 DT 13-MAY-1999 (first entry)
 XX
 DE Human serine protease BSSP-3.
 XX
 KW Serine protease; BSSP-3; brain tissue.
 XX
 OS Homo sapiens.
 XX
 PN WO9905290-A1.
 XX
 PD 04-FEB-1999.
 XX
 PF 24-JUL-1998; 98WO-JP003324.
 XX
 PR 24-JUL-1997; 97JP-00213969.
 XX
 PA (SUNR) SUNTORY LTD.
 XX
 PI Tsuruoka N, Yamashiro K, Yamaguchi N;
 XX
 DR WPI; 1999-142942/12.
 DR N-PSDB; AAX19024.
 XX
 PT New serine protease expressed in brain tissue - used in screening for

PT potential serine protease inhibitors for drug use.
 XX
 PS Claim 1; Page 61-65; 69pp; Japanese.
 XX
 CC The present sequence is a serine protease designated BSSP-3, which is
 CC isolated from human brain tissue. Transformants may be used to produce
 CC the enzyme or its partial sequences. Products from the present invention
 CC are used for screening for potential peptide or non-peptide serine
 CC protease inhibitors or expression regulators for use as drugs
 XX
 SQ Sequence 822 AA;
 Query Match 56.2%; Score 41; DB 2; Length 822;
 Best Local Similarity 54.5%; Pred. NO. 4.8e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 NVRCRGDSSK 11
 DB 183 NVRCRGDENI 193
 ||||||:
 RESULT 21
 AAW83361
 ID AAW83361 standard; protein; 875 AA.
 XX
 AC AAW83361;
 XX
 DT 17-FEB-1999 (first entry)
 XX
 DE Human neurotrypsin.
 XX
 KW Human; neurotrypsin; tumour inhibition; neurological disease;
 KW lung disease; gene therapy; drug development; stroke; brain injury;
 KW neurodegeneration; neuroinflammatory disease; multiple sclerosis;
 KW epilepsy; hypoxia; ischaemia; nerve transection; neovascularisation;
 KW emphysema; bronchitis.
 XX
 OS Homo sapiens.
 XX
 PN WO9849322-A1.
 XX
 PD 05-NOV-1998.
 XX
 PF 24-APR-1998; 98WO-IB000625.
 XX
 PR 26-APR-1997; 97CH-00000966.
 XX
 PA (SOND/) SONDEREGGER P.
 XX
 PI Sonderegger P;
 XX
 DR WPI; 1999-009438/01.
 DR N-PSDB; AAV72589.
 XX
 PT New human and murine neurotrypsin - used, e.g. for inhibiting tumours,
 PT treatment of neurological or lung disease, including by gene therapy and
 PT in drug development.
 XX
 PS Claim 1; Page 20-24; 50pp; English.
 XX
 CC The present sequence represents human neurotrypsin. Neurotrypsin proteins
 CC and polynucleotides can be used: (i) to inhibit tumours, including
 CC metastases, e.g. of brain or retina; (ii) to minimise tissue damage
 CC caused by stroke or brain injury (having a protective effect on the
 CC penumbra zone); (iii) to treat or prevent neurodegeneration,
 CC neuroinflammatory disease (e.g. multiple sclerosis) or epilepsy; (iv) to
 CC increase survival of damaged neurons (e.g. in cases of hypoxia,
 CC ischaemia, nerve transection) and to stimulate regeneration and/or
 CC restoration of synapses; (v) to treat or prevent retinal disorders (e.g.
 CC degeneration or neovascularisation); (vi) to prevent apoptosis (or other
 CC causes of cell death) in the nervous system; (vii) to regenerate brain
 CC and/or nervous tissue; (viii) to treat pain; (ix) to improve brain
 CC performance, including learning and memory; (x) to treat or prevent a

```
CC wide range of psychiatric disorders; and (xi) to treat brain or lung
CC injury associated with protease expression (specifically emphysema or
CC bronchitis)
XX
SQ Sequence 875 AA;
  Query Match          56.2%; Score 41; DB 2; Length 875;
  Best Local Similarity 54.5%; Pred. No. 5.1e+02;
  Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 NVRCRGDDSKV 11
  |||||:
Db 236 NVRCRGDBENI 246

RESULT 22
ADQ21226
ID ADQ21226 standard; protein; 875 AA.
XX
AC ADQ21226;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4046.
XX
KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
XX
OS Homo sapiens.
XX
PN WO2004048938-A2.
XX
PD 10-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-US038193.
XX
PR 26-NOV-2002; 2002US-0429739P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Aziz N, Ginsburg WM, Zlotnik A;
XX
WPI; 2004-441208/41.
XX
PT Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
PS Example 2; SEQ ID NO 4046; 210pp; English.
XX
CC The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC protein of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
SQ Sequence 875 AA;
  Query Match          56.2%; Score 41; DB 8; Length 875;
  Best Local Similarity 54.5%; Pred. No. 5.1e+02;
  Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 NVRCRGDDSKV 11
  |||||:
Db 236 NVRCRGDBENI 246
```

```
RESULT 23
ADQ89082
ID ADQ89082 standard; protein; 875 AA.
XX
AC ADQ89082;
XX
DT 21-OCT-2004 (first entry)
XX
DE Human urological disorder related protein 14063 SEQ:34.
XX
KW urological disorder; uropathic; cytostatic; urinary incontinence;
KW benign prostatic hyperplasia; human.
XX
OS Homo sapiens.
XX
PN WO2004065576-A2.
XX
PD 05-AUG-2004.
XX
PF 14-JAN-2004; 2004WO-US000750.
XX
PR 15-JAN-2003; 2003US-0440318P.
PR 04-FEB-2003; 2003US-0444783P.
PR 27-MAR-2003; 2003US-0457901P.
PR 08-MAY-2003; 2003US-0468775P.
PR 19-MAY-2003; 2003US-0471614P.
PR 16-JUN-2003; 2003US-0478742P.
PR 18-JUL-2003; 2003US-048529P.
PR 30-JUL-2003; 2003US-0491156P.
PR 02-SEP-2003; 2003US-0499594P.
PR 26-SEP-2003; 2003US-0506332P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Karicheti V, Silos-Santiago I, Eliasof SD;
XX
WPI; 2004-562167/54.
XX
N-PSDB; ADQ89081.
XX
PT Use of polypeptides related to urological disorders, e.g. 44390, 54181,
PT 211 or for identifying a compound capable of treating a urological
PT disorder or identifying and treating a subject having a urological
PT disorder.
XX
PS Claim 1; SEQ ID NO 34; 542pp; English.
XX
CC The present invention describes the use of polypeptides related to
CC urological disorders for identifying a compound capable of treating a
CC urological disorder, identifying a subject having a urological disorder,
CC or treating a subject having a urological disorder. Also described: (1) a
CC method for identifying a compound capable of treating a urological
CC disorder; (2) a method for identifying a subject having a urological
CC disorder; and (3) a method for treating a subject having a urological
CC disorder. The compound has uropathic and cytostatic activities. The
CC polypeptides related to urological disorders are useful for identifying a
CC compound capable of treating a urological disorder, identifying a subject
CC having a urological disorder, or treating a subject having a urological
CC disorder. Disorders include urinary incontinence and benign prostatic
CC hyperplasia. The present sequence represents a human urological disorder
CC related protein, which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 875 AA;
  Query Match          56.2%; Score 41; DB 8; Length 875;
  Best Local Similarity 54.5%; Pred. No. 5.1e+02;
  Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 NVRCRGDDSKV 11
  |||||:
Db 236 NVRCRGDBENI 246
```

RESULT 24
 ABP56183
 ID ABP56183 standard; peptide; 20 AA.
 AC
 XX
 DT 28-MAR-2003 (first entry)
 DE
 XX
 DE Chimeric peptide sequence #5.
 XX
 KW Mitochondrial membrane permeabilisation; mitochondrion; PTPC; chimeric;
 KW permeability transition pore complex; virucide; neuroprotective;
 KW vasotropic; cytosolic; infection; cell death regulation; apoptosis;
 KW mitochondrial permeability transition pore complex modulator; cancer;
 KW apoptogenic; ischaemia; neurodegenerative disease; fulminant hepatitis.
 XX
 OS Synthetic.
 XX
 PN WO200261105-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 01-FEB-2002; 2002WO-EP001633.
 XX
 PR 02-FEB-2001; 2001US-0265594P.
 XX
 PA (INSP) INST PASTEUR.
 PA (CNRS) CENT NAT RECH SCT.
 XX
 PI Edelman L, Jacotot E, Briand J;
 XX
 DR WPI; 2002-619260/66.
 XX
 XX New chimeric bifunctional molecules that target specific cells and
 PT regulate the apoptosis function of the permeability transition pore
 PT complex of the mitochondria, useful for treating or preventing e.g.
 PT cancer or ischemia.
 XX
 PS Disclosure; Page 23; 76pp; English.
 XX
 CC The present invention describes a chimeric bifunctional molecule (I)
 CC comprising at least a first functional molecule covalently linked to a
 CC second functional molecule, which is able to modulate the activity of the
 CC permeability transition pore complex (PTPC) of the mitochondria. (I) has
 CC the function of specifically targeting and entering a tissue cell
 CC population. The second functional molecule has the function of
 CC specifically targeting, and inducing or preventing the death of the cells
 CC by apoptosis by regulating the opening or the closing of the PTPC of the
 CC mitochondria or its fragment. (I) has virucide, neuroprotective,
 CC vasotropic and cytostatic activities, and can be used as a mitochondrial
 CC permeability transition pore complex (PTPC) modulator. (I) is useful for
 CC treating or preventing a pathological infection or disease. (I) is also
 CC useful for regulating cell death regulatory molecules, specifically the
 CC apoptogenic function of the PTPC, for treating e.g. cancer, ischaemia,
 CC neurodegenerative diseases, fulminant hepatitis or viral infections. The
 CC present sequence represents a chimeric peptide which is given in the
 CC exemplification of the present invention
 XX
 XX Sequence 20 AA;
 SQ
 Query Match 54.8%; Score 40; DB 5; Length 20;
 Best Local Similarity 58.3%; Pred No. 16;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 NYRCRGDSDSKVQ 12
 Db ||||| :
 2 NGRCGGDDKRTQ 13
 RESULT 25
 ABB99111
 ID ABB99111 standard; protein; 282 AA.
 AC
 XX
 DT 29-OCT-2002 (first entry)
 DE
 XX
 DE Rat phosphatase #1.
 KW Phosphatase; prenlyphosphoric acid; prenyl alcohol; rat.
 XX
 OS Rattus norvegicus.
 XX
 PN WO200253751-A1.
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-JP011223.
 XX
 PR 28-DEC-2000; 2000JP-00401515.
 PR 28-DEC-2000; 2000JP-00401806.
 XX
 PA (TOYM) TOYOTA CHUO KENKYUSHO KK.
 PA (TOYT) TOYOTA JIDOSHA KK.
 XX
 PI Tokuhiko K, Muramoto N, Yamada Y, Asami O, Hirai M, Ohto C;
 PI Obata S, Muramatsu M;
 XX
 DR WPI; 2002-643303/69.
 DR N-PSDB; ABQ78947.
 XX
 PT Phosphatase polypeptides and encoded polynucleotides with substrate-
 PT specificity for prenlyphosphoric acid, applicable in mass-production of
 PT all-trans-prenyl alcohols by culturing transformants.
 XX
 PS Claim 1; Page 64-65; 93pp; Japanese.
 XX
 CC The invention relates to a novel phosphatase polypeptide, exhibiting
 CC substrate-specificity for not less than 15C prenlyphosphoric acid. The
 CC polynucleotides and encoded polypeptides are applicable in mass-
 CC production of all-trans-prenyl alcohols. The sequence represents a rat
 CC phosphatase polypeptide of the invention
 XX
 SQ Sequence 282 AA;
 Query Match 54.8%; Score 40; DB 5; Length 282;
 Best Local Similarity 46.2%; Pred No. 2,4e+02;
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 NYRCRGDSDSKVQE 13
 Db ||||| :
 150 NFVCGQNEQKVRE 162
 RESULT 26
 ADE58904
 ID ADE58904 standard; protein; 282 AA.
 AC
 XX
 AC ADE58904;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Rat Protein NP_071983, SEQ ID NO 4792.
 XX
 KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX
 OS Rattus norvegicus.
 XX
 PN WO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 DR GENBANK; NP_071983.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 282 AA;
 Query Match 54.8%; Score 40; DB 7; Length 282;
 Best Local Similarity 46.2%; Pred. No. 2.4e+02;
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 NYRCRGDDSKVOE 13
 Db 150 NFVQCQNEQKRE 162
 RESULT 27
 ADE58900
 ID ADE58900 standard; protein; 282 AA.
 XX
 AC ADE58900;
 XX
 XX 29-JAN-2004 (first entry)
 DT Rat Protein NP_071983, SEQ ID NO 4788.
 XX
 DE Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX Rattus norvegicus.
 OS
 XX WO2003016475-A2.
 PN

XX 27-FEB-2003.
 PD
 XX 14-AUG-2002; 2002WO-US025765.
 PF
 XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 DR GENBANK; NP_071983.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 282 AA;
 Query Match 54.8%; Score 40; DB 7; Length 282;
 Best Local Similarity 46.2%; Pred. No. 2.4e+02;
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 NYRCRGDDSKVOE 13
 Db 150 NFVQCQNEQKRE 162
 RESULT 28
 ADD45532
 ID ADD45532 standard; protein; 282 AA.
 XX
 AC ADD45532;
 XX
 XX 29-JAN-2004 (first entry)
 DT Rat Protein NP_071983, SEQ ID NO 11196.
 XX
 DE Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 KW

ADS27091
ID ADS27091 standard; protein; 301 AA.
XX AC ADS27091;
XX DT 02-DEC-2004 (first entry)
XX DE Bacterial polypeptide #16124.
XX KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX OS Bacteria.
XX PN US2003233675-A1.
XX PD 19-DEC-2003.
XX PF 20-FEB-2003; 2003US-00369493.
XX PR 21-FEB-2002; 2002US-0360039P.
XX PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX PS Claim 1; SEQ ID NO 16124; 122pp; English.
XX CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX SQ Sequence 301 AA;
Query Match 54.8%; Score 40; DB 8; Length 301;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 CRGDSKVOE 13
DB 200 CRGDDARIHD 209
RESULT 31
ADS26338
ID ADS26338 standard; protein; 302 AA.
XX AC ADS26338;
XX DT 02-DEC-2004 (first entry)
XX DE Bacterial polypeptide #15371.
XX KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX OS Bacteria.
XX PN US2003233675-A1.
XX PD 18-DEC-2003.
XX PF 20-FEB-2003; 2003US-00369493.
XX PR 21-FEB-2002; 2002US-0360039P.
XX PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX PS Claim 1; SEQ ID NO 15371; 122pp; English.
XX CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic

CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 302 AA;

Query Match 54.8%; Score 40; DB 8; Length 302;

Best Local Similarity 50.0%; Pred. No. 2.5e+02;

Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 CRGDDSKVOE 13

|||||:::;

Db 203 CRGDDARIHD 212

RESULT 32

ABU31582

ID ABU31582 standard; protein; 400 AA.

XX AC ABU31582;

XX DT 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #17109.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX OS Klebsiella pneumoniae.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyekind JW;

XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX DR WPI; 2003-029926/02.

XX DR N-PSDB; ACA35452.

XX PT New antisense nucleic acids, useful for identifying proteins or screening

for homologous nucleic acids required for cellular proliferation to

isolate candidate molecules for rational drug discovery programs.

XX PS Claim 25; SEQ ID NO 59506; 1766pp; English.

XX CC The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid
encoding a polypeptide whose expression is inhibited by the antisense
nucleic acid; (2) a host cell containing the vector; (3) an isolated
polypeptide or its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
proliferation or the activity of a gene in an operon required for

CC proliferation; (7) identifying a compound that influences the activity of
the gene product or that has an activity against a biological pathway
required for proliferation, or that inhibits cellular proliferation; (8)
identifying a gene required for cellular proliferation or the biological
pathway in which a proliferation-required gene or its gene product lies
or a gene on which the test compound that inhibits proliferation of an
organism acts; (9) manufacturing an antibiotic; (10) profiling a
compound's activity; (11) a culture comprising strains in which the gene
product is overexpressed or underexpressed; (12) determining the extent
to which each of the strains is present in a culture or collection of

CC strains; or (13) identifying the target of a compound that inhibits the
proliferation of an organism. The antisense nucleic acids are useful for
identifying proteins or screening for homologous nucleic acids required
for cellular proliferation to isolate candidate molecules for rational
drug discovery programs, or for screening homologous nucleic acids
required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
K. pneumoniae or *P. aeruginosa*. The present sequence is encoded by one of
the target prokaryotic essential genes. Note: The sequence data for this
patent did not form part of the printed specification, but was obtained
in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 400 AA;

Query Match 54.8%; Score 40; DB 6; Length 400;

Best Local Similarity 85.7%; Pred. No. 3.4e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8

:|||||

Db 39 FRCRGDD 45

RESULT 33

ABU45262

ID ABU45262 standard; protein; 400 AA.

XX AC ABU45262;

XX DT 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #30789.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX OS Salmonella paratyphi.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyekind JW;

XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX DR WPI; 2003-029926/02.

XX DR N-PSDB; ACA49132.

XX PT New antisense nucleic acids, useful for identifying proteins or screening
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.

XX PS Claim 25; SEQ ID NO 73186; 1766pp; English.

XX CC The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
encoding a polypeptide whose expression is inhibited by the antisense
nucleic acid; (2) a host cell containing the vector; (3) an isolated
polypeptide or its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
proliferation or the activity of a gene in an operon required for

CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 400 AA;

Query Match 54.8%; Score 40; DB 6; Length 400;
 Best Local Similarity 85.7%; Pred. No. 3.4e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
 :|||||
 Db 39 FRCRGDD 45

RESULT 34
 ABU48051
 ID ABU48051 standard; protein; 400 AA.
 XX
 AC ABU48051;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #33578.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Salmomella typhi.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US0009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-0299926/02.
 DR N-PSDB; ACA51921.
 DR
 XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 75975; 1766pp; English.
 XX

CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 400 AA;

Query Match 54.8%; Score 40; DB 6; Length 400;
 Best Local Similarity 85.7%; Pred. No. 3.4e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
 :|||||
 Db 39 FRCRGDD 45

RESULT 35
 ABU15369
 ID ABU15369 standard; protein; 400 AA.
 XX
 AC ABU15369;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #896.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Escherichia coli.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US0009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.
 DR N-PSDB; ACA19239.
 XX
 XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 FT isolate candidate molecules for rational drug discovery programs.
 XX
 XX Claim 25; SEQ ID NO 43293; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway;
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 400 AA;
 SQ
 Query Match 54.8%; Score 40; DB 6; Length 400;
 Best Local Similarity 85.7%; Pred. No. 3.4e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 YRCRGDD 8
 Db :|||||
 39 FRCRGDD 45
 RESULT 36
 ID ABO65513 standard; protein; 424 AA.
 XX ABO65513;
 AC ABO65513;
 XX
 XX 29-JUL-2004 (first entry)
 DT
 XX Klebsiella pneumoniae polypeptide segid 12030.
 DE
 XX Recombinant expression vector; transcription regulatory element;
 KW Klebsiella pneumoniae protein; antibacterial; Vaccine.
 KW
 XX Klebsiella pneumoniae.
 OS
 XX US6610836-B1.
 PN
 XX 26-AUG-2003.
 PD
 XX 27-JAN-2000; 2000US-00489039.
 PF

XX 29-JAN-1999; 99US-0117747P.
 PR (GENO-) GENOME THERAPEUTICS CORP.
 PA
 XX Breton GL, Osborne M;
 FI
 XX WPI; 2003-895346/82.
 DR N-PSDB; ACH99064.
 DR
 XX New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
 PT preparing a vaccine composition against Klebsiella pneumoniae.
 FT
 XX Disclosure; SEQ ID NO 12030; 932pp; English.
 PS
 CC The invention describes a new isolated nucleic acid encoding a Klebsiella
 CC pneumoniae polypeptide. Also described are: a recombinant expression
 CC vector comprising the nucleic acid, operably linked to a transcription
 CC regulatory element; and a cell comprising the recombinant expression
 CC vector. The nucleic acid is useful for preparing a vaccine composition
 CC against Klebsiella pneumoniae. This is the amino acid sequence of a
 CC Klebsiella pneumoniae polypeptide of the invention
 XX
 XX Sequence 424 AA;
 SQ
 Query Match 54.8%; Score 40; DB 7; Length 424;
 Best Local Similarity 85.7%; Pred. No. 3.6e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 YRCRGDD 8
 Db :|||||
 63 FRCRGDD 69
 RESULT 37
 ID ABO65513 standard; protein; 1299 AA.
 XX ABO65513;
 AC ABO65513;
 XX
 XX 22-APR-2003 (first entry)
 DT
 XX Plasmodium yoelii modular secreted protein PySR.
 DE
 XX PfSR; protein secretion; malaria; diagnosis; vaccine; antimalarial;
 KW protozoacide.
 KW
 XX Plasmodium yoelii.
 OS
 XX Key Location/Qualifiers
 FH Peptide 1..22
 FT /label= signal_peptide
 FT Protein 23..2399
 FT /label= Mature_protein
 FT Misc-difference 175
 FT /note= "encoded by ATK"
 XX
 XX WO2003004524-A2.
 PN
 XX 16-JAN-2003.
 PD
 XX 02-JUL-2002; 2002WO-GB003045.
 PF
 XX 02-JUL-2001; 2001GB-00016185.
 PR
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 PA
 XX Claudianos C, Crompton TK, Dessens JT, Sinden RE, Trueman HF;
 PI
 XX WPI; 2003-210339/20.
 DR N-PSDB; ABZ58198.
 DR
 XX New secreted proteins from malarial parasites (e.g. Plasmodium
 FT

PR 20-OCT-2000; 2000US-02411786P.
 PR 20-OCT-2000; 2000US-02411787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 20-OCT-2000; 2000US-0241826P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246612P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 01-DEC-2000; 2000US-0250100P.
 PR 01-DEC-2000; 2000US-0250101P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Barash SC, Ruben SM;
 PI
 XX WPI; 2001-451937/48.
 DR N-PSDB; AAL35678.
 XX

PT Isolated polypeptide for treating, preventing and/or prognosing
 PT disorders related to the musculoskeletal system including musculoskeletal
 PT cancers and also for testing and detection e.g. diagnosis.
 XX
 XX Claim 11; SEQ ID NO 2043; 781pp + Sequence Listing; English.
 XX
 XX The invention relates to novel genes (AAL34669-AAL37666) and proteins
 CC (ABB03087-ABB04109) associated with the musculoskeletal system useful for
 CC preventing, treating or ameliorating medical conditions e.g. by protein
 CC or gene therapy. The genes are isolated from a range of human tissues
 CC disclosed in the specification. The nucleic acids, proteins, antibodies

CC and (ant)agonists are useful in the diagnosis, treatment and prevention
 CC of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the
 CC adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,
 CC lung, or urogenital; (b) immune disorders e.g. Addison's disease,
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
 CC arthritis and ulcerative colitis; (c) cardiovascular disorders such as
 CC myocardial ischaemia; (d) wound healing; (e) neurological diseases e.g.
 CC cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,
 CC bacterial, fungal and parasitic infections. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIFO at
 CC ftp.wifo.int/pub/published_pct_sequences
 XX
 XX Sequence 74 AA;
 SQ
 Query Match 53.4%; Score 39; DB 4; Length 74;
 Best Local Similarity 63.6%; Pred. No. 87;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 3 RCRGDSKVQE 13
 Db 23 RCRGDSRSQE 33
 RESULT 39
 ABUI3390
 ID ABUI3390 standard; protein; 74 AA.
 XX
 AC ABUI3390;
 XX
 DT 26-FEB-2003 (first entry)
 XX
 DE Novel human musculoskeletal system antigen #1010.
 XX
 KW Musculoskeletal system antigen; cancer; metastasis; re-vascularisation;
 KW thrombosis; arteriosclerosis; mineral content; cardiovascular condition;
 KW wound; injury; burn; angiogenesis; ulcer; post-operative tissue repair;
 KW limb regeneration; neuronal growth; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; AIDS-related complex;
 KW chondrocyte growth; bone regeneration; periodontal regeneration;
 KW tissue transport; bone graft; skin aging; keratinocyte growth; hair loss;
 KW melanocyte growth; cell proliferation; cell growth; organ transplant;
 KW cell differentiation; body height; weight; hair colour; eye colour; skin;
 KW percentage of adipose tissue; pigmentation; cosmetic surgery; metabolism;
 KW biohythm; cardiac rhythm; depression; tendency for violence; pain;
 KW reproductive capability; hormone level; endocrine level; appetite;
 KW libido; memory; stress; storage capability; fat content; lipid content;
 KW protein content; carbohydrate content; vitamin content; cofactor content;
 KW nutritional component.
 OS Homo sapiens.
 XX
 XX US2002147140-A1.
 PN
 XX 10-OCT-2002.
 PD
 XX
 XX 17-JAN-2001; 2001US-00764877.
 PF
 XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216809P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 22-AUG-2000; 2000US-0225758P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 08-SEP-2000; 2000US-0231413P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 27-SEP-2000; 2000US-0235834P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 17-NOV-2000; 2000US-0249299P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.

XX (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.

XX Rosen CA, Ruben SM, Barash SC;
XX WPI; 2003-128199/12.

XX Isolated nucleic acid molecules encoding musculoskeletal system
PT associated polypeptides, useful for detecting disorders, e.g. cancer.
XX Disclosure; SEQ ID NO 2043; 321pp; English.

CC The invention describes an isolated nucleic acid molecule comprising a
CC sequence encoding musculoskeletal system associated polypeptides useful
CC for detecting disorders, e.g., cancer or cancer metastases, in animals or
CC humans. The nucleic acid; stimulates re-vascularisation of ischaemic
CC tissues associated with conditions such as thrombosis, arteriosclerosis,
CC and other cardiovascular conditions; treats wounds due to injuries,
CC burns, post-operative tissue repair, and ulcers; stimulates angiogenesis
CC and limb regeneration; stimulates neuronal growth; can treat and prevent
CC neuronal damage occurring in certain disorders or neurodegenerative
CC conditions, such as, Alzheimer's disease, Parkinson's disease, and AIDS-
CC related complex; stimulates chondrocyte growth, thus they can be used to
CC enhance bone and periodontal regeneration and aid in tissue transports or
CC bone grafts; prevents skin aging due to sunburn by stimulating
CC keratinocyte growth; prevents hair loss, since RGF family members
CC activate hair-forming cells and promotes melanocyte growth; stimulates
CC growth and differentiation of hematopoietic cells and bone marrow cells
CC when used in combination with other cytokines; maintains organs before
CC transplantation or for supporting cell culture of primary tissues;
CC induces tissue of mesodermal origin to differentiate in early embryos;
CC increases or decreases the differentiation or proliferation of embryonic
CC stem cells, besides, haematopoietic lineage; modulates mammalian
CC characteristics, such as, body height, weight, hair colour, eye colour,
CC skin, percentage of adipose tissue, pigmentation, size, and shape (e.g.,

CC cosmetic surgery); modulates mammalian metabolism; changes mammal's metal
CC state or physical state by influencing biorhythms, cardiac rhythms,
CC depression, tendency for violence, tolerance for pain, reproductive
CC capabilities, hormonal or endocrine levels, appetite, libido, memory, or
CC stress; increases or decreases storage capabilities, fat content, lipid,
CC protein, carbohydrate, vitamins, minerals, cofactors or other nutritional
CC components. This is the amino acid sequence of a novel human
CC musculoskeletal system antigen. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from the US patent office at
XX ftp.seqdata.uspto.gov/sequence.html?DocID=20020147140

XX Sequence 74 AA;

Query Match 53.4%; Score 39; DB 6; Length 74;
Best Local Similarity 63.6%; Pred. No. 87;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 RCRGDDSKVQE 13
Db 23 RCGRDSRSQ 33
||:|:|:|:
||:|:|:|:

RESULT 40

ADJ29416

ID ADJ29416 standard; protein; 74 AA.

XX ADJ29416;

XX 20-MAY-2004 (first entry)

DE Human musculoskeletal system-associated protein - SEQ ID 2043.

XX musculoskeletal system; cytostatic; osteopathic; cancer; osteoporosis;
XX gene therapy; vaccine; human.

XX Homo sapiens.

XX US2004009488-A1.

XX 15-JAN-2004.

XX 13-SEP-2002; 2002US-00242515.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225477P.

PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.

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PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234998P.
PR 25-SEP-2000; 2000US-0234999P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241807P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-00764877.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Barash SC;
PI WPI; 2004-090458/09.
DR N-PSDB; ADJ28393.
XX
PT New nucleic acid molecule, useful for preparing a medicament for
PT preventing, treating or ameliorating a medical condition e.g., cancer of
PT musculoskeletal tissues or osteoporosis.
XX Claim 11; SEQ ID NO 2043; 289pp; English.
XX The invention relates to a novel isolated musculoskeletal system-
XX associated nucleic acid molecule. The nucleic acid of the invention
XX demonstrates cytostatic and osteopathic activities and may be useful for
XX preparing a medicament for preventing, treating or ameliorating a medical
XX condition such as cancer of the musculoskeletal tissues or osteoporosis,
XX possibly via gene therapy or vaccine production. The current sequence is
XX that of the human musculoskeletal system-associated polypeptide of the
XX invention. The current sequence is not shown within the specification per
XX se but is available on the USPTO web-site
XX http:seqdata.uspto.gov/sequence.html?DocID=20040009488.
SQ Sequence 74 AA;
Query Match 53.4%; Score 39; DB 8; Length 74;
Best Local Similarity 63.6%; Pred. No. 87;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 3 RCRGDSKVQE 13
|||: |||: ||
Db 23 RCQGRDSRSQE 33
RESULT 41
ADE61256
```

ID ADE61256 standard; protein; 283 AA.
AC ADE61256;
XX
XX 29-JAN-2004 (first entry)
XX
XX Rat Protein BAA12335, SEQ ID NO 7174.
XX
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
XX Rattus norvegicus.
XX
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
PA
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI: 2003-268312/26.
DR GENBANK; BAA12335.
DR
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
PT
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC the sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 283 AA;
SQ
Query Match 53.4%; Score 39; DB 7; Length 283;
Best Local Similarity 46.2%; Pred. No. 3.5e+02;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 1 NYRCRGDSKVQE 13
Db 150 DYICQNEKVKVE 162

RESULT 42
ADR41635
ID ADR41635 standard; protein; 305 AA.
XX
XX ADR41635;
AC
XX 21-OCT-2004 (first entry)
DT
XX
XX Lipid acyltransferase, SEQ ID 28.
DE
XX
XX Antimicrobial; fungicide; herbicide; insecticide; cytostatic;
KW carbohydrate ester; protein ester; hydroxy acid ester;
KW lipid acyltransferase; enzyme; pharmaceutical; cosmetic; foodstuff;
KW paint.
XX
XX Streptomyces coelicolor A3(2).
OS
XX
XX WO2004064987-A2.
PN
XX
XX 05-AUG-2004.
PD
XX
XX 15-JAN-2004; 2004WO-IB000575.
PF
XX
XX 17-JAN-2003; 2003GB-00001117.
PR 17-JAN-2003; 2003GB-00001118.
PR 17-JAN-2003; 2003GB-00001119.
PR 17-JAN-2003; 2003GB-00001120.
PR 17-JAN-2003; 2003GB-00001121.
PR 17-JAN-2003; 2003GB-00001122.
PR 23-JUL-2003; 2003US-0489441P.
PR 24-DEC-2003; 2003GB-00030016.
XX
XX (DANI-) DANISCO AS.
XX
XX Kreij AD, Madrid SM, Mikkelsen JD, Soe JB;
PI
XX WPI; 2004-593357/57.
XX N-PSDB; ADR41636.
XX
XX Producing carbohydrate ester, protein ester, hydroxy acid ester, by
PT admixing acyl donor e.g., phospholipid, acyl acceptor e.g., carbohydrate,
PT contacting admixture with lipid acyltransferase for alcoholysis or
PT transesterification reaction.
XX
XX Claim 7; Fig 24; 157pp; English.
XX
XX The present invention relates to a method (M1) for producing one or more
CC of a carbohydrate ester, protein ester, protein subunit ester or a
CC hydroxy acid ester. (M1) involves admixing an acyl donor, an acyl
CC acceptor and water, where the acyl donor is a lipid substrate chosen from
CC phospholipid and glycolipid, and acyl acceptor is chosen from
CC carbohydrate, and protein, and contacting the admixture with lipid
CC acyltransferase, such that the lipid acyltransferase catalyses one or
CC both of the alcoholysis or transesterification reactions. The lipid
CC acyltransferase comprises the amino acid sequence motif ADR41663. (M1)
CC enables bioconversion of lipids to form one or more of a carbohydrate
CC ester, protein ester, protein subunit ester or hydroxy acid ester, in a
CC high water environment, which comprises no organic solvent or a reduced
CC amount of organic solvent. The lipid acyltransferases have unique
CC properties when compared to lipolytic enzymes in that they have a marked
CC preference for transfer of acyl groups from lipids to acceptors other
CC than water, even in the presence of significant water. (M1) enables
CC production of esters at reduced cost, reduced human and/or environmental
CC exposures to organic solvents, and simplification of the production
CC process. The carbohydrate ester, protein ester, protein subunit ester or
CC hydroxy acid ester produced by (M1) is useful in pharmaceutical,
CC cosmetic, foodstuff, feedstuff and paint. The esters produced by (M1) are
CC functionally important and useful emulsifiers that are used in food
CC industry, feed industry, cosmetics industry (for e.g., in cosmetic bases)
CC and pharmaceutical industry. The emulsifiers are useful as wetting
CC agents, food ingredients and active ingredients. The esters produced by

CC (M1) are useful in personal hygiene products. The protein esters of (M1)
 CC are useful in shower and bath preparations and in shampoos and body
 CC cleansers. The protein-fatty acid condensates produced by (M1) form a
 CC protective layer on the skin, which reduces the excessive attack of
 CC surfactants on the upper layer of the skin, their strong degreasing
 CC effect and the direct interaction of anionic surfactants with the skin.
 CC The carbohydrate esters produced by (M1) are useful in oral-care
 CC products, as antibiotics, antitumorals, fungicides and insecticides. The
 CC esters produced by (M1) are useful in cosmetics including essential oil
 CC emulsions, paraffin oil emulsions, pharmaceutical preparations including
 CC drug emulsions, ointment bases, agricultural including cleaners for fruit
 CC and vegetables, crop protection including insecticides and herbicides,
 CC and food industry including bread, cakes, chocolate, margarine, custard
 CC powder, and in drinks industry. The present sequence is one such lipid
 CC acyltransferase, used in the method of the invention.

XX SQ Sequence 305 AA;

Query Match 53.4%; Score 39; DB 8; Length 305;
 Best Local Similarity 63.6%; Pred. No. 3.7e+02;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 RCRGDSKVQE 13
 |||||
 Db 258 RCRSDDGAVHE 268

RESULT 43
 ADR41585
 ID ADR41585 standard; protein; 305 AA.

XX AC ADR41585;

XX DT 21-OCT-2004 (first entry)

XX DE Lipid acyltransferase, SEQ ID 28.

XX KW Antiarteriosclerotic; Cardiant; Antilipemic; cholesterol; lipoprotein;
 KW emulsifier; foodstuff; lipid acyltransferase; enzyme;
 KW blood serum cholesterol; low density lipoprotein; atherosclerosis;
 KW heart disease.

XX OS Streptomyces coelicolor A3(2).

XX PN WO2004064537-A2.

XX PD 05-AUG-2004.

XX PF 15-JAN-2004; 2004WO-IB000655.

XX PR 17-JAN-2003; 2003GB-00001117.

XX PR 17-JAN-2003; 2003GB-00001118.

XX PR 17-JAN-2003; 2003GB-00001119.

XX PR 17-JAN-2003; 2003GB-00001120.

XX PR 17-JAN-2003; 2003GB-00001121.

XX PR 17-JAN-2003; 2003GB-00001122.

XX PR 23-JUL-2003; 2003US-048941P.

XX PR 24-DEC-2003; 2003GB-00030016.

XX PA (DANI-) DANISCO AS.

XX PI De Kreij A, Madrid SM, Mikkelsen JD, Soe JB;

XX DR WPI; 2004-593271/57.

XX DR N-PSDB; ADR41586.

XX PT In situ production of emulsifier in foodstuffs, involves addition of
 PT lipid acyltransferase to foodstuff.

XX PS Claim 13; Fig 24; 257pp; English.

XX CC The present invention relates to a method (M1) for the in situ production
 CC of an emulsifier in a foodstuff, wherein a lipid acyltransferase (I) is

CC added to the foodstuff. (I) enables in situ emulsifier production,
 CC without increasing or without substantially increasing the free fatty
 CC acid in the foodstuffs. (I) also produces foodstuffs having improved
 CC appearance, stability, thermal stability, taste, softness, resilience and
 CC emulsification. (I) comprises the motif ADR41613. (M1) or (I) is useful
 CC for in situ production of an emulsifier in a foodstuff. (I) is useful for
 CC preparing a foodstuff (e.g., egg-based products, salad dressings sauces,
 CC ice creams, egg powder, modified egg yolk or bread) which in turn is
 CC useful for reducing blood serum cholesterol and/or to reduce low density
 CC lipoprotein, or for treating and/or preventing atherosclerosis and/or
 CC heart disease. (I) is useful for preparing medicament, flavouring agent
 CC and/or texturizer. (I) is useful for producing acylated proteins,
 CC cosmetic composition or food or feed enzyme composition. The present
 CC sequence is one such lipid acyltransferase used to illustrate the
 CC invention.

XX SQ Sequence 305 AA;

Query Match 53.4%; Score 39; DB 8; Length 305;
 Best Local Similarity 63.6%; Pred. No. 3.7e+02;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 RCRGDSKVQE 13
 |||||
 Db 258 RCRSDDGAVHE 268

RESULT 44
 ADR48160
 ID ADR48160 standard; protein; 393 AA.

XX AC ADR48160;

XX DT 01-JUL-2004 (first entry)

XX DE Thermococcus kodakaraensis KOD1 protein sequence SeqID2038.

XX KW gene disruption; gene targeting; marker gene; transformation;
 KW homologous recombination; hyperthermostable archaeobacterium; KOD1;
 KW gene structure; gene function; enzyme activity; medicine; immunology.
 KW forensic science; food; drug inspection; molecular biology; immunology.

XX OS Thermococcus kodakaraensis.

XX PN WO2004022736-A1.

XX PD 18-MAR-2004.

XX PF 29-AUG-2003; 2003WO-IB003597.

XX PR 30-AUG-2002; 2002JP-00319011.

XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX PI Imanaka T, Atomi H;

XX DR WPI; 2004-257583/24.

XX PT Method for disrupting targeted gene in genome of organism particularly
 PT thermostable bacterium and with genome chips for analysis, applicable in
 PT studying gene structure and functions.

XX PS Claim 9; SEQ ID NO 2038; 598pp; Japanese.

XX CC This invention relates to a novel method for targeting disruption of an
 CC arbitrary gene in a genome of an organism which comprises providing the
 CC whole sequential data of the genome of such organism, selecting at least
 CC 1 arbitrary region in the sequence, providing a vector that contains a
 CC sequence homologous with the selected region and a marker gene,
 CC transformation, and homologous recombination. The genome is preferably
 CC the genome of a hyperthermostable archaeobacterium, particularly
 CC Thermococcus kodakaraensis KOD1. The method is for targeting the
 CC disruption of a gene in the genome of an organism, which is applicable in

CC studying gene structure and functions as well as enzyme activities of
CC encoded proteins and useful in medicine, forensic science, food or drug
CC inspection, molecular biology and immunology. With this method, the
CC disruption of a gene at an arbitrary position in a genome can be achieved
CC efficiently and reliably. The present sequence is that of a protein
CC encoded by the genome of *Thermococcus kodakaraensis* which was derived
CC using the method of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 393 AA;
SQ

Query Match 53.4%; Score 39; DB 8; Length 393;
Best Local Similarity 53.8%; Pred. No. 4.8e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 NYRCRGDDSKVQ 13
DB 279 STRAGDDKATQE 291

RESULT 45
ADG33762
ID ADG33762 standard; protein; 461 AA.
XX AC ADG33762;
XX
XX 26-FEB-2004 (first entry)
XX
XX Actinomycetes dual condensation/epimerisation NRPS domain protein ID 21.
XX
XX non-ribosomal peptide synthetase; NRPS; dual condensation; epimerisation;
KW ramoplanin; complestatin; actinomycetes taxon.
XX
XX *Pseudomonas syringae* pv. *syringae*.
XX
XX WO2003089641-A2.
XX
XX 30-OCT-2003.
XX
XX 17-APR-2003; 2003WO-CA000575.
XX
XX 17-APR-2002; 2002US-0372790P.
PR
XX (ECOP-) ECOPIA BIOSCIENCES INC.
XX
XX Farnet CM, Staffa A;
XX
XX WPI; 2003-854123/79.
DR
XX N-PSDB; ADG33763.
XX
XX New dual condensation/epimerization non-ribosomal peptide synthetase
PT domain and encoding polynucleotide, useful for modifying the
PT stereochemistry of synthesized peptides (e.g. ramoplanin or complestatin)
PT in vitro or in vivo.
XX
XX Claim 9; SEQ ID NO 21; 245pp; English.
XX
XX This invention relates to novel domains of non-ribosomal peptide
CC synthetases (NRPSs) that exhibit dual condensation and epimerisation
CC activities. Specifically, these domains allow incorporation of non-
CC proteinogenic substrates (e.g. D-amino acids) into peptide products.
CC Furthermore, they can be used in vivo to modify the stereochemistry of
CC synthesized peptides (e.g. ramoplanin or complestatin) at selected amino
CC acid sites by the addition of non-chiral residues. The present invention
CC describes the identification of isolated polynucleotide NRPS domains in
CC various organisms from the actinomycetes taxon, and the encoded
CC polypeptides thereof, as well as suitable expression vectors. This
CC polypeptide sequence is a dual condensation/ epimerisation NRPS domain
CC protein of the invention.
XX
XX Sequence 461 AA;
SQ

Query Match 53.4%; Score 39; DB 7; Length 461;
Best Local Similarity 50.0%; Pred. No. 5.7e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDDSKVQ 12
DB 341 NYRHQGDNRILQ 352

RESULT 46
ADS44300
ID ADS44300 standard; protein; 690 AA.
XX AC ADS44300;
XX
XX 02-DEC-2004 (first entry)
XX
XX Bacterial polypeptide #22730.
XX
XX Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; omeosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomanan;
KW bacterial polypeptide.
XX
XX Bacteria.
XX
XX US2003233675-A1.
XX
XX 18-DEC-2003.
XX
XX 20-FEB-2003; 2003US-00369493.
XX
XX 21-FEB-2002; 2002US-0360039P.
XX
XX (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 22730; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content. Improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC

CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 690 AA;

SQ Query Match 53.4%; Score 39; DB 8; Length 690;

Best Local Similarity 80.0%; Pred. No. 8.6e+02;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 RCRGDDSKVQ 12

Db 561 RVRGDDSDVQ 570

RESULT 47

ADD46237

ID ADD46237 standard; protein; 1269 AA.

XX ADD46237;

XX 29-JAN-2004 (first entry)

XX Rat Protein U49055, SEQ ID NO 11912.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;

XX Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX Rattus norvegicus.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GENO) GEN HOSPITAL CORP.

XX (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

XX GENBANK; U49055.

XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more

CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1269 AA;

SQ Query Match 52.7%; Score 38.5; DB 7; Length 1269;

Best Local Similarity 72.7%; Pred. No. 2e+03;

Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 2 YRCRGDD-SKV 11

Db 100 YRCPGDDSKI 110

RESULT 48

ADD46239

ID ADD46239 standard; protein; 1272 AA.

XX AC ADD46239;

XX 29-JAN-2004 (first entry)

XX Human Protein AB029039, SEQ ID NO 11914.

XX Human; pain; neuronal tissue; gene therapy;

XX spinal segmental nerve injury; chronic constriction injury; CCI;

XX spared nerve injury; SNI; Chung.

XX Homo sapiens.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GENO) GEN HOSPITAL CORP.

XX (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

XX GENBANK; AB029039.

XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the

CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNII) in an animal (e.g. gene
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 1272 AA;
 Query Match 52.7%; Score 38.5; DB 7; Length 1272;
 Best Local Similarity 72.7%; Pred. No. 2e+03;
 Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
 QY 2 YRCRGDD-SKV 11
 ||| |||
 Db 100 YRCFGDDSKI 110

RESULT 49
 AAU60236
 ID AAU60236 standard; protein; 84 AA.
 AC AAU60236;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DE Propionibacterium acnes immunogenic protein #21132.
 XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.

XX
 OS Propionibacterium acnes.
 XX
 PN WO200181581-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 20-APR-2001; 2001WO-US012865.
 XX
 PR 21-APR-2000; 2000US-0199047P.
 PR 02-JUN-2000; 2000US-0208841P.
 PR 07-JUL-2000; 2000US-0216747P.
 XX
 XX (CORI-) CORIXA CORP.

XX
 PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'Maisonneuve J, Zhang Y, Jen S, Carter D;
 XX
 DR WPI; 2001-616774/71.
 DR N-PSDB; AAS59608.
 XX
 PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris.

PS Example 1; SEQ ID NO 21431; 1069pp; English.
 XX
 CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central

CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 84 AA;
 Query Match 52.1%; Score 38; DB 4; Length 84;
 Best Local Similarity 38.5%; Pred. No. 1.5e+02;
 Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 1 NYRCRGDDSKVQ 13
 :| |||: :|:
 Db 36 HYACRGEGVRIQD 48

RESULT 50
 ABM56755
 ID ABM56755 standard; protein; 84 AA.
 XX
 AC ABM56755;
 XX
 DT 20-OCT-2003 (first entry)
 XX
 DE Propionibacterium acnes predicted ORF-encoded polypeptide #21431.
 XX
 KW Acne vulgaris; antiseborrheic; dermatological; antibacterial;
 KW immunostimulant; immune response; vaccine.

XX
 OS Propionibacterium acnes.
 XX
 PN WO2003033515-A1.
 XX
 PD 24-APR-2003.
 XX
 PF 11-OCT-2002; 2002WO-US032727.
 XX
 PR 15-OCT-2001; 2001US-00978825.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
 PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
 PI Barth B, Vallieue-Douglas J;
 XX
 DR WPI; 2003-381789/36.
 DR N-PSDB; ACF64537.

XX
 PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX
 PS Example 1; SEQ ID NO 21431; 1481pp; English.

XX
 CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC polynucleotide of the invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared

CC via this method; a vaccine composition (comprising P. acnes polypeptides,
CC polynucleotides, antibodies, fusion proteins, T cell populations, or
CC antigen-presenting cells that express the polypeptide); a method and kit
CC for detecting or determining the presence or absence of P. acnes in a
CC patient; and a method for inhibiting the development of P. acnes in a
CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations or antigen-presenting cells that express the
CC polypeptides are useful for diagnosing, preventing or treating acne
CC vulgaris, or for stimulating an immune response specific for a P. acnes
CC protein. The polynucleotides can also be used as probes or primers for
CC nucleic acid hybridisation. The vaccine composition is useful for the
CC stimulation of an immune response against P. acnes, or for treating acne,
CC and the kit is useful for performing a diagnostic assay. The present
CC sequence represents a polypeptide predicted to be encoded by an ORF (open
CC reading frame) contained within the P. acnes polynucleotides of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 84 AA;

Query Match 52.1%; Score 38; DB 6; Length 84;
Best Local Similarity 38.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 NYRCRGDSKVQE 13
:| |||: :|:
Db 36 HYACRGEGVRIQD 48

Search completed: September 7, 2005, 19:55:12
Job time : 109.721 secs

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OM protein - protein search, using sw model

Run on: September 7, 2005, 19:49:10 ; Search time 9.97674 Seconds
(without alignments)
125.373 Million cell updates/sec

Title: US-10-812-238B-23

Perfect score: 73

Sequence: 1 NYRCRDDSKEVQE 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	60.3	504	2 C64398	hypothetical prote
2	44	60.3	705	2 A70669	probable acid-CoA
3	42	57.5	513	2 B87484	anthranilate synth
4	40	54.8	150	2 G83840	ferric uptake regu
5	40	54.8	179	2 T22521	hypothetical prote
6	40	54.8	303	2 T29321	hypothetical prote
7	40	54.8	400	1 A39130	nicotinate phospho
8	40	54.8	400	1 JQ0756	nicotinate phospho
9	40	54.8	400	2 AB0617	nicotinate phospho
10	40	54.8	400	2 P90755	nicotinate phospho
11	40	54.8	400	2 D85619	nicotinate phospho
12	40	54.8	577	2 T18646	hypothetical prote
13	40	54.8	721	2 H82528	L-ascorbate oxidas
14	39	53.4	280	2 T43011	suppressor protein
15	39	53.4	325	2 S66668	hydrogen peroxide-
16	39	53.4	507	2 AD3382	ABC transporter-as
17	39	53.4	662	2 T41442	omnipotent nonsens
18	39	53.4	662	2 T51948	omnipotent nonsens
19	39	53.4	9376	2 T14593	synergomycin synth
20	38.5	52.7	1268	2 T31420	C-terminal domain-
21	38	52.1	172	2 F81439	translation initia
22	38	52.1	389	2 T27085	hypothetical prote
23	38	52.1	1071	2 E85343	hypothetical prote
24	38	52.1	1267	1 MWXR31	lambda 3 protein -
25	38	52.1	1267	1 MWXR32	lambda 3 protein -
26	38	52.1	1267	1 MWXR33	lambda 3 protein -
27	38	52.1	2212	2 T28157	erythrocyte membra
28	38	52.1	2647	2 T28161	hypothetical prote
29	38	52.1	3228	2 T21381	hypothetical prote

30	37	50.7	185	2 H87107	ribosome recycling
31	37	50.7	258	2 T21959	hypothetical prote
32	37	50.7	324	2 H86244	lysophospholipase
33	37	50.7	410	2 T21960	hypothetical prote
34	37	50.7	430	2 S75313	serine-tRNA ligase
35	37	50.7	489	2 C87480	conserved hypotet
36	37	50.7	518	2 T19133	hypothetical prote
37	37	50.7	564	2 T19132	hypothetical prote
38	37	50.7	801	2 A89862	Na+/H+ antiporter
39	37	50.7	873	2 T19131	hypothetical prote
40	37	50.7	988	2 F86316	protein T10022.13
41	37	50.7	1030	2 F96763	hypothetical prote
42	36	49.3	138	2 C90460	hypothetical prote
43	36	49.3	180	2 AC3270	hypothetical expor
44	36	49.3	248	2 F64908	probable dehydroge
45	36	49.3	248	2 D90897	probable oxidoredu
46	36	49.3	248	2 C85720	probable oxidoredu
47	36	49.3	329	2 T20546	hypothetical prote
48	36	49.3	347	2 T35013	probable membrane
49	36	49.3	411	2 H72494	hypothetical prote
50	36	49.3	435	2 A46206	voltage-gated sodi
51	36	49.3	461	1 E69360	4-hydroxyphenylac
52	36	49.3	470	2 E72376	hypothetical prote
53	36	49.3	644	2 B72559	probable arginyl-t
54	36	49.3	707	2 F86925	probable acyl-CoA
55	36	49.3	752	1 P1IVBC	RNA-directed RNA p
56	36	49.3	752	1 P1IVBL	RNA-directed RNA p
57	36	49.3	752	1 P1IVBW	RNA mismatch repai
58	36	49.3	822	2 S77112	DNA mismatch repai
59	36	49.3	1812	2 I49350	breast/ovarian can
60	35	47.9	187	2 A10520	AmpD protein (anhy
61	35	47.9	200	2 T02826	ribosomal protein
62	35	47.9	269	2 A46506	leukocyte activati
63	35	47.9	274	2 T32736	hypothetical prote
64	35	47.9	342	2 T45577	protein kinase-lik
65	35	47.9	346	2 T49085	hypothetical prote
66	35	47.9	347	2 B72596	hypothetical prote
67	35	47.9	392	2 A86252	hypothetical prote
68	35	47.9	422	2 S34199	polygalacturonase
69	35	47.9	435	2 T32195	hypothetical prote
70	35	47.9	453	2 T24127	probable chitinase
71	35	47.9	471	2 S09110	hypothetical prote
72	35	47.9	482	2 H71400	hypothetical prote
73	35	47.9	502	2 S38139	LASI protein - yea
74	35	47.9	656	2 T10664	serine/threonine-s
75	35	47.9	662	2 I37892	IL12 receptor comp
76	35	47.9	1035	2 T42093	phospholipase D (E
77	35	47.9	1036	2 T13732	phospholipase D (E
78	35	47.9	1037	2 T13943	phospholipase D (E
79	35	47.9	1074	2 T17203	phospholipase (EC
80	35	47.9	1074	2 T13725	phospholipase D (E
81	35	47.9	1075	2 T46635	phospholipase D (E
82	35	47.9	1323	2 T37533	coronin-like prote
83	35	47.9	1390	2 S51364	sperm tail-splici
84	35	47.9	2153	2 T14893	scavenger receptor
85	34.5	47.3	325	2 B81364	probable periplasm
86	34	46.6	112	2 H70232	hypothetical prote
87	34	46.6	116	2 H75591	hypothetical prote
88	34	46.6	122	2 T04118	mitochondrial proc
89	34	46.6	137	2 T33210	hypothetical prote
90	34	46.6	225	2 T20325	hypothetical prote
91	34	46.6	238	2 T11718	hypothetical prote
92	34	46.6	255	2 G64320	hypothetical prote
93	34	46.6	259	2 E84427	hypothetical prote
94	34	46.6	270	2 C96731	unknown protein F5
95	34	46.6	273	2 T10610	hypothetical prote
96	34	46.6	285	2 S36903	Fc gamma (IgG) rec
97	34	46.6	296	2 A95408	hypothetical prote
98	34	46.6	302	2 S65021	chitinase (EC 3.2.
99	34	46.6	308	2 D86742	thioredoxin-disulf
100	34	46.6	311	2 F84030	porphobilinogen de
101	34	46.6	313	1 I8EC	hydroxymethylbilan
102	34	46.6	324	2 S56694	chitinase (EC 3.2.

103	34	46.6	327	1	JQ0965	chitinase (EC 3.2.	176	33	45.2	370	2	F84550	hypothetical prote
104	34	46.6	341	2	H95930	hypothetical prote	177	33	45.2	372	2	A34261	alanine dehydrogen
105	34	46.6	344	2	T05437	hypothetical prote	178	33	45.2	375	2	AP1720	N-acetylmuramoyl-L
106	34	46.6	348	2	H85256	hypothetical prote	179	33	45.2	387	2	JI0101	methane monooxygen
107	34	46.6	358	2	T32238	hypothetical prote	180	33	45.2	389	1	A48329	histidinol-phospha
108	34	46.6	375	2	B96551	hypothetical prote	181	33	45.2	393	2	A75079	hypothetical prote
109	34	46.6	375	2	AC1350	N-acetylmuramoyl-L	182	33	45.2	408	2	S76678	hypothetical prote
110	34	46.6	393	2	B86189	protein T25N20.9 l	183	33	45.2	421	2	AE3467	glutamate dehydrog
111	34	46.6	407	2	C36786	hypothetical prote	184	33	45.2	428	2	S58735	homocitrate syntha
112	34	46.6	413	2	F96743	probable C2H2-type	185	33	45.2	435	2	A49171	translation elonga
113	34	46.6	505	2	A55923	KNR4 protein - yea	186	33	45.2	438	2	E70883	probable proteinas
114	34	46.6	521	2	T18896	glypican 1 precurs	187	33	45.2	456	2	SI1665	translation elonga
115	34	46.6	559	2	S04531	thrombospondin-rel	188	33	45.2	460	2	JC4214	translation elonga
116	34	46.6	572	1	BGN2BA	cell fusion glycop	189	33	45.2	484	2	E64432	spore coat polysac
117	34	46.6	596	2	A41627	furin (EC 3.4.21.7	190	33	45.2	503	2	T46852	anchranilate synth
118	34	46.6	692	2	T32980	hypothetical prote	191	33	45.2	514	2	T00934	probable cytochrom
119	34	46.6	710	1	IS1283	hepatocyte growth	192	33	45.2	524	2	A32617	phytoene dehydroge
120	34	46.6	731	2	T29129	probable ATP/GTP b	193	33	45.2	527	2	T41856	ACMNPV orf119 - Bo
121	34	46.6	732	1	HYHUK	Kell blood group p	194	33	45.2	531	2	T51922	hypothetical prote
122	34	46.6	757	1	A60008	RNA-directed RNA p	195	33	45.2	532	2	S18448	variant surface gl
123	34	46.6	757	1	B60011	RNA-directed RNA p	196	33	45.2	552	2	S48328	hypothetical prote
124	34	46.6	757	1	PI1V61	RNA-directed RNA p	197	33	45.2	552	2	D85354	hypothetical prote
125	34	46.6	757	1	PI1V33	RNA-directed RNA p	198	33	45.2	573	2	H86313	protein F2H15.10 l
126	34	46.6	757	1	PI1V34	RNA-directed RNA p	199	33	45.2	574	1	VGNZR2	cell fusion glycop
127	34	46.6	757	1	PI1V68	RNA-directed RNA p	200	33	45.2	574	1	VGNZA2	cell fusion glycop
128	34	46.6	757	2	S06212	RNA-directed RNA p	201	33	45.2	574	1	VGNZHB	cell fusion glycop
129	34	46.6	783	2	A41627	furin (EC 3.4.21.7	202	33	45.2	574	1	VGNZL	cell fusion glycop
130	34	46.6	808	2	H64474	hypothetical prote	203	33	45.2	574	2	B28929	cell fusion glycop
131	34	46.6	850	2	S54553	Sn3 protein-bindi	204	33	45.2	574	2	S37254	cell fusion protei
132	34	46.6	1036	2	T18530	phospholipase D (E	205	33	45.2	587	2	C71433	probable membrane
133	34	46.6	1116	2	T38073	serine/threonine-p	206	33	45.2	589	2	F70033	glucan 1,4-alpha-m
134	34	46.6	1494	2	T13798	hypothetical prote	207	33	45.2	600	2	E87665	arganyl-tRNA synth
135	34	46.6	1750	2	H64403	ribonucleoside-tri	208	33	45.2	662	2	T18233	probable transcrip
136	34	46.6	1763	2	T19183	hypothetical prote	209	33	45.2	675	2	S74399	sensory transducti
137	34	46.6	1769	2	T13184	hypothetical prote	210	33	45.2	680	2	G82526	ATP-dependent DNA
138	33-5	45.9	268	2	F87076	probable reductase	211	33	45.2	718	1	A69084	DNA topoisomerase
139	33-5	45.9	348	2	G69142	GDP-D-mannose dehy	212	33	45.2	725	2	JE0100	neural cell adhesi
140	33-5	45.9	370	2	T22082	hypothetical prote	213	33	45.2	730	2	JH0798	fasciclin IV precu
141	33	45.2	60	2	A54369	fibrinogen recepto	214	33	45.2	789	2	T51310	RNA helicase RH28
142	33	45.2	112	2	B86263	Fl3K23.19 protein	215	33	45.2	842	2	C83177	probable phosphotr
143	33	45.2	152	2	AI0448	probable ribonucle	216	33	45.2	860	2	T16892	hypothetical prote
144	33	45.2	161	2	AC0883	conserved hypotet	217	33	45.2	864	2	T30441	probable capsid-as
145	33	45.2	162	2	F82084	probable 2-demethy	218	33	45.2	938	2	A56731	chromatin assembly
146	33	45.2	167	2	B84536	hypothetical prote	219	33	45.2	955	2	T18435	hypothetical prote
147	33	45.2	169	2	C70207	outer membrane pro	220	33	45.2	969	2	H69425	modification methy
148	33	45.2	170	2	AC2917	invasion protein A	221	33	45.2	996	2	T25512	hypothetical prote
149	33	45.2	175	2	T18773	hypothetical prote	222	33	45.2	1034	2	A36108	integrin alpha-v c
150	33	45.2	184	2	T13186	hypothetical prote	223	33	45.2	1041	2	PQ0442	polyprotein - barl
151	33	45.2	191	2	AG2916	conserved hypotet	224	33	45.2	1042	2	T10050	integrin alpha-v c
152	33	45.2	194	2	F97691	hypothetical prote	225	33	45.2	1045	2	S60571	integrin alpha v c
153	33	45.2	195	2	S38667	ribonuclease (EC 3	226	33	45.2	1048	2	A27421	integrin alpha-5 c
154	33	45.2	198	2	S06176	cytotoxic T-lympho	227	33	45.2	1092	1	JN0635	neural cell adhesi
155	33	45.2	205	2	S34833	stylar protein (al	228	33	45.2	1174	2	S28976	DNA-directed RNA p
156	33	45.2	210	2	T18778	hypothetical prote	229	33	45.2	1202	2	PQ0440	polyprotein - barl
157	33	45.2	214	2	S46476	cysteine proteinas	230	33	45.2	1231	1	NBHUH	complement factor
158	33	45.2	219	2	T10520	ribonuclease (EC 3	231	33	45.2	1289	2	AB2217	hypothetical prote
159	33	45.2	221	2	T04238	hypothetical prote	232	33	45.2	1436	2	A46496	antigen Wc1.1 prec
160	33	45.2	226	2	AD2198	hypothetical prote	233	33	45.2	1470	2	S45323	genome polyprotein
161	33	45.2	235	2	B97691	pBP protein (AF02	234	33	45.2	2043	2	T18524	scavenger receptor
162	33	45.2	242	2	A36148	flbN protein precu	235	33	45.2	2051	2	T30938	receptor tyrosine
163	33	45.2	244	2	A87505	flagellar L-ring p	236	33	45.2	2410	1	JQ1948	genome polyprotein
164	33	45.2	248	2	A33412	cytotoxic T-lympho	237	33	45.2	2412	1	JQ1537	LDL-receptor-relat
165	33	45.2	273	2	D81878	probable oxidoredu	238	33	45.2	4753	1	A47437	LDL-receptor-relat
166	33	45.2	324	2	S20981	chitinase (EC 3.2.	239	32.5	44.5	186	2	AE3624	hypothetical prote
167	33	45.2	328	2	AG2987	hypothetical prote	240	32.5	44.5	435	2	C59194	L-asparaginase I -
168	33	45.2	329	2	S08627	chitinase (EC 3.2.	241	32.5	44.5	571	2	AI0506	probable sulfatase
169	33	45.2	332	2	A96296	hypothetical prote	242	32	43.8	46	2	D84334	hypothetical prote
170	33	45.2	336	2	G82228	forminoglutamase	243	32	43.8	66	1	DNVPB	DNA-binding protei
171	33	45.2	336	2	T31249	hypothetical prote	244	32	43.8	74	1	DNVPAS	DNA-binding protei
172	33	45.2	350	2	D83102	xenobiotic reducta	245	32	43.8	75	2	B36119	preoptic area regu
173	33	45.2	352	2	C96643	hypothetical prote	246	32	43.8	97	2	A82158	hypothetical prote
174	33	45.2	352	2	C84603	probable pectinest	247	32	43.8	98	2	F70769	hypothetical prote
175	33	45.2	362	2	T49078	probable serine/th	248	32	43.8	111	2	C71401	hypothetical prote

249	32	43.8	116	2	H69023	conserved hypothet	322	32	43.8	486	2	T21566	hypothetical prote
250	32	43.8	129	2	AF0527	conserved hypothet	323	32	43.8	489	2	C84725	probable protein k
251	32	43.8	142	2	JO5866	ribosomal protein	324	32	43.8	491	2	E87452	ankyrin-related pr
252	32	43.8	145	2	A83010	conserved hypothet	325	32	43.8	504	2	F82253	amidophosphoribos
253	32	43.8	150	2	T25581	hypothetical prote	326	32	43.8	505	2	T19106	probable serine ca
254	32	43.8	152	2	C83896	potassium channel	327	32	43.8	509	2	T02864	probable Zn finger
255	32	43.8	154	2	A60398	replication protei	328	32	43.8	516	2	D26682	protein FLE22.18 (
256	32	43.8	158	2	AB0426	transcription elon	329	32	43.8	516	2	T06716	hypothetical prote
257	32	43.8	161	1	TPH0CC	troponin C, cardia	330	32	43.8	522	2	S33029	hypothetical prote
258	32	43.8	161	1	TPBOCC	troponin C, cardia	331	32	43.8	531	2	S07881	hypothetical prote
259	32	43.8	161	1	TPRBCW	troponin C, cardia	332	32	43.8	534	2	T19944	hypothetical prote
260	32	43.8	161	1	S07450	troponin C - quail	333	32	43.8	536	2	T20736	hypothetical prote
261	32	43.8	161	2	A27204	troponin C, cardia	334	32	43.8	539	2	A54294	cell division cont
262	32	43.8	161	2	JU0035	troponin C, cardia	335	32	43.8	551	2	S58238	DHR38 protein - fr
263	32	43.8	161	2	JW0064	slow cardiac tropo	336	32	43.8	554	2	B85072	hypothetical prote
264	32	43.8	161	2	A32620	troponin C, cardia	337	32	43.8	562	2	AF0852	secretory protein i
265	32	43.8	171	1	RWHUD1	T-cell surface gly	338	32	43.8	563	2	S54420	invasion protein i
266	32	43.8	176	2	G70138	purine-binding che	339	32	43.8	576	2	T41587	probable carbon ca
267	32	43.8	178	2	AB3279	invasion protein A	340	32	43.8	581	2	F84657	hypothetical prote
268	32	43.8	183	2	AF0904	probable exported	341	32	43.8	591	2	T02402	beta-glucosidase h
269	32	43.8	190	2	T46053	ADP-ribosylation f	342	32	43.8	606	2	T16449	hypothetical prote
270	32	43.8	204	2	E84173	hypothetical prote	343	32	43.8	607	2	S77092	hypothetical prote
271	32	43.8	221	2	T26921	hypothetical prote	344	32	43.8	632	2	T00325	hypothetical prote
272	32	43.8	226	2	T14675	hypothetical prote	345	32	43.8	646	2	S30180	phosphoenolpyruvat
273	32	43.8	229	2	I46614	nerve growth facto	346	32	43.8	660	2	T20569	hypothetical prote
274	32	43.8	229	2	B95147	lncC protein (impo	347	32	43.8	664	2	E70770	probable atp-depen
275	32	43.8	229	2	H98014	hypothetical prote	348	32	43.8	710	1	S70965	serine/threonine-s
276	32	43.8	232	2	T14939	hypothetical prote	349	32	43.8	729	2	T45951	hypothetical prote
277	32	43.8	234	2	I56140	NK and T lymphocy	350	32	43.8	729	2	T23972	hypothetical prote
278	32	43.8	241	2	JL0097	nerve growth facto	351	32	43.8	736	2	D86271	protein F16A14.2 (
279	32	43.8	245	2	I56570	beta-nerve growth	352	32	43.8	738	2	A40096	platelet-endotheli
280	32	43.8	245	2	D82680	conserved hypothet	353	32	43.8	767	2	AE3370	sensory transducti
281	32	43.8	248	1	S01007	granzyme F (EC 3.4	354	32	43.8	775	2	S35543	DNA-directed DNA p
282	32	43.8	253	2	S53760	triose-phosphate i	355	32	43.8	862	1	S56766	replication licens
283	32	43.8	253	2	A05283	spectrin alpha cha	356	32	43.8	1027	2	S37711	kinesin heavy chai
284	32	43.8	259	2	T01008	ribonuclease (EC 3	357	32	43.8	1032	2	I38510	neuronal kinesin h
285	32	43.8	266	1	NGHUBM	nerve growth facto	358	32	43.8	1048	2	C86189	protein T2SN20.11
286	32	43.8	287	2	D81295	cytochrome-c oxida	359	32	43.8	1094	2	C59434	KIAA1688 protein (
287	32	43.8	289	2	T44599	oligopeptide trans	360	32	43.8	1095	2	T00329	hypothetical prote
288	32	43.8	303	1	NGRTBA	nerve growth facto	361	32	43.8	1096	2	T16875	hypothetical prote
289	32	43.8	305	2	E84261	glycosyl transfera	362	32	43.8	1224	2	A25884	DNA-directed RNA p
290	32	43.8	307	1	NGMSMG	nerve growth facto	363	32	43.8	1263	2	T15496	hypothetical prote
291	32	43.8	308	2	AF1990	hypothetical prote	364	32	43.8	1283	2	T13799	neurexin IV - frui
292	32	43.8	320	2	T02285	hypothetical prote	365	32	43.8	1331	2	S05011	calcium channel al
293	32	43.8	321	2	S58686	hypothetical prote	366	32	43.8	1331	2	S05011	calcium channel al
294	32	43.8	345	2	T46962	8-oxoguanine DNA-g	367	32	43.8	1429	2	JN0609	nitric-oxide synth
295	32	43.8	350	2	T25451	transforming growt	368	32	43.8	1433	2	G01946	nitric-oxide synth
296	32	43.8	354	2	T41377	rna binding protei	369	32	43.8	1451	1	JQ1719	B2 glycoprotein pr
297	32	43.8	357	2	AG1072	conserved hypothet	370	32	43.8	1453	2	S41453	spike protein - ca
298	32	43.8	363	2	G95937	probable murein pep	371	32	43.8	1520	2	T30820	carbamoyl-phosphat
299	32	43.8	368	2	S62412	2-dehydro-3-deoxy-	372	32	43.8	1589	1	RGBYC5	cell division cont
300	32	43.8	383	2	A96704	hypothetical prote	373	32	43.8	1984	2	A44396	p-type cation tran
301	32	43.8	385	2	G84051	hypothetical prote	374	32	43.8	2042	2	T18399	variant-specific s
302	32	43.8	387	1	A60345	protein-tyrosine-p	375	32	43.8	2166	2	S11339	calcium channel pr
303	32	43.8	394	2	S77272	hypothetical prote	376	32	43.8	2171	2	S05054	calcium channel al
304	32	43.8	415	1	A33899	protein-tyrosine-p	377	32	43.8	2204	1	RRNZNV	genome polypeptid
305	32	43.8	415	2	T12974	hypothetical prote	378	32	43.8	2274	2	T30258	adenomatous polyo
306	32	43.8	427	2	G02034	killer cell inhibi	379	32	43.8	2657	2	T18497	hypothetical prote
307	32	43.8	428	2	S36856	glycolipid 2-alpha	380	32	43.8	2692	2	T23768	hypothetical prote
308	32	43.8	429	2	S23581	lamb protein precu	381	32	43.8	2911	2	T20566	hypothetical prote
309	32	43.8	429	2	S59773	26S proteasome reg	382	32	43.8	4687	1	A39638	plectin - rat
310	32	43.8	444	2	G01924	KIR (cl-2) NK rece	383	31.5	43.2	189	2	G96514	hypothetical prote
311	32	43.8	444	2	G01925	KIR (cl-11) NK rec	384	31.5	43.2	205	2	F87560	ribosomal protein
312	32	43.8	447	2	C82958	probable two-compo	385	31.5	43.2	473	1	A38874	protein-tyrosine-p
313	32	43.8	449	2	F83627	hypothetical prote	386	31.5	43.2	645	2	G72256	hydrogenase (EC 1.
314	32	43.8	455	2	G01923	KIR (cl-5) NK rece	387	31.5	43.2	782	2	T43277	host cell factor 1
315	32	43.8	457	2	T48036	hypothetical prote	388	31.5	43.2	888	2	H88085	protein T11F1.8 (i
316	32	43.8	458	2	S53936	hypothetical prote	389	31.5	43.2	1016	2	T05066	conserved hypothet
317	32	43.8	462	2	H95914	asparagine synthas	390	31.5	43.2	1367	2	H82874	titin, cardiac mus
318	32	43.8	466	2	H69153	hypothetical membr	391	31.5	43.2	26926	1	I38344	hypothetical prote
319	32	43.8	474	1	OMHUB	alpha-1-B-glycopro	392	31	42.5	77	2	A38345	tachyplestin I prec
320	32	43.8	478	2	JQ2034	RNA-directed RNA p	393	31	42.5	86	2	S38920	hypothetical prote
321	32	43.8	486	2	A83284	probable oxidoredu	394	31	42.5	120	1	PSRF3U	phospholipase A2 (

395	31	42.5	125	2	T32471	hypothetical prote	468	31	42.5	367	1	S02193	cellular tumor ant
396	31	42.5	129	2	A48902	hypothetical prote	469	31	42.5	369	2	JQ2278	hydroxymethylbilan
397	31	42.5	134	2	AF3482	hypothetical prote	470	31	42.5	374	2	AG3337	transcription regu
398	31	42.5	135	2	I49275	protein kinase Sry	471	31	42.5	377	2	B72275	probable aspartate
399	31	42.5	137	2	E86251	protein F25C20.8 [472	31	42.5	384	2	A11843	hypothetical prote
400	31	42.5	145	2	F82133	hypothetical prote	473	31	42.5	385	2	F69941	conserved hypotet
401	31	42.5	146	2	T29401	hypothetical prote	474	31	42.5	389	2	C82637	porphyrin biosynth
402	31	42.5	147	2	T18586	hypothetical prote	475	31	42.5	405	2	T27509	homeotic protein 1
403	31	42.5	157	2	B29555	gamma-crystallin I	476	31	42.5	411	2	G69185	collagenase - Meth
404	31	42.5	167	2	T33368	hypothetical prote	477	31	42.5	411	2	T13315	hypothetical prote
405	31	42.5	170	2	AD0114	conserved hypotet	478	31	42.5	417	2	T33376	hypothetical prote
406	31	42.5	170	2	AG2479	aminoglycoside N6'	479	31	42.5	418	2	G84164	hypothetical prote
407	31	42.5	172	2	D72368	hypothetical prote	480	31	42.5	428	2	D97010	5-enolpyruvylshiki
408	31	42.5	173	2	S04266	gamma-crystallin I	481	31	42.5	428	2	A89759	seryl-tRNA synthet
409	31	42.5	173	2	C82062	hypothetical prote	482	31	42.5	429	2	S48172	variable surface g
410	31	42.5	182	2	JC7515	VPS29-like phospho	483	31	42.5	434	2	T47575	hypothetical prote
411	31	42.5	182	2	A52468	T-cell surface gly	484	31	42.5	454	2	A86221	hypothetical prote
412	31	42.5	188	2	H95211	anthranilate synth	485	31	42.5	459	2	A35291	adenylosuccinate 1
413	31	42.5	188	2	B98076	anthranilate synth	486	31	42.5	461	2	T33747	hypothetical prote
414	31	42.5	190	2	JC4514	TATA-binding prote	487	31	42.5	462	2	A84327	photolyase/cryptoc
415	31	42.5	191	2	E75072	transcription init	488	31	42.5	467	2	A47388	serine/threonine p
416	31	42.5	191	2	D71093	probable tRNA-bind	489	31	42.5	474	2	T29336	hypothetical prote
417	31	42.5	192	2	S42381	hypothetical prote	490	31	42.5	475	2	C96503	protein F9C16.7 [1
418	31	42.5	207	2	A75475	probable acetyltra	491	31	42.5	476	2	G90512	p60-like (mycoplas
419	31	42.5	222	2	S26594	cellulose 1,4-beta	492	31	42.5	483	2	A39676	protein kinase Sry
420	31	42.5	224	2	S28737	hypothetical prote	493	31	42.5	488	2	D82991	conserved hypotet
421	31	42.5	228	2	S26995	cellulose 1,4-beta	494	31	42.5	489	2	AF2800	ABC transporter su
422	31	42.5	228	2	T47425	NAC domain-like pr	495	31	42.5	497	2	B97555	hypothetical prote
423	31	42.5	236	2	S26993	cellulose 1,4-beta	496	31	42.5	497	2	AD2775	fumurate hydratase
424	31	42.5	240	2	E86418	probable eukaryoti	497	31	42.5	501	2	T37747	hypothetical prote
425	31	42.5	240	2	T23797	hypothetical prote	498	31	42.5	503	2	AC1042	probable DNA helic
426	31	42.5	245	2	G82175	hypothetical prote	499	31	42.5	510	2	S41943	cellulose 1,4-beta
427	31	42.5	250	1	ISUTTB	triose-phosphate i	500	31	42.5	511	2	S44716	cellulose 1,4-beta
428	31	42.5	252	2	D91031	probable chaperrone							
429	31	42.5	252	2	E85875	probable fibrinall							
430	31	42.5	253	1	ISZMT	triose-phosphate i							
431	31	42.5	253	2	A32187	triose-phosphate i							
432	31	42.5	260	2	B70419	hypothetical prote							
433	31	42.5	263	2	H82134	conserved hypotet							
434	31	42.5	267	2	JN0845	enterohemolysin 1							
435	31	42.5	268	2	T31699	phosphomethylpyrim							
436	31	42.5	271	2	AF1157	phosphomethylpyrim							
437	31	42.5	271	2	AC1516	phosphomethylpyrim							
438	31	42.5	274	2	T10270	protein kinase (EC							
439	31	42.5	284	2	AG3231	conjugal transfer							
440	31	42.5	285	2	G85016	probable myb-relat							
441	31	42.5	286	2	S50855	neurotrophin-6 - s							
442	31	42.5	287	2	T25064	hypothetical prote							
443	31	42.5	289	2	E64330	dihydrodipicolinat							
444	31	42.5	290	2	AH2001	hypothetical prote							
445	31	42.5	292	2	T10106	chitinase (EC 3.2.							
446	31	42.5	293	2	AE3253	chromosome partiti							
447	31	42.5	306	2	I49068	protein kinase Sry							
448	31	42.5	307	2	T21879	hypothetical prote							
449	31	42.5	311	2	E96714	probable DNA-bind							
450	31	42.5	314	2	C90256	conserved hypotet							
451	31	42.5	317	2	T18695	hypothetical prote							
452	31	42.5	318	2	C93297	conserved hypotet							
453	31	42.5	319	2	T27700	hypothetical prote							
454	31	42.5	320	2	A86067	porphobilinogen de							
455	31	42.5	320	2	G91220	porphobilinogen de							
456	31	42.5	320	2	B44059	36K protein - appl							
457	31	42.5	321	2	S57482	chitinase class 1							
458	31	42.5	321	2	H87683	transcription regu							
459	31	42.5	323	2	T27640	hypothetical prote							
460	31	42.5	336	2	E69845	thiamin biosynthes							
461	31	42.5	338	2	H83228	hypothetical prote							
462	31	42.5	341	2	B95403	probable ABC trans							
463	31	42.5	342	2	A89846	hypothetical prote							
464	31	42.5	344	2	T27664	hypothetical prote							
465	31	42.5	347	2	JC7828	glucuronyltransfer							
466	31	42.5	359	2	AF3184	beta-lactamase [im							
467	31	42.5	364	2	E69131	tryptophan-tRNA li							

ALIGNMENTS

RESULT 1

C64398

hypothetical protein homolog MJ0787 - Methanococcus jannaschii

C:Species: Methanococcus jannaschii

C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C:Accession: C64398

R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, C.;

; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;

rsen, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.

Science 273, 1058-1073, 1996

A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.

A>Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.

A:Reference number: A64300; MUID:96337999; PMID:8688087

A:Accession: C64398

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-504 <BUL>

A:Cross-references: UNIPROT:Q58197; GB:U67523; GB:L77117; NID:g2826319; PIDN:AAB98783.1;

C:Genetics:

A:Map position: FOR710775-712289

Query Match 60.3%; Score 44; DB 2; Length 504;

Best Local Similarity 66.7%; Pred. NO. 5.4;

Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 YRCGGDSKVOE 13

DB 463 YPCGGDDKKVLE 474

RESULT 2

A70659

probable acid-CoA ligase (EC 6.2.1.-) fadD22 [similarity] - Mycobacterium tuberculosis (H37Rv)

N:Alternate names: hypothetical protein pks002a

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C/Accession: A70669; S73073
 R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
 A/Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A/Reference number: A70669
 A/Accession: A70669
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-705 <COL>
 A/Cross-references: UNIPROT:P96283; GB:283858; GB:AL123456; NID:g3261675; PIDN:CAB06101.
 R/Smith, D.R.; Robison, K.
 A/Description: The EMBL Data Library, September 1994
 A/Reference number: S73053
 A/Accession: S73073
 A/Molecule type: DNA
 A/Residues: 1-486, 'QQ', 489-705 <SMI>
 A/Cross-references: EMBL:U00024; NID:g560506; PIDN:AAA50930.1; PID:g560509
 C/Genetics:
 A/Gene: fadD22
 C/Keywords: acid-thiol ligase; carrier protein; phosphopantetheine; phosphoprotein
 F:51-486/Domain: acetate-CoA ligase homology <ACL>
 F:544-615/Domain: acyl carrier protein homology <ACPI>
 F:579/Binding site: phosphopantetheine (Ser) (covalent) #status predicted
 Query Match 60.3%; Score 44; DB 2; Length 705;
 Best Local Similarity 70.0%; Pred. No. 7.3;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 2 YRCRGDSDSKV 11
 |||||
 Db 383 YRCRADDTTEV 392
 |||||
 RESULT 3
 B87484
 anthranilate synthase component I [imported] - Caulobacter crescentus
 C/Species: Caulobacter crescentus
 C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C/Accession: B87484
 R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Emolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A/Title: Complete Genome Sequence of Caulobacter crescentus.
 A/Reference number: A87249; MUID:21173698; PMID:11259647
 A/Accession: B87484
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-513 <STO>
 A/Cross-references: UNIPROT:Q9A731; GB:AE005673; NID:g13423344; PIDN:AAK23870.1; GSPDB:G
 C/Genetics:
 C/Superfamily: anthranilate synthase component I
 Query Match 57.5%; Score 42; DB 2; Length 513;
 Best Local Similarity 50.0%; Pred. No. 12;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 2 YRCRGDSDSKVQ 13
 :|||||
 Db 73 WRCRGDAETAE 84
 |||||
 RESULT 4
 G83840
 ferric uptake regulation protein BH1527 [imported] - Bacillus halodurans (strain C-125)
 C/Species: Bacillus halodurans

C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C/Accession: G83840
 R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
 A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A/Reference number: A83650; MUID:20512582; PMID:11058132
 A/Accession: G83840
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-150 <STO>
 A/Cross-references: UNIPROT:Q9KCP2; GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BA0524
 C/Genetics:
 C/Superfamily: ferric uptake regulator
 Query Match 54.8%; Score 40; DB 2; Length 150;
 Best Local Similarity 66.7%; Pred. No. 9;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 2 YRCRGDSDSK 10
 :|||||
 Db 141 HRCQGDSEK 149
 |||||
 RESULT 5
 T22521
 hypothetical protein F52H3.5 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T22521
 R/Gardner, A.
 A/Status: preliminary; translated from GB/EMBL/DBBJ
 A/Reference number: Z19575
 A/Accession: T22521
 A/Molecule type: DNA
 A/Residues: 1-179 <WIL>
 A/Cross-references: UNIPROT:Q20683; EMBL:Z66512; PIDN:CAA91325.1; GSPDB:GN00020; CESP:F5;
 A/Experimental source: clone F52H3
 C/Genetics:
 A/Gene: CESP:F52H3.5
 A/Map position: 2
 A/Introns: 88/2; 95/1; 135/3
 Query Match 54.8%; Score 40; DB 2; Length 179;
 Best Local Similarity 63.6%; Pred. No. 11;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 YRCRGDSDSKVQ 12
 |||||
 Db 125 YRLRGDDDKAR 135
 |||||
 RESULT 6
 T29321
 hypothetical protein M01E11.4 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
 C/Accession: T29321
 R/Pauley, A.; Gattung, S.
 A/Status: preliminary; translated from GB/EMBL/DBBJ
 A/Reference number: Z20605
 A/Accession: T29321
 A/Molecule type: DNA
 A/Residues: 1-303 <PAU>
 A/Cross-references: EMBL:U80450; PIDN:AAB37827.1; GSPDB:GN00019; CESP:M01E11.4
 A/Experimental source: strain Bristol N2; clone M01E11
 C/Genetics:
 A/Gene: CESP:M01E11.4
 A/Map position: 1

A; Introns: 32/3; 135/2; 152/2; 267/3

C; Superfamily: Caenorhabditis elegans hypothetical protein M01E11.4

Query Match 54.8%; Score 40; DB 2; Length 303;

Best Local Similarity 70.0%; Pred. No. 17;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 CRGDDSKVOE 13

|||||

Db 42 CRGLDSQIOE 51

RESULT 7

A39130

nicotinate phosphoribosyltransferase (EC 2.4.2.11) - Salmonella typhimurium

C; Species: Salmonella typhimurium

C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C; Accession: A39130

R; Vinitzky, A.; Teng, H.; Grubmeyer, C.T.

J. Bacteriol. 173, 536-540, 1991

A; Title: Cloning and nucleic acid sequence of the Salmonella typhimurium pncB gene and

A; Reference number: A39130; MUID:91100340; PMID:1987148

A; Accession: A39130

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-400 <VIN>

A; Cross-references: UNIPROT:P22253; GB:M55986; NID:gl54268; PIDN:AAA27190.1; PID:gl54269

C; Genetics:

A; Gene: pncB

C; Function:

A; Pathway: nicotinate and nicotinamide metabolism

C; Superfamily: nicotinate phosphoribosyltransferase

C; Keywords: glycosyltransferase; pentosyltransferase

Query Match 54.8%; Score 40; DB 1; Length 400;

Best Local Similarity 85.7%; Pred. No. 22;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8

|||||

Db 39 FRCRGDD 45

RESULT 8

JQ0756

nicotinate phosphoribosyltransferase (EC 2.4.2.11) - Escherichia coli (strain K-12)

C; Species: Escherichia coli

C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C; Accession: JQ0756; B64833

R; Wubboldt, M.G.; Terpstra, P.; van Beilen, J.B.; Kingma, J.; Meesters, H.A.R.; Witholt,

J. Biol. Chem. 265, 17665-17672, 1990

A; Title: Variation of cofactor levels in Escherichia coli; sequence analysis and expres

A; Reference number: JQ0756; MUID:91009224; PMID:2211655

A; Accession: JQ0756

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-400 <WUB>

A; Cross-references: UNIPROT:P18133; GB:J05568; NID:gl47306; PIDN:AAA24400.1; PID:gl47307

A; Experimental source: strain GEC70

R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A; Title: The complete genome sequence of Escherichia coli K-12.

A; Reference number: A64720; MUID:97426617; PMID:9278503

A; Accession: B64833

A; Status: nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA

A; Residues: 1-400 <BLAT>

A; Cross-references: GB:AE000195; GB:U00096; NID:gl787156; PIDN:AACT4017.1; PID:gl787162;

A; Experimental source: strain K-12, substrain MG1655

C; Genetics:

A; Gene: pncB

C; Function:

A; Pathway: nicotinate and nicotinamide metabolism

C; Superfamily: nicotinate phosphoribosyltransferase

C; Keywords: glycosyltransferase; pentosyltransferase

Query Match 54.8%; Score 40; DB 1; Length 400;

Best Local Similarity 85.7%; Pred. No. 22;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8

|||||

Db 39 FRCRGDD 45

RESULT 9

AB0617

nicotinate phosphoribosyltransferase [imported] - Salmonella enterica subsp. enterica ser

C; Species: Salmonella enterica subsp. enterica serovar Typhi

A; Note: this species has also been called Salmonella typhi

C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C; Accession: AB0617

R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Connerton, P.; Cronin, A.; Davies, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serova

A; Reference number: AB0502; MUID:21534947; PMID:11677608

A; Accession: AB0617

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-400 <PAR>

A; Cross-references: GB:AL513382; PIDN:CAD05404.1; PID:gl6502165; GSPDB:GN00176

C; Genetics:

A; Gene: STY1010

C; Superfamily: nicotinate phosphoribosyltransferase

Query Match 54.8%; Score 40; DB 2; Length 400;

Best Local Similarity 85.7%; Pred. No. 22;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8

|||||

Db 39 FRCRGDD 45

RESULT 10

F90755

nicotinate phosphoribosyltransferase [imported] - Escherichia coli (strain O157:H7, subst

C; Species: Escherichia coli

C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C; Accession: F90755

R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hatcori, M.; Shingagawa, H.

gasa Res. 8, 11-22, 2001

A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genon

A; Reference number: A99629; MUID:21156231; PMID:11258796

A; Accession: F90755

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-400 <HAY>

A; Cross-references: UNIPROT:Q8XDE8; GB:BA000007; PIDN:BA034437.1; PID:gl3360473; GSPDB:GN

A; Experimental source: strain O157:H7, substrain RIMD 0509952

C; Genetics:

A; Gene: ECs1014

C; Superfamily: nicotinate phosphoribosyltransferase

Query Match 54.8%; Score 40; DB 2; Length 400;

Best Local Similarity 85.7%; Pred. No. 22;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8

|||||

Db 39 FRCRGDD 45

```
RESULT 11
D85619
nicotinate phosphoribosyltransferase [imported] - Escherichia coli (strain O157:H7, sube
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: D85619
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
filler, L.; Grothbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoudis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: D85619
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-400 <STO>
A:Cross-references: UNIPROT:O8XD8; GB:AE005174; NID:g12514106; PIDN:AAG55416.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: pncB
C:Superfamily: nicotinate phosphoribosyltransferase

Query Match 54.8%; Score 40; DB 2; Length 400;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
:|||||
Db 39 FRCRGDD 45

RESULT 12
T18646
hypothetical protein B0024.11 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18646
R:McMurray, A.
submitted to the EMBL Data Library, April 1996
A:Reference number: Z19001
A:Accession: T18646
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-577 <WIL>
A:Cross-references: UNIPROT:Q17426; EMBL:Z71178; PIDN:CAA94883.1; GSPDB:GN00023; CESP:B0
A:Experimental source: clone B0024
C:Genetics:
A:Gene: CESP.B0024.11
A:Map position: 5
A:Intron: 37/1; 175/2; 271/1; 308/1; 458/2

Query Match 54.8%; Score 40; DB 2; Length 577;
Best Local Similarity 46.2%; Pred. No. 32;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 NYRCRGDDSKVQR 13
:::|||||
Db 544 SPKTRGDDEKTEE 556

RESULT 13
H82528
L-ascorbate oxidase XF2677 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: H82528
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: H82528
```

```
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-721 <SIM>
A:Cross-references: UNIPROT:Q9PA43; GB:AE004073; GB:AE003849; NID:g9107904; PIDN:AAF85474
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al
Briones, M.R.S.; Bueno, M.R.P.; Canargo, L.E.A.; Carraro, D.M.; Carrer, H.
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A:Authors: Martins, E.M.P.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF2677

Query Match 54.8%; Score 40; DB 2; Length 721;
Best Local Similarity 54.5%; Pred. No. 39;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 YRCRGDDSKVQ 12
:|||||
Db 282 YACRGNDCKLK 292

RESULT 14
T43011
suppressor protein homolog - fission yeast (Schizosaccharomyces pombe) (fragment)
C:Species: Schizosaccharomyces pombe
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43011
R:Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A:Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A:Reference number: Z17323; MUID:98162722; PMID:9501991
A:Accession: T43011
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-280 <YOS>
A:Cross-references: UNIPROT:P78857; EMBL:D89207; NID:g1749621; PIDN:BAAL3868.1; PID:g174
A:Experimental source: strain PR745
C:Superfamily: suppressor 2 protein; translation elongation factor Tu homology

Query Match 53.4%; Score 39; DB 2; Length 280;
Best Local Similarity 80.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 RCRGDDSKVQ 12
:|||||
Db 151 RVRGDDSDVQ 160

RESULT 15
S66668
hydrogen peroxide-inducible protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S66668
R:Egawa, K.; Yoshiwara, M.; Shibamura, M.; Nose, K.
FEBS Lett. 372, 74-77, 1995
A:Title: Isolation of a novel ras-recision gene that is induced by hydrogen peroxide from
A:Reference number: S66668; MUID:96032549; PMID:7556647
A:Accession: S66668
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-325 <EGA>
A:Cross-references: UNIPROT:Q61469; EMBL:L43371; NID:g1161099; PIDN:AAA85353.1; PID:g1161
```


A,Note: in the authors' translation residues 241-260 do not match the nucleotide sequend

Query Match 53.4%; Score 39; DB 2; Length 325;
Best Local Similarity 46.2%; Pred. No. 28;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 NYRCRGDDSKVQ 13
:|:|:|:|:|
Db 261 DYICQGNKEKVE 273

RESULT 16
AD3382
ABC transporter-associated protein BMEI1042 [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AD3382
R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elizer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AD3382
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-507 <KUR>
A:Cross-references: UNIPROT:Q8YGW3; GB:AE008917; PIDN:AAL52223.1; PID:G17983006; GSPDB:C
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI1042
A:Map position: 1
C:Superfamily: conserved hypothetical protein b1683

Query Match 53.4%; Score 39; DB 2; Length 507;
Best Local Similarity 75.0%; Pred. No. 42;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 CRGDDSKV 11
|||:|:|
Db 319 CRGDSKI 326

RESULT 17
T41442
Omnipotent nonsense suppressor, efl alpha factor-like gtp-bindingprotein - fission yeast
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
R:Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1998
A:Reference number: Z21993
A:Accession: T41442
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-662 <SEE>
A:Cross-references: UNIPROT:O74718; EMBL:AL032824; PIDN:CAA21821.1; GSPDB:GN00068; SPDB:
A:Experimental source: strain 972h-; cosmid c584
C:Genetics:
A:Gene: SPDB:SPCC584.04
A:Map position: 3
A:Introns: 44/1
C:Superfamily: suppressor 2 protein; translation elongation factor Tu homology

F:239-387/Domain: translation elongation factor Tu homology <ETU>
Query Match 53.4%; Score 39; DB 2; Length 662;
Best Local Similarity 80.0%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 RCRGDDSKVQ 12
|:|:|:|:|
Db 533 RVRGDDSDVQ 542

RESULT 18
T51948
Omnipotent nonsense suppressor SUP35/erF-3 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C:Accession: T51948
R:Ito, K.; Ebihara, K.; Nakamura, Y.
RNA 4, 958-972, 1998
A:Title: The stretch of C-terminal acidic amino acids of translational release factor erF
A:Reference number: Z25883
A:Accession: T51948
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-662 <ITO>
A:Cross-references: UNIPROT:O74718; EMBL:D79214; PIDN:BAA33530.1
A:Experimental source: strain JY333
C:Genetics:
A:Gene: sup35
A:Introns: 44/1
C:Superfamily: suppressor 2 protein; translation elongation factor Tu homology

Query Match 53.4%; Score 39; DB 2; Length 662;
Best Local Similarity 80.0%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 RCRGDDSKVQ 12
|:|:|:|:|
Db 533 RVRGDDSDVQ 542

RESULT 19
T14593
syringomycin synthetase - Pseudomonas syringae pv. syringae
C:Species: Pseudomonas syringae pv. syringae
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T14593
R:Guenzi, E.; Galli, G.; Grgurina, I.; Gross, D.C.; Grandi, G.
J. Biol. Chem. 273, 32857-32863, 1998
A:Title: Characterization of the syringomycin synthetase gene cluster. A link between prc
A:Reference number: Z18153; MUID:99047670; PMID:9830033
A:Accession: T14593
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-9376 <GUE>
A:Cross-references: UNIPROT:O85168; EMBL:AF047828; MID:g3510628; PID:g3510629; PIDN:AAC8(
C:Genetics:
A:Gene: syzE
C:Keywords: carrier protein; phosphopantetheine; phosphoprotein
F:441-896/Domain: acetate-CoA ligase homology <ACL1>
F:914-981/Domain: acyl carrier protein homology <ACP1>
F:1529-1984/Domain: acetate-CoA ligase homology <ACL2>
F:2002-2069/Domain: acyl carrier protein homology <ACP2>
F:2613-3071/Domain: acetate-CoA ligase homology <ACL3>
F:3089-3156/Domain: acyl carrier protein homology <ACP3>
F:3700-4158/Domain: acetate-CoA ligase homology <ACL4>
F:4176-4244/Domain: acyl carrier protein homology <ACP4>
F:4768-5224/Domain: acetate-CoA ligase homology <ACL5>
F:5242-5310/Domain: acyl carrier protein homology <ACP5>
F:5834-6280/Domain: acetate-CoA ligase homology <ACL6>
F:6298-6366/Domain: acyl carrier protein homology <ACP6>
F:6892-7352/Domain: acetate-CoA ligase homology <ACL7>
F:7370-7437/Domain: acyl carrier protein homology <ACP7>
F:7950-8440/Domain: acetate-CoA ligase homology <ACL8>
F:8458-8526/Domain: acyl carrier protein homology <ACP8>
F:9015-9083/Domain: acyl carrier protein homology <ACP>
F:946,2034,3121,4208,5274,6330/Binding site: phosphopantetheine (Ser) (covalent) #status

Query Match 53.4%; Score 39; DB 2; Length 9376;
Best Local Similarity 50.0%; Pred. No. 6.5e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDDSKVQ 12
|||:|:|:|
Db 533 RVRGDDSDVQ 542

Db 3548 NYRHQGDNRLO 3559

RESULT 20
T31420
C-terminal domain-binding protein rAB - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31420
R:Yuryev, A.; Patturajan, M.; Litington, Y.; Joshi, R.V.; Gentile, C.; Gebara, M.; Cord
Proc. Natl. Acad. Sci. U.S.A. 93, 6975-6980, 1996
A:Title: The C-terminal domain of the largest subunit of RNA polymerase II interacts wit
A:Reference number: Z21024; MUID:96293459; PMID:8692929
A:Accession: T31420
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1268 <YUR>
A:Cross-references: UNIPROT:Q63623; EMBL:U49055; NID:g1438530; PIDN:AA526
A:Experimental source: hippocampus

Query Match 52.7%; Score 38.5; DB 2; Length 1268;
Best Local Similarity 72.7%; Pred. No. 1.2e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 2 YRCGDD-SKV 11
||| ||| ||| |||
Db 100 YRCFGDDSKI 110

RESULT 21
F81439
translation initiation factor IF-3 Cj0207 [imported] - Campylobacter jejuni (strain NCTC
C:Species: Campylobacter jejuni
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: F81439
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: F81439
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-172 <PAR>
A:Cross-references: UNIPROT:Q9PI2; GB:AL139074; GB:AL111168; NID:g6967505; PIDN:CAB7269
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: InfC; Cj0207
C:Superfamily: translation initiation factor IF-3

Query Match 52.1%; Score 38; DB 2; Length 172;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 RCGDDSKV 11
||| ||| ||| |||
Db 19 RCVGDDGKV 27

RESULT 22
T27085
hypothetical protein Y51A2D.17 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004
C:Accession: T27085; T27320
R:McMurray, A.
submitted to the EMBL Data Library, January 1998
A:Reference number: Z20307
A:Accession: T27085
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-389 <WIL>
A:Cross-references: UNIPROT:Q9XTG0; UNIPROT:Q9GTD6; EMBL:AL021497; PIDN:CAA16413.1; GSPD

A:Experimental source: clone Y51A2D
R:McMurray, A.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z20343
A:Accession: T27320
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-389 <WIL>
A:Cross-references: EMBL:Z98877; PIDN:CAB11571.1; GSPDB:GN00023; CESP:Y51A2D.17
A:Experimental source: clone Y69H2
C:Genetics:
A:Gene: CESP:Y51A2D.17
A:Map position: 5
A:Introns: 29/2; 58/1; 162/3; 204/3; 228/1; 305/1; 356/3
C:Superfamily: erBA transforming protein homology

Query Match 52.1%; Score 38; DB 2; Length 389;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGD 7
||| ||| ||| |||
Db 45 YRCRGD 50

RESULT 23
E85343
hypothetical protein AT4G29440 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: E85343
R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: E85343
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1071 <STO>
A:Cross-references: UNIPROT:Q9MOD9; GB:NC_001268; NID:g7269843; PIDN:CAB79702.1; GSPDB:GN
C:Genetics:
A:Gene: AT4G29440
A:Map position: 4

Query Match 52.1%; Score 38; DB 2; Length 1071;
Best Local Similarity 77.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 RCGDDSKVQE 13
: ||| ||| ||| |||
Db 640 QGDDSKTQE 648

RESULT 24
MWXR31
lambda 3 protein - reovirus type 1 (strain Lang)
N:Alternate names: minor core protein
C:Species: reovirus type 1
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: A30121
R:Wiener, J.R.; Joklik, W.K.
Virology 169, 194-203, 1989
A:Title: The sequences of the reovirus serotype 1, 2, and 3 L1 genome segments and analyt
A:Reference number: A94390; MUID:89163254; PMID:2922925
A:Accession: A30121
A:Molecule type: genomic RNA
A:Residues: 1-1267 <WIE>
A:Cross-references: UNIPROT:P17376; GB:M24734; NID:g499863
A>Note: this sequence, which matches the sequence attributed to type 1 in Fig. 2, matched
he translations in entries REO1LAM3P and REO3LAM3P now differ only by the sequence correct
C:Comment: See also PIR:MWXR33.
C:Genetics:
A:Map position: segment L1

C:Superfamily: reovirus lambda 3 protein
C:Keywords: core protein

Query Match 52.1%; Score 38; DB 1; Length 1267;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYVCRGDD 8
||| |||
Db 728 NYVCGDD 735

RESULT 25

MWXR32

lambda 3 protein - reovirus type 2 (strain D5/Jones)

N:Alternate names: minor core protein

C:Species: reovirus type 2

A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: B30121

R:Wiener, J.R.; Joklik, W.K.

Virology 169, 194-203, 1989

A:Title: The sequences of the reovirus serotype 1, 2, and 3 L1 genome segments and analysis
A:Reference number: A94390; MUID:89163254; PMID:2922925

A:Accession: B30121

A:Molecule type: genomic RNA

A:Residues: 1-1267 <WIE>

A:Cross-references: UNIPROT:P17377; GB:M31057; NID:G499865; PIDN:AAA47245.1; PID:G499865

C:Genetics:

A:Map position: segment L1

C:Superfamily: reovirus lambda 3 protein

C:Keywords: core protein

Query Match 52.1%; Score 38; DB 1; Length 1267;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYVCRGDD 8
||| |||
Db 728 NYVCGDD 735

RESULT 26

MWXR33

lambda 3 protein - reovirus type 3 (strain Dearing)

N:Alternate names: minor core protein

C:Species: reovirus type 3

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: C30121

R:Wiener, J.R.; Joklik, W.K.

Virology 169, 194-203, 1989

A:Title: The sequences of the reovirus serotype 1, 2, and 3 L1 genome segments and analysis
A:Reference number: A94390; MUID:89163254; PMID:2922925

A:Accession: C30121

A:Molecule type: genomic RNA

A:Residues: 1-1267 <WIE>

A:Cross-references: UNIPROT:P17378; GB:M31058; NID:G499867; GB:M24734; NID:G499863; PIDN:AAA47245.1; PID:G499863
A:Note: this sequence, which matches the sequence attributed to type 3 in Fig. 2, matches
naries R01LAM3P and R03LAM3P now differ only by the sequence correction apparently made
C:Comment: See also PIR:MWXR31.

C:Genetics:

A:Map position: segment L1

C:Superfamily: reovirus lambda 3 protein

C:Keywords: core protein

Query Match 52.1%; Score 38; DB 1; Length 1267;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYVCRGDD 8
||| |||
Db 728 NYVCGDD 735

RESULT 27

T28157

erythrocyte membrane protein 1 - malaria parasite (Plasmodium falciparum)

C:Species: Plasmodium falciparum

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T28157

R:Yang, S.Q.; Wollish, W.S.; Gut, J.; Wu, J.; Ahn, J.; Petersen, C.; Fujioka, H.; Aikawa,
submitted to the EMBL Data Library, July 1995

A:Description: The molecular cloning and DNA sequence analysis of Plasmodium falciparum
A:Reference number: Z20479

A:Accession: T28157

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-2212 <YAN>

A:Cross-references: UNIPROT:Q94657; EMBL:U31083; NID:G1517813; PID:G1517814; PIDN:AAB0696

C:Genetics:

A:Gene: EMP1

Query Match 52.1%; Score 38; DB 2; Length 2212;
Best Local Similarity 45.5%; Pred. No. 2.5e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 YRCRGDDSKVQ 12
::| ||| ::
Db 1770 FKCGDDCRVR 1780

RESULT 28

T28161

hypothetical protein FCR3-varT11-1 - malaria parasite (Plasmodium falciparum) (fragments)

C:Species: Plasmodium falciparum

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T28161

R:Hernandez-Kivas, R.; Mattei, D.; Sterkers, Y.; Peterson, D.S.; Welles, T.E.; Scherf, F.
Mol. Cell. Biol. 17, 604-611, 1997

A:Title: Expressed var genes are found in Plasmodium falciparum subtelomeric regions.

A:Reference number: Z20483; MUID:97154495; PMID:9001213

A:Accession: T28161

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-2647 <HER>

A:Cross-references: UNIPROT:P90580; EMBL:U67959; NID:G1794255; PID:G1809295; PIDN:AAC474:

A:Experimental source: strain FCQ27/PNG

C:Genetics:

A:Introns: 2158/3

A:Note: FCR3-varT11-1

Query Match 52.1%; Score 38; DB 2; Length 2647;
Best Local Similarity 45.5%; Pred. No. 3e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 YRCRGDDSKVQ 12
::| ||| ::
Db 1778 FKCGDDCRVR 1788

RESULT 29

T21381

hypothetical protein F26A3.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21381

R:McMurray, A.

submitted to the EMBL Data Library, August 1996

A:Reference number: Z19415

A:Accession: T21381

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-3228 <WIL>

A:Cross-references: UNIPROT:Q93593; EMBL:Z78419; PIDN:CAB01701.1; GSPDB:GN00019; CESP:F26A3

A:Experimental source: clone F26A3

C:Genetics:

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A:Gene: CESP:F26A3.3
A:Map position: 1
A:Introns: 36/3; 91/3; 216/3; 263/3; 308/3; 702/3; 828/3; 866/1; 1013/3; 1171/3; 1231/3;
; 2443/1; 2595/3; 2663/1; 2753/3; 2813/3; 2859/1; 3052/3; 3136/1; 3176/1

Query Match 52.1%; Score 38; DB 2; Length 3228;
Best Local Similarity 46.2%; Pred. No. 3.6e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 NYRCRGDSDSKVQ 13
||| | |
Db 2836 NYRCEDPDQEVK 2848

RESULT 30
H87107
ribosome recycling factor [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: H87107
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S
A;Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: H87107
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-185 <STO>
A:Cross-references: UNIPROT:O33046; GB:AL450380; NID:gl3093386; PIDN:CAC30541.1; GSPDB:G
C:Genetics:
A:Gene: frr
C:Superfamily: ribosome releasing factor

Query Match 50.7%; Score 37; DB 2; Length 185;
Best Local Similarity 55.6%; Pred. No. 38;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 RCRGDDSKV 11
|.|.|.|.
Db 118 KCKGEDAKV 126

RESULT 31
T21959
hypothetical protein F38C2.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21959
R;Mortimore, B.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19494
A:Accession: T21959
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-258 <WIL>
A:Cross-references: UNIPROT:O45489; EMBL:Z82267; PIDN:CAB05189.1; GSPDB:GN000022; CESP:F3
A:Experimental source: clone F38C2
C:Genetics:
A:Gene: CESP:F38C2.2
A:Map position: 4
A:Introns: 56/2; 100/3; 184/2

Query Match 50.7%; Score 37; DB 2; Length 258;
Best Local Similarity 58.3%; Pred. No. 51;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 NYRCRGDSDSKVQ 12
||| | |
Db 103 NYKWRIEDQKVQ 114

RESULT 32
H86244
lysophospholipase homolog, 25331-24357 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 12-Jul-2004
C:Accession: H86244
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H86244
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-324 <STO>
A:Cross-references: UNIPROT:O04083; GB:AE005172; NID:gl931639; PIDN:AAB65474.1; GSPDB:GN
C:Genetics:
A:Map position: 1
C:Superfamily: tropinesterase

Query Match 50.7%; Score 37; DB 2; Length 324;
Best Local Similarity 58.3%; Pred. No. 64;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 NYRCRGDSDSKVQ 12
||| | |
Db 312 NDRCGGDKTKTQ 323

RESULT 33
T21960
hypothetical protein F38C2.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21960
R;Mortimore, B.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19494
A:Accession: T21960
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-410 <WIL>
A:Cross-references: UNIPROT:O45490; EMBL:Z82267; PIDN:CAB05190.1; GSPDB:GN000022; CESP:F3
A:Experimental source: clone F38C2
C:Genetics:
A:Gene: CESP:F38C2.4
A:Map position: 4
A:Introns: 63/1; 79/3; 103/1; 138/1; 220/2; 279/3; 346/3; 367/2

Query Match 50.7%; Score 37; DB 2; Length 410;
Best Local Similarity 58.3%; Pred. No. 79;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 NYRCRGDSDSKVQ 12
||| | |
Db 3 NYKWRIEDQKVQ 14

RESULT 34
S75313
serine-tRNA ligase (EC 6.1.1.11) - Synecocystis sp. (strain PCC 6803)
N:Alternate names: protein slr1703; seryl-tRNA synthetase
C:Species: Synecocystis sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S75313

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R.; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* s.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S75313

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-430 <KAN>

A:Cross-references: UNIPROT:P73201; EMBL:D50904; GB:AB001339; NID:g1522225; PIDN:BAAL1722

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Genetics:

A:Gene: sers

A:Start codon: GTG

C:Function:

A:Description: charges tRNA(Ser) with serine

A:Pathway: protein biosynthesis

C:Superfamily: serine-tRNA ligase

C:Keywords: aminoacyl-tRNA synthetase; ATP; ligase; protein biosynthesis

Query Match 50.7%; Score 37; DB 2; Length 430;
Best Local Similarity 62.5%; Pred. No. 83;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
:::|||||

Db 225 SFQCRGDD 232

RESULT 35

C87480

conserved hypothetical protein CC1864 [imported] - *Caulobacter crescentus*

C:Species: *Caulobacter crescentus*

C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C:Accession: C87480

R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.; B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Esmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of *Caulobacter crescentus*.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: C87480

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-489 <STO>

A:Cross-references: UNIPROT:Q9A762; GB:AE005673; NID:g13423307; PIDN:AAK23839.1; GSPDB:C

C:Genetics:

A:Gene: CC1864

C:Superfamily: conserved hypothetical protein b1683

Query Match 50.7%; Score 37; DB 2; Length 489;
Best Local Similarity 87.5%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CRGDDSKV 11
|||||

Db 301 CRGDRSKV 308

RESULT 36

T19133

hypothetical protein C09F9.5b - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T19133

R.Smye, R.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19078

A:Accession: T19133

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-518 <WIL>

A:Cross-references: EMBL:Z81465; PIDN:CAB03864.1; GSPDB:GN00020; CESP:C09F9.5b

A:Experimental source: clone C09F9

C:Genetics:

A:Gene: CESP:C09F9.5b

A:Map position: 2

A:Introns: 34/2; 69/3; 139/3; 222/3; 284/2; 335/2; 377/1

Query Match 50.7%; Score 37; DB 2; Length 518;
Best Local Similarity 58.3%; Pred. No. 99;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 YRCRGDDSKVQE 13
|||:|:|

Db 55 YRCFPDESQVYE 66

RESULT 37

T19132

hypothetical protein C09F9.5a - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T19132

R.Smye, R.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19078

A:Accession: T19132

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-564 <WIL>

A:Cross-references: EMBL:Z81465; PIDN:CAB03863.1; GSPDB:GN00020; CESP:C09F9.5a

A:Experimental source: clone C09F9

C:Genetics:

A:Gene: CESP:C09F9.5a

A:Map position: 2

A:Introns: 34/2; 69/3; 139/3; 222/3; 284/2; 335/2; 377/1; 505/1

Query Match 50.7%; Score 37; DB 2; Length 564;
Best Local Similarity 58.3%; Pred. No. 1.1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 YRCRGDDSKVQE 13
|||:|:|

Db 55 YRCFPDESQVYE 66

RESULT 38

A89862

Na+/H+ antiporter subunit [imported] - *Staphylococcus aureus* (strain N315)

C:Species: *Staphylococcus aureus*

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: A89862

R.Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; t C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: A89862

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-801 <KUR>

A:Cross-references: UNIPROT:P60674; UNIPROT:P60675; GB:BA000018; PID:g13700756; PIDN:BAB4

A:Experimental source: strain N315

C:Genetics:

A:Gene: mnhA

C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5

Query Match 50.7%; Score 37; DB 2; Length 801;
Best Local Similarity 54.5%; Pred. No. 1.5e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 NYRCRGDDSKV 11
:|:|||||

Db 322 SYHYQGDDSKI 332

RESULT 39

T19131

hypothetical protein C09F9.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T19131

R:Smyle, R.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19078

A:Accession: T19131

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-873 <WIL>

A:Cross-references: EMBL:Z81465; PIDN:CAB03862.1; GSPDB:GN00020; CESP:C09F9.3

A:Experimental source: clone C09F9

C:Genetics:

A:Gene: CESP:C09F9.3

A:Map position: 2

A:Introns: 66/1; 168/2; 293/1; 343/2; 378/3; 448/3; 531/3; 593/2; 644/2; 686/1; 814/1

Query Match 50.7%; Score 37; DB 2; Length 873;

Best Local Similarity 58.3%; Pred. No. 1.6e+02;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 YRCRGDDSKVQE 13

Db 364 YRCFPDESQVYE 375

RESULT 40

F86316

protein T10022.13 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: F86316

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Liu, X.; Lin, S.X.; Liu, Z.A.; Luroe, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Iker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: F86316

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-988 <STO>

A:Cross-references: UNIPROT:Q9LM32; GB:AE005172; NID:g8671767; PIDN:AAF78373.1; GSPDB:GN

C:Genetics:

A:Gene: T10022.13

A:Map position: 1

Query Match 50.7%; Score 37; DB 2; Length 988;

Best Local Similarity 54.5%; Pred. No. 1.8e+02;

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 NYRCRGDDSKV 11

Db 164 NYNCLGVDDKI 174

RESULT 41

F96763

hypothetical protein F25P22.8 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: F96763

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Liu, X.; Lin, S.X.; Liu, Z.A.; Luroe, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Iker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: F86316

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-988 <STO>

A:Cross-references: UNIPROT:Q9LM32; GB:AE005172; NID:g8671767; PIDN:AAF78373.1; GSPDB:GN

C:Genetics:

A:Gene: T10022.13

A:Map position: 1

Query Match 50.7%; Score 37; DB 2; Length 988;

Best Local Similarity 54.5%; Pred. No. 1.8e+02;

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 NYRCRGDDSKV 11

Db 164 NYNCLGVDDKI 174

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Liu, X.; Lin, S.X.; Liu, Z.A.; Luroe, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Iker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: F96763

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1030 <STO>

A:Cross-references: UNIPROT:Q9C9U5; GB:AE005173; NID:g6692730; PIDN:AAF24836.1; GSPDB:GN

C:Genetics:

A:Gene: F25P22.8

A:Map position: 1

Query Match 50.7%; Score 37; DB 2; Length 1030;

Best Local Similarity 54.5%; Pred. No. 1.9e+02;

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 NYRCRGDDSKV 11

Db 188 NYNCLGVDDKI 198

RESULT 42

C90460

hypothetical protein SSO2828 [imported] - Sulfolobus solfataricus

C:Species: Sulfolobus solfataricus

C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C:Accession: C90460

R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-vong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A:Description: Sulfolobus solfataricus complete genome.

A:Reference number: A99139

A:Accession: C90460

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-138 <KUR>

A:Cross-references: UNIPROT:Q97V09; GB:AE006641; NID:gl3816183; PIDN:AAK42938.1; GSPDB:GN

C:Genetics:

A:Gene: SSO2828

Query Match 49.3%; Score 36; DB 2; Length 138;

Best Local Similarity 60.0%; Pred. No. 43;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 YRCRGDDSKV 11

Db 45 YRCGDIGKL 54

RESULT 43

AC3270

hypothetical exported protein BMEI0144 [imported] - Brucella melitensis (strain 16M)

C:Species: Brucella melitensis

C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C:Accession: AC3270

R:DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujeer, C.; Los, T.; Ivanova, I.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A:Reference number: AD3252; PMID:11756688

A:Accession: AC3270

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-180 <KUR>

```

Db      187 NVRFKGGDGAEK 199      |||:::
RESULT 46
C85720
probable oxidoreductase ydfG [imported] - Escherichia coli (strain O157:H7, substrain EDI
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C/Accession: C85720
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: C85720
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-248 <STO>
A/Cross-references: UNIPROT:Q8X505; GB:AE005174; NID:gl2515117; PIDN:AAG56223.1; GSPDB:G
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Gene: ydfG
C/Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match      49.3%; Score 36; DB 2; Length 248;
Best Local Similarity 46.2%; Pred. No. 75;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1 NYRCRGDDSKVOE 13      |||:::
Db      187 NVRFKGGDGAEK 199

RESULT 47
T20546
hypothetical protein F07C6.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T20546
R:Steward, C.
submitted to the EMBL Data Library, February 1996
A/Reference number: Z19290
A/Accession: T20546
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-329 <WTL>
A/Cross-references: UNIPROT:Q19157; EMBL:Z69659; PIDN:CAA93483.1; GSPDB:GN00022; CESP:F0
A/Experimental source: clone F07C6
C/Genetics:
A/Gene: CESP:F07C6.1
A/Map position: 4
A/Introns: 14/2; 47/2; 85/1; 146/1; 226/3; 299/2

Query Match      49.3%; Score 36; DB 2; Length 329;
Best Local Similarity 50.0%; Pred. No. 98;
Matches 9; Conservative 0; Mismatches 3; Indels 6; Gaps 1;

QY      2 YRCRGDD-----SKVOE 13      |||||
Db      287 YRCRGDKVLHYKDKVME 304      |||||

RESULT 48
T35013
probable membrane protein - Streptomyces coelicolor
C/Species: Streptomyces coelicolor
C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C/Accession: T35013
R;Seeger, S.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999
A/Reference number: Z21565
A/Accession: T35013

```

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-347 <SEE>
A;Cross-references: UNIPROT:Q9XAN5; EMBL:AL079355; PIDN:CAB45569.1; GSPDB:GN00070; SCOE
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC4C6.05C
C;Superfamily: Streptomyces coelicolor probable membrane protein SC4C6.05c

Query Match 49.3%; Score 36; DB 2; Length 347;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YRCRGDDSK 10
|:|:|:|:
DB 206 YKCPGDTSK 214

RESULT 49
H72494
hypothetical protein APE2599 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: H72494
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: H72494
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-411 <XAW>
A;Cross-references: UNIPROT:Q9Y8N4; DDBJ:AP000064; NID:G5105945; PIDN:BAAB1616.1; PID:G5
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE2599
C;Superfamily: Aeropyrum pernix hypothetical protein APE2599

Query Match 49.3%; Score 36; DB 2; Length 411;
Best Local Similarity 54.5%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 YRCRGDDSKVQ 12
|:|:|:|:
DB 225 YNCRDEDNVVQ 235

RESULT 50
A46206
voltage-gated sodium channel alpha subunit - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46206
R;Gautron, S.; Dos Santos, G.; Pinto-Henrique, D.; Koulakoff, A.; Gros, F.; Berwald-Nett
Proc. Natl. Acad. Sci. U.S.A. 89, 7272-7276, 1992
A;Title: The glial voltage-gated sodium channel: cell- and tissue-specific mRNA expressi
A;Reference number: A46206; MUID:92357813; PMID:1379737
A;Accession: A46206
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-435 <GAU>
A;Cross-references: UNIPROT:Q01340; GB:M96578; NID:G204544; PIDN:AAA41303.1; PID:G204545
A;Experimental source: 1-day-old Wistar, astrocyte cultures
A;Note: sequence extracted from NCBI backbone (NCBIP:113349)
C;Superfamily: sodium channel protein

Query Match 49.3%; Score 36; DB 2; Length 435;
Best Local Similarity 46.2%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 NYRCRGDDSKVQE 13
|:|:|:|:|:
DB 1 NYRCRGDDSKVQE 13

Db 392 SYRLRQSDKKIQD 404

Search completed: September 7, 2005, 20:04:01
Job time : 14.9767 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 7, 2005, 19:43:14 ; Search time 45.6512 Seconds
(without alignments)
145.824 Million cell updates/sec

Title: US-10-812-238B-23
Perfect score: 73
Sequence: 1 NYRCRGDDSKVQE 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73	100.0	311	1 LPP3_HUMAN	O14495 h lipid pho
2	69	94.5	312	1 LPP3_MOUSE	Q991y8 mus musculus
3	69	94.5	312	1 LPP3_RAT	P97544 rattus norv
4	69	94.5	312	1 Q6INX4	Q6inx4 rattus norv
5	46	63.0	307	2 Q68F34	Q68f34 xenopus lae
6	46	63.0	776	2 Q73RY0	Q73ry0 mycobacteri
7	44	60.3	167	2 Q95L84	Q95l84 oryctolagus
8	44	60.3	504	1 Y787_METJA	Q58197 methanococc
9	44	60.3	705	2 Q50468	Q50468 mycobacteri
10	44	60.3	705	2 P96283	P96283 mycobacteri
11	44	60.3	705	2 Q7TXK7	Q7txk7 mycobacteri
12	43	58.9	307	2 Q6AX87	Q6ax87 xenopus lae
13	42	57.5	73	2 Q7QP19	Q7qp19 giardia lam
14	42	57.5	265	2 Q86KQ7	Q86kq7 dictyosteli
15	42	57.5	513	2 Q9A731	Q9a731 caulobacter
16	42	57.5	845	2 Q8WQJ3	Q8wgj3 plasmodium
17	42	57.5	1304	2 Q8WT63	Q8wt63 plasmodium
18	41	56.2	37	2 Q8P0M2	Q8p0m2 streptococ
19	41	56.2	226	2 Q69XV4	Q69xv4 oryza sativ
20	41	56.2	428	2 Q8TBF1	Q8tbf1 homo sapien
21	41	56.2	461	2 Q69XV5	Q69xv5 oryza sativ
22	41	56.2	489	2 Q8N9B8	Q8n9b8 homo sapien
23	41	56.2	505	2 Q96I80	Q96i80 homo sapien
24	41	56.2	875	1 NETR_HUMAN	P56730 homo sapien
25	41	56.2	1334	2 Q97322	Q97322 plasmodium
26	41	56.2	2736	2 Q7RTC3	Q7rtc3 plasmodium
27	40	54.8	150	2 Q9KCP2	Q9kcp2 bacillus ha
28	40	54.8	179	2 Q20683	Q20683 caenorhabdi
29	40	54.8	244	2 Q95ZL6	Q95z16 caenorhabdi
30	40	54.8	252	2 Q95ZL7	Q95z17 caenorhabdi
31	40	54.8	269	2 Q7R8M3	Q7r8m3 plasmodium

32	40	54.8	282	1 LPP1_RAT	Q08564 rattus norv
33	40	54.8	282	2 Q6P766	Q6p766 rattus norv
34	40	54.8	288	2 Q9DW23	Q9dw23 rat cytomog
35	40	54.8	304	1 HEN3_XANCP	Q8p536 xanthomonas
36	40	54.8	309	1 PNCB_ECOS7	Q8x536 escherichia
37	40	54.8	399	1 PNCB_ECOLI	P18133 escherichia
38	40	54.8	399	1 PNCB_SALTI	Q8t7y9 salmonella
39	40	54.8	399	1 PNCB_SALTY	P22253 salmonella
40	40	54.8	400	2 Q7UD27	Q7ud27 shigella fl
41	40	54.8	416	2 Q83LN3	Q83ln3 shigella fl
42	40	54.8	416	2 Q8FJ98	Q8fj98 escherichia
43	40	54.8	577	1 YQ4B_CAEEL	Q17426 caenorhabdi
44	40	54.8	586	2 Q62YB1	Q62yb1 bacillus li
45	40	54.8	587	2 Q65MW8	Q65mw8 bacillus li
46	40	54.8	721	2 Q9PA43	Q9pa43 xylella fas
47	40	54.8	1129	2 Q7RQD4	Q7rqd4 rhodospirell
48	40	54.8	1615	2 Q7RQM4	Q7rqm4 plasmodium
49	39	53.4	46	2 Q848W4	Q848w4 bacillus me
50	39	53.4	154	2 Q8BUS2	Q8bus2 mus musculu
51	39	53.4	278	2 Q6DHF1	Q6dhf1 brachydanio
52	39	53.4	280	2 P78857	P78857 schizosacch
53	39	53.4	283	1 LPP1_MOUSE	Q61469 mus musculu
54	39	53.4	305	2 Q9RDP5	Q9rdp5 streptomyce
55	39	53.4	403	2 Q6MQE4	Q6mqe4 bdellovibri
56	39	53.4	503	2 Q6FZW1	Q6fzw1 bartonella
57	39	53.4	503	2 Q6G3B9	Q6g3b9 bartonella
58	39	53.4	507	2 Q8YGW3	Q8ygw3 bruceella me
59	39	53.4	507	2 Q8G100	Q8gi100 bruceella su
60	39	53.4	528	2 Q97379	Q97379 strongyloce
61	39	53.4	540	2 Q76771	Q76771 dictyosteli
62	39	53.4	588	2 Q70681	Q70681 sugarcane s
63	39	53.4	662	1 ERF2_SCHPO	Q74718 schizosacch
64	39	53.4	750	2 Q26188	Q26188 plasmodium
65	39	53.4	1015	2 Q6C6V1	Q6c6v1 yarrowia li
66	39	53.4	1420	2 Q9YNB1	Q9ynb1 sugarcane s
67	39	53.4	1450	2 Q815X9	Q815x9 plasmodium
68	39	53.4	1778	2 Q9BPP7	Q9bpb7 anthersea y
69	39	53.4	1778	2 Q9GUX5	Q9gux5 antheraea p
70	39	53.4	9376	2 Q85168	Q85168 pseudomonas
71	38.5	52.7	1268	2 Q63623	Q63623 rattus norv
72	38.5	52.7	1268	2 Q6D1D3	Q6did3 mus musculu
73	38.5	52.7	1271	1 RBMG_HUMAN	Q6d1d3 mus sapien
74	38.5	52.7	1271	2 Q6NSK3	Q6nsk3 homo sapien
75	38.5	52.7	1362	2 Q80TJ3	Q80tj3 mus musculu
76	38.5	52.7	1364	2 Q8I3E6	Q8i3e6 plasmodium
77	38	52.1	121	2 Q8Q0W8	Q8q0w8 methanosarc
78	38	52.1	121	2 Q8V163	Q8vi63 reovirus sp
79	38	52.1	121	2 Q8V164	Q8vi64 reovirus sp
80	38	52.1	121	2 Q8V165	Q8vi65 reovirus sp
81	38	52.1	121	2 Q8V166	Q8vi66 reovirus sp
82	38	52.1	121	2 Q8V167	Q8vi67 reovirus sp
83	38	52.1	121	2 Q8V168	Q8vi68 reovirus sp
84	38	52.1	121	2 Q8V169	Q8vi69 reovirus sp
85	38	52.1	121	2 Q8V170	Q8vi70 reovirus sp
86	38	52.1	121	2 Q8V171	Q8vi71 reovirus sp
87	38	52.1	121	2 Q8V172	Q8vi72 reovirus sp
88	38	52.1	121	2 Q8V173	Q8vi73 reovirus sp
89	38	52.1	121	2 Q8V174	Q8vi74 reovirus sp
90	38	52.1	121	2 Q8V175	Q8vi75 reovirus sp
91	38	52.1	121	2 Q8V176	Q8vi76 reovirus sp
92	38	52.1	121	2 Q8V177	Q8vi77 reovirus sp
93	38	52.1	121	2 Q8V178	Q8vi78 reovirus sp
94	38	52.1	121	2 Q8V179	Q8vi79 reovirus sp
95	38	52.1	121	2 Q8V180	Q8vi80 reovirus sp
96	38	52.1	121	2 Q8V181	Q8vi81 reovirus sp
97	38	52.1	121	2 Q8V182	Q8vi82 reovirus sp
98	38	52.1	121	2 Q8V183	Q8vi83 reovirus sp
99	38	52.1	121	2 Q8V184	Q8vi84 reovirus sp
100	38	52.1	121	2 Q8V185	Q8vi85 reovirus sp
101	38	52.1	121	2 Q8V186	Q8vi86 reovirus sp
102	38	52.1	121	2 Q8V187	Q8vi87 reovirus sp
103	38	52.1	121	2 Q8V188	Q8vi88 reovirus sp
104	38	52.1	121	2 Q8V189	Q8vi89 reovirus sp

105	38	52.1	121	2	Q8V190	Q8v190 reovirus sp	178	37	50.7	467	1	VE2_HP24	P50770 human papil
106	38	52.1	121	2	Q8V191	Q8v191 reovirus sp	179	37	50.7	485	2	Q8P748	Q8p748 xanthomonas
107	38	52.1	121	2	Q8V192	Q8v192 reovirus sp	180	37	50.7	489	2	Q8A762	Q8a762 caulobacter
108	38	52.1	121	2	Q8V193	Q8v193 reovirus sp	181	37	50.7	490	2	Q82137	Q82137 streptomyce
109	38	52.1	121	2	Q8V194	Q8v194 reovirus sp	182	37	50.7	566	2	Q8S313	Q8s313 phytophthor
110	38	52.1	121	2	Q8V195	Q8v195 reovirus sp	183	37	50.7	743	2	Q8T1S1	Q8t1s1 methanosarc
111	38	52.1	121	2	Q8V196	Q8v196 reovirus sp	184	37	50.7	801	1	MNHA_STAAM	P60674 staphylococ
112	38	52.1	121	2	Q8V197	Q8v197 reovirus sp	185	37	50.7	801	1	MNHA_STAAM	P60675 staphylococ
113	38	52.1	121	2	Q8V198	Q8v198 reovirus sp	186	37	50.7	801	1	MNHA_STAAU	Q92ng6 staphylococ
114	38	52.1	121	2	Q8V199	Q8v199 reovirus sp	187	37	50.7	801	1	MNHA_STAAW	Q8nxf6 staphylococ
115	38	52.1	121	2	Q8V1A0	Q8v1a0 reovirus sp	188	37	50.7	801	2	Q6GAX4	Q6gax4 staphylococ
116	38	52.1	121	2	Q8V1A1	Q8v1a1 reovirus sp	189	37	50.7	801	2	Q6GID6	Q6gid6 staphylococ
117	38	52.1	121	2	Q8V1A2	Q8v1a2 reovirus sp	190	37	50.7	808	2	Q7Q4C6	Q7q4c6 anopheles g
118	38	52.1	121	2	Q8V1A3	Q8v1a3 reovirus sp	191	37	50.7	850	2	Q6C6X5	Q6c6x5 yarrowia li
119	38	52.1	121	2	Q6RJU0	Q6rju0 reovirus sp	192	37	50.7	868	2	Q6CFX2	Q6cfx2 yarrowia li
120	38	52.1	130	2	Q9YHG0	Q9yhg0 ginglymosto	193	37	50.7	888	2	Q75AE3	Q75ae3 ashbya goss
121	38	52.1	172	1	IF3_CAMJE	Q9pis2 campylobact	194	37	50.7	953	2	Q7PGN3	Q7pgn3 anopheles g
122	38	52.1	172	2	Q897T4	Q897t4 clostridium	195	37	50.7	966	2	Q9LMS1	Q9lms1 arabidopsis
123	38	52.1	191	2	Q9AY16	Q9ay16 funaria apo	196	37	50.7	970	2	Q7X8K7	Q7x8k7 brassica ju
124	38	52.1	193	2	Q9AY18	Q9ay18 entosthodon	197	37	50.7	988	2	Q9LM32	Q9lm32 arabidopsis
125	38	52.1	206	2	Q8TBK8	Q8tbk8 homo sapien	198	37	50.7	992	2	Q8LPH3	Q8lph3 arabidopsis
126	38	52.1	285	1	LPPI_CAVPO	Q88956 cavia porce	199	37	50.7	1022	2	Q8XM34	Q8xm34 clostridium
127	38	52.1	298	2	Q7Q232	Q7q232 anopheles g	200	37	50.7	1030	2	Q8L625	Q8l625 arabidopsis
128	38	52.1	298	2	Q8AKP4	Q8akp4 cyanidiosch	201	37	50.7	1030	2	Q9C9U5	Q9c9u5 arabidopsis
129	38	52.1	304	1	HEM3_XANAC	Q8ppr3 xanthomonas	202	37	50.7	1257	2	Q7QCZ7	Q7qc27 anopheles g
130	38	52.1	310	2	Q8D1T7	Q8dit7 synechococ	203	37	50.7	1325	2	Q95ZZ0	Q95zz0 caenorhabdi
131	38	52.1	311	2	Q8N4J2	Q8n4j2 homo sapien	204	37	50.7	1583	2	Q7RRC0	Q7rrc0 plasmodium
132	38	52.1	383	2	Q9GTD8	Q9gtd8 caenorhabdi	205	37	50.7	1756	2	Q8PMS	Q8pms oikopleura
133	38	52.1	387	2	Q9GTD7	Q9gtd7 caenorhabdi	206	37	50.7	1969	2	Q89HL6	Q89hl6 ciona inte
134	38	52.1	388	2	Q9GTD6	Q9gtd6 caenorhabdi	207	37	50.7	4569	2	Q7PS35	Q7pe35 anopheles g
135	38	52.1	389	2	Q9XTG0	Q9xtg0 caenorhabdi	208	36.5	50.0	459	2	Q7QJN6	Q7qjn6 anopheles g
136	38	52.1	435	2	Q8JTB2	Q8jtb2 golden ide	209	36.5	50.0	1193	2	Q7Z8L8	Q7z8l8 cochlilobolu
137	38	52.1	454	2	Q9H648	Q9h648 homo sapien	210	36	49.3	63	2	Q9BS83	Q9bs83 homo sapien
138	38	52.1	476	2	Q6B8Q6	Q6b8q6 gracilaria	211	36	49.3	84	2	Q9RIJ0	Q9rij0 streptococ
139	38	52.1	542	2	Q8N3Z6	Q8n3z6 homo sapien	212	36	49.3	122	2	Q85KS8	Q85ks8 bacillus li
140	38	52.1	639	2	Q8DID1	Q8did1 synechococ	213	36	49.3	138	2	Q97V09	Q97v09 sulfolobus
141	38	52.1	661	2	Q8JTB6	Q8jtb6 striped bas	214	36	49.3	142	2	Q87I31	Q87i31 vibrio para
142	38	52.1	750	2	Q6CI30	Q6ci30 yarrowia li	215	36	49.3	147	1	Y237_TROWT	P67323 tropheryma
143	38	52.1	915	2	Q7UV66	Q7uv66 rhodopirell	216	36	49.3	147	1	Y533_TROW8	P67324 tropheryma
144	38	52.1	973	2	Q9NC89	Q9nc89 strongyloce	217	36	49.3	158	2	Q8LNX9	Q8lnx9 zinnia eleg
145	38	52.1	1073	2	Q9M0D9	Q9m0d9 arabidopsis	218	36	49.3	160	1	RRAL_VIBPA	Q87sd2 vibrio para
146	38	52.1	1075	2	Q9NC90	Q9nc90 strongyloce	219	36	49.3	164	2	Q7Q0D5	Q7q0d5 anopheles g
147	38	52.1	1240	2	Q8VA42	Q8va42 chum salmon	220	36	49.3	165	2	Q9GLE6	Q9gle6 sus scrofa
148	38	52.1	1267	1	VL3_REOVD	P17378 reovirus ty	221	36	49.3	176	2	Q8XN04	Q8xn04 clostridium
149	38	52.1	1267	1	VL3_REOVJ	P17377 reovirus ty	222	36	49.3	180	2	Q8YJE2	Q8yje2 bruceella me
150	38	52.1	1267	1	VL3_REOVL	P17376 reovirus ty	223	36	49.3	180	2	Q8FYG1	Q8fyg1 bruceella su
151	38	52.1	1267	2	Q8V5E5	Q8v5e5 ndelle viru	224	36	49.3	188	2	Q83XE8	Q63xe8 burkholderi
152	38	52.1	1267	2	Q85665	Q85665 reovirus ty	225	36	49.3	225	1	CLD8_HUMAN	P56748 homo sapien
153	38	52.1	1274	2	Q8JU61	Q8ju61 golden shin	226	36	49.3	225	1	CLD8_MOUSE	Q92260 mus musculu
154	38	52.1	1274	2	Q9E3V9	Q9e3v9 grass carp	227	36	49.3	248	1	YDFG_ECOLI	P39831 escherichia
155	38	52.1	1601	2	Q9NDH1	Q9ndh1 caenorhabdi	228	36	49.3	248	2	Q621I5	Q621i5 burkholderi
156	38	52.1	2212	2	Q9A657	Q9a657 plasmodium	229	36	49.3	248	2	Q63RB3	Q63rb3 burkholderi
157	38	52.1	2647	2	P90580	P90580 plasmodium	230	36	49.3	248	2	Q7UCH2	Q7uch2 shigella fl
158	37	50.7	59	2	Q6ETU2	Q6etu2 oryza sativ	231	36	49.3	248	2	Q8X505	Q8x505 escherichia
159	37	50.7	97	2	Q72N54	Q72n54 leptospira	232	36	49.3	250	2	Q6KCK6	Q6kcx6 escherichia
160	37	50.7	97	2	Q8F8G5	Q8f8g5 leptospira	233	36	49.3	250	2	Q8CVU9	Q8cvu9 escherichia
161	37	50.7	108	2	Q6ESN2	Q6ean2 oryza sativ	234	36	49.3	252	2	Q937E7	Q937e7 nostoc punc
162	37	50.7	141	2	Q7MUA2	Q7mu2 porphyromon	235	36	49.3	253	2	Q83RE8	Q83re8 shigella fl
163	37	50.7	142	2	Q88Z98	Q88z98 lactobacill	236	36	49.3	253	2	Q8FHD2	Q8fhd2 escherichia
164	37	50.7	158	2	Q86D08	Q86d08 caenorhabdi	237	36	49.3	266	2	Q8EJ20	Q8ej20 shewanella
165	37	50.7	159	2	Q67VQ7	Q67vq7 oryza sativ	238	36	49.3	279	2	Q80VI5	Q80vi5 mus musculu
166	37	50.7	185	1	RRF_MYCLE	Q33046 mycobacteri	239	36	49.3	280	2	Q95698	Q95698 homo sapien
167	37	50.7	187	2	Q8HU07	Q8hu07 rhodobryum	240	36	49.3	280	2	Q9H160	Q9h160 homo sapien
168	37	50.7	187	2	Q68IK5	Q68ik5 helicobacte	241	36	49.3	281	2	Q8BGU8	Q8bgu8 m mus muscu
169	37	50.7	255	2	Q8MI30	Q8mi30 equus cabal	242	36	49.3	281	2	Q9ESK4	Q9esk4 mus musculu
170	37	50.7	324	2	O04083	O04083 arabidopsis	243	36	49.3	292	2	Q90Z34	Q90z34 brachydanio
171	37	50.7	330	2	Q82MFO	Q82mf0 streptomyce	244	36	49.3	306	2	Q7RIN6	Q7rin6 plasmodium
172	37	50.7	338	2	Q8SSM8	Q8ssm8 encephalito	245	36	49.3	328	2	Q98K20	Q98k20 rhizobium l
173	37	50.7	356	2	Q919T1	Q919t1 influenza a	246	36	49.3	329	1	PIN2_CAEEL	Q19157 caenorhabdi
174	37	50.7	383	2	Q6EDQ1	Q6edq1 hirundo pyr	247	36	49.3	340	2	Q8V256	Q8v286 helicoverpa
175	37	50.7	394	2	Q8EVB5	Q8evb5 mycoplasma	248	36	49.3	340	2	Q77LV8	Q77lv8 helicoverpa
176	37	50.7	410	2	O45490	O45490 caenorhabdi	249	36	49.3	340	2	Q9E219	Q9e219 helicoverpa
177	37	50.7	430	1	SYS_SYNY3	P73201 synechocyt	250	36	49.3	340	2	Q91FJ4	Q91fj4 helicoverpa

251	36	49.3	347	2	Q9XAN5	Q9xan5 streptomyce	324	36	49.3	822	1	MUS2_SYN3	P73625 synechocyst
252	36	49.3	401	2	Q6D454	Q6d454 erwinia car	325	36	49.3	897	2	Q93Y95	Q93y95 bacte mayr (m
253	36	49.3	402	2	Q93YD4	Q93yd4 nicotiana t	326	36	49.3	996	2	Q89ZU9	Q89zu9 bacteroides
254	36	49.3	402	2	Q93Y85	Q93ye5 nicotiana t	327	36	49.3	1063	2	Q61FK6	Q61fk6 plasmodium
255	36	49.3	402	2	Q948Y4	Q948y4 nicotiana t	328	36	49.3	1168	2	Q7RH99	Q7rh99 plasmodium
256	36	49.3	402	2	Q9XG74	Q9xg74 nicotiana t	329	36	49.3	1247	2	Q817Z6	Q817z6 toxoplasma
257	36	49.3	404	2	Q7N621	Q7n621 photorhabdu	330	36	49.3	1363	2	Q81AM5	Q81am5 plasmodium
258	36	49.3	406	2	Q93YC1	Q93yc1 nicotiana t	331	36	49.3	1702	2	P97706	P97706 rattus norv
259	36	49.3	411	2	Q9Y8N4	Q9y8n4 aeropyrum p	332	36	49.3	1907	2	Q96L96	Q96l96 homo sapien
260	36	49.3	428	2	Q6GD81	Q6gd81 staphylococ	333	36	49.3	2209	2	Q9U0G6	Q9u0g6 plasmodium
261	36	49.3	435	2	Q01340	Q01340 rattus norv	334	36	49.3	3454	2	Q7Y1G0	Q7y1g0 oryza sativ
262	36	49.3	461	2	Q28377	Q28377 archaeoglob	335	36	49.3	5432	2	Q7RXP5	Q7rxp5 plasmodium
263	36	49.3	466	2	Q9S5X4	Q9s5x4 thermotoga	336	35.5	48.6	468	2	Q72WL4	Q72wl4 desulfovibr
264	36	49.3	470	2	Q7WYR5	Q7wyrs thermotoga	337	35.5	48.6	2112	2	Q9VEL9	Q9vel9 drosophila
265	36	49.3	481	2	Q7MXE2	Q7mxex porphyromon	338	35	47.9	55	2	Q6SA81	Q6sa81 salmonella
266	36	49.3	485	2	Q8CFK1	Q8cfk1 mus musculu	339	35	47.9	104	2	Q51757	Q51757 pseudomonas
267	36	49.3	488	2	Q75DX4	Q75dx4 ashbya gos	340	35	47.9	110	2	Q942Y1	Q942y1 oryza sativ
268	36	49.3	498	1	NMT2_HUMAN	Q60551 homo sapien	341	35	47.9	112	2	Q46132	Q46132 clostridium
269	36	49.3	498	2	Q8NM54	Q8nm54 bradyrhizob	342	35	47.9	119	2	Q8XK90	Q8xk90 bradyrhizob
270	36	49.3	505	2	Q98NR7	Q98nr7 rhizobium l	343	35	47.9	128	2	Q74FF9	Q74ff9 geobacter s
271	36	49.3	510	2	Q6M0Z3	Q6m0z3 methanococ	344	35	47.9	137	2	Q88JY2	Q88jy2 pseudomonas
272	36	49.3	514	2	Q8KZ28	Q8kz28 uncultured	345	35	47.9	140	2	Q6JLB3	Q6jlb3 francisella
273	36	49.3	523	2	Q6K632	Q6k632 oryza sativ	346	35	47.9	173	2	Q8BIH1	Q8bihi shewanella
274	36	49.3	529	1	NMT2_MOUSE	Q70311 mus musculu	347	35	47.9	179	2	Q67BF6	Q67bf6 haemophilus
275	36	49.3	529	2	Q700Q7	Q700q7 rattus norv	348	35	47.9	179	2	Q7VN40	Q7vn40 haemophilus
276	36	49.3	530	2	Q6BQJ5	Q6bjj5 debaryomyce	349	35	47.9	187	1	AMPD_SALTY	P30013 salmonella
277	36	49.3	532	2	Q8KX52	Q8kx52 synechococ	350	35	47.9	187	2	Q8Z9F5	Q8z9f5 salmonella
278	36	49.3	537	2	Q6Z543	Q6z543 oryza sativ	351	35	47.9	190	2	Q96BF5	Q96bf5 homo sapien
279	36	49.3	601	2	Q75DW2	Q75dw2 ashbya gos	352	35	47.9	195	2	Q9VRN5	Q9vrn5 drosophila
280	36	49.3	609	2	Q81ER1	Q81er1 plasmodium	353	35	47.9	200	2	O02498	Q02498 leishmania
281	36	49.3	620	2	Q6UJF6	Q6ujf6 drosophila	354	35	47.9	205	1	BASI_BOVIN	Q865r3 bos taurus
282	36	49.3	620	2	Q6UJF7	Q6ujf7 drosophila	355	35	47.9	217	2	Q6PVK2	Q6pvk2 pseudomonas
283	36	49.3	620	2	Q6UJF9	Q6ujf9 drosophila	356	35	47.9	221	2	Q9ALZ8	Q9alz8 fremyella d
284	36	49.3	621	2	Q6UJG2	Q6ujg2 drosophila	357	35	47.9	229	2	Q6M9T8	Q6m9t8 parachlamyd
285	36	49.3	621	2	Q9NAY2	Q9nay2 drosophila	358	35	47.9	237	2	Q6AME6	Q6ame6 desulfotale
286	36	49.3	621	2	Q9NGM3	Q9ngm3 drosophila	359	35	47.9	237	2	Q8BDM8	Q8bmd8 mus musculu
287	36	49.3	630	2	Q6UJF8	Q6ujf8 drosophila	360	35	47.9	239	2	O44730	O44730 caenorhabdi
288	36	49.3	630	2	Q6UJG0	Q6ujg0 drosophila	361	35	47.9	252	2	Q9LIQ7	Q9liq7 streptomyce
289	36	49.3	630	2	Q9NAY3	Q9nay3 drosophila	362	35	47.9	255	2	Q86KQ6	Q86kq6 dictyosteli
290	36	49.3	630	2	Q9NAY4	Q9nay4 drosophila	363	35	47.9	256	2	Q86KQ8	Q86kq8 dictyosteli
291	36	49.3	635	1	HS6E DROME	Q97125 drosophila	364	35	47.9	259	2	Q6LGM9	Q6lgw9 photobacter
292	36	49.3	639	2	Q7QUK1	Q7quk1 giardia lam	365	35	47.9	262	2	Q8Y1G0	Q8y1g0 ralatonia s
293	36	49.3	644	1	SYR_AERPE	Q9y339 aeropyrum p	366	35	47.9	283	2	Q9W057	Q9w057 drosophila
294	36	49.3	687	2	Q69DK8	Q69dk8 sus scrofa	367	35	47.9	284	1	LPPI_HUMAN	O14494 homo sapien
295	36	49.3	707	2	Q9CD82	Q9cd82 mycobacteri	368	35	47.9	292	2	Q7NFX3	Q7nfx3 gloeobacter
296	36	49.3	711	2	Q81292	Q81292 plasmodium	369	35	47.9	293	2	Q8RYM8	Q8rym8 oryza sativ
297	36	49.3	732	2	Q86UF2	Q86uf2 homo sapien	370	35	47.9	320	2	Q702C4	Q702c4 uncultured
298	36	49.3	747	2	Q8QPW0	Q8qpw0 influenza b	371	35	47.9	321	2	Q9GRJ9	Q9grj9 leishmania
299	36	49.3	752	1	RRP1_INBAC	P13871 influenza b	372	35	47.9	321	2	Q8RYK1	Q8ryk1 oryza sativ
300	36	49.3	752	1	RRP1_INBAC	P13872 influenza b	373	35	47.9	341	2	Q9HLX8	Q9hlx8 thermoplasma
301	36	49.3	752	1	RRP1_INBLE	P07832 influenza b	374	35	47.9	342	2	Q8LCP0	Q8lcp0 arabidopsis
302	36	49.3	752	1	RRP1_INBP9	Q36430 influenza b	375	35	47.9	342	2	Q9SND6	Q9snd6 arabidopsis
303	36	49.3	752	2	Q681P2	Q681p2 influenza b	376	35	47.9	346	2	Q9SUZ8	Q9suz8 arabidopsis
304	36	49.3	752	2	Q77SM9	Q77sm9 influenza b	377	35	47.9	347	2	Q9YCM3	Q9ycm3 aeropyrum p
305	36	49.3	752	2	Q77SN0	Q77sn0 influenza b	378	35	47.9	362	2	Q6L191	Q6l191 drosophila
306	36	49.3	752	2	Q77SN1	Q77sn1 influenza b	379	35	47.9	377	2	Q88DG5	Q88dg5 pseudomonas
307	36	49.3	752	2	Q77SN2	Q77sn2 influenza b	380	35	47.9	382	2	Q7UJS6	Q7ujs6 rhodospirell
308	36	49.3	752	2	Q80DM8	Q80dm8 influenza b	381	35	47.9	385	1	BASI_HUMAN	P35613 h basigin p
309	36	49.3	752	2	Q80DN5	Q80dn5 influenza b	382	35	47.9	392	2	Q94B20	Q94b20 arabidopsis
310	36	49.3	752	2	Q9IMP8	Q9imp8 influenza b	383	35	47.9	392	2	Q9SA96	Q9sa96 arabidopsis
311	36	49.3	752	2	Q9FWU1	Q9fwu1 influenza b	384	35	47.9	401	2	Q82N33	Q82n33 streptomyce
312	36	49.3	752	2	Q9QLJ8	Q9qlj8 influenza b	385	35	47.9	415	2	Q8LB99	Q8lb99 arabidopsis
313	36	49.3	752	2	Q9QLJ9	Q9qlj9 influenza b	386	35	47.9	415	2	Q9LJ68	Q9lj68 arabidopsis
314	36	49.3	752	2	Q9QLK0	Q9qlk0 influenza b	387	35	47.9	419	2	Q7RLU9	Q7rlu9 plasmodium
315	36	49.3	752	2	Q9QLK1	Q9qlk1 influenza b	388	35	47.9	419	2	Q73UF6	Q73uf6 mycobacteri
316	36	49.3	752	2	Q9QLK2	Q9qlk2 influenza b	389	35	47.9	422	1	PGL1_ARATH	P49062 arabidopsis
317	36	49.3	752	2	Q9QLK3	Q9qlk3 influenza b	390	35	47.9	422	2	Q9K426	Q9k426 streptomyce
318	36	49.3	752	2	Q9QLK4	Q9qlk4 influenza b	391	35	47.9	431	2	Q8PDE1	Q8ped1 xanthomonas
319	36	49.3	752	2	Q9QLK5	Q9qlk5 influenza b	392	35	47.9	435	2	O16968	O16968 caenorhabdi
320	36	49.3	752	2	Q9QLK6	Q9qlk6 influenza b	393	35	47.9	439	1	L1A3_HUMAN	Q8n6c8 homo sapien
321	36	49.3	752	2	Q9QLK7	Q9qlk7 influenza b	394	35	47.9	447	2	Q9F0G1	Q9f0g1 streptococ
322	36	49.3	752	2	Q9QLK8	Q9qlk8 influenza b	395	35	47.9	447	2	Q9FDM8	Q9fdm8 streptococ
323	36	49.3	752	2	Q9QLK9	Q9qlk9 influenza b	396	35	47.9	447	2	Q9RPL5	Q9rpl5 streptococ

397	35	47.9	453	2	P92013	P92013	caenorhabdi	470	34	46.6	122	2	Q40738	Q40738 oryza sativ
398	35	47.9	471	1	Y1R1 DROME	P16424	drosophila	471	34	46.6	124	2	Q91TY9	Q91TY9 influenza a
399	35	47.9	482	2	O23260	O23260	arabidopsis	472	34	46.6	129	2	Q91TZ1	Q91TZ1 influenza a
400	35	47.9	488	2	O8K0T4	O8K0T4	mus musculus	473	34	46.6	137	2	Q8NAF9	Q8NAF9 homo sapien
401	35	47.9	502	1	LASI YEAST	F36146	saccharomyc	474	34	46.6	146	2	Q9CTI3	Q9CTI3 mus musculus
402	35	47.9	502	2	O6GR55	O66R55	saccharomyc	475	34	46.6	159	2	Q8N8D2	Q8N8D2 homo sapien
403	35	47.9	503	2	O6BK51	O6BK51	debaryomyce	476	34	46.6	164	2	Q8HRE9	Q8HRE9 bryum gemm
404	35	47.9	508	2	Q7UXZ0	Q7UXZ0	rhodopirell	477	34	46.6	186	2	Q8HRF4	Q8HRF4 anomobryum
405	35	47.9	521	2	O7S3M1	Q7S3M1	neurospora	478	34	46.6	187	2	O8MG45	O8MG45 rosulabryum
406	35	47.9	521	2	Q8AR16	Q8AR16	arabidopsis	479	34	46.6	188	2	O63005	O63005 bryum alpin
407	35	47.9	546	1	PTR2 MOUSE	Q91V95	mus musculus	480	34	46.6	188	2	Q9AY14	Q9AY14 physcometri
408	35	47.9	551	2	O8T294	O8T294	dictyosteli	481	34	46.6	188	2	Q91RL9	Q91RL9 arabidopsis
409	35	47.9	562	2	Q6ZMG3	Q6ZMG3	homo sapien	482	34	46.6	188	2	Q6JKP4	Q6JKP4 influenza a
410	35	47.9	569	2	O84H24	O84H24	pseudomonas	483	34	46.6	188	2	O6JKP5	Q6JKP5 influenza a
411	35	47.9	575	2	O8WTU2	O8WTU2	homo sapien	484	34	46.6	188	2	O6JKP6	Q6JKP6 influenza a
412	35	47.9	575	2	Q96G45	Q96G45	homo sapien	485	34	46.6	188	2	Q6JKP7	Q6JKP7 influenza a
413	35	47.9	581	2	O89244	O89244	marek's dis	486	34	46.6	189	2	O63006	O63006 bryum caesp
414	35	47.9	581	2	Q782P8	Q782P8	gallid herp	487	34	46.6	189	2	O63011	O63011 rhodobryum
415	35	47.9	622	2	Q653D2	Q653D2	oryza sativ	488	34	46.6	189	2	Q6JE74	Q6JE74 splichnum w
416	35	47.9	626	2	O81129	O81129	plasmodium	489	34	46.6	190	2	O62998	O62998 funaria hyg
417	35	47.9	627	2	Q7RWT2	Q7RWT2	neurospora	490	34	46.6	190	2	O63009	O63009 bryum steno
418	35	47.9	628	2	Q6A849	Q6A849	propionibac	491	34	46.6	190	2	Q8HU00	Q8HU00 bryum pallie
419	35	47.9	631	2	Q8SVW5	Q8SVW5	encephalico	492	34	46.6	190	2	Q8MCT1	Q8MCT1 haplodontiu
420	35	47.9	638	2	Q9GLR0	Q9GLR0	bos taurus	493	34	46.6	190	2	Q6K3W6	Q6K3W6 oryza sativ
421	35	47.9	656	2	Q9M092	Q9M092	arabidopsis	494	34	46.6	190	2	Q9AY13	Q9AY13 aphanorrrheg
422	35	47.9	662	1	I12R HUMAN	P42701	homo sapien	495	34	46.6	191	2	Q9AY15	Q9AY15 physcometri
423	35	47.9	727	2	Q6RKB2	Q6RKB2	rattus norv	496	34	46.6	191	2	O6W760	Q6W760 influenza a
424	35	47.9	735	2	Q9N8A6	Q9N8A6	trypanosoma	497	34	46.6	191	2	Q8W761	Q8W761 influenza a
425	35	47.9	739	2	Q9Q0S6	Q9Q0S6	influenza a	498	34	46.6	191	2	Q8BCD5	Q8BCD5 influenza a
426	35	47.9	757	2	Q6LTA6	Q6LTA6	photobacter	499	34	46.6	191	2	Q8BCD6	Q8BCD6 influenza a
427	35	47.9	782	2	O8PP65	O8PP65	xanthomonas	500	34	46.6	191	2	Q8BCE4	Q8BCE4 influenza a
428	35	47.9	837	1	NCM2 HUMAN	O15394	homo sapien							
429	35	47.9	837	1	NCM2 MOUSE	Q35136	mus musculus							
430	35	47.9	837	2	Q727F2	Q727F2	homo sapien							
431	35	47.9	837	2	Q6RKB3	Q6RKB3	rattus norv							
432	35	47.9	849	2	Q815V7	Q815V7	plasmodium							
433	35	47.9	958	2	Q7NNV9	Q7NNV9	chromobacte							
434	35	47.9	1019	2	Q6CVF3	Q6CVF3	klyuveromyc							
435	35	47.9	1036	2	Q6NVF2	Q6NVF2	mus musculus							
436	35	47.9	1065	2	Q6P2X0	Q6P2X0	oryza sativ							
437	35	47.9	1074	1	FLD1 MOUSE	P22280	mus musculus							
438	35	47.9	1074	1	FLD1 RAT	P70496	rattus norv							
439	35	47.9	1137	2	Q8T9H7	Q8T9H7	drosophila							
440	35	47.9	1137	2	Q9VXF4	Q9VXF4	strongyloce							
441	35	47.9	1181	2	Q96JV0	Q96JV0	homo sapien							
442	35	47.9	1234	2	Q7PLQ7	Q7PLQ7	anopheles g							
443	35	47.9	1322	2	Q7FNR7	Q7FNR7	anopheles g							
444	35	47.9	1322	2	Q9NAT0	Q9NAT0	anopheles g							
445	35	47.9	1322	2	Q9NJS5	Q9NJS5	anopheles g							
446	35	47.9	1323	2	O13686	O13686	schizosacch							
447	35	47.9	1402	2	Q7RBO6	Q7RBO6	plasmodium							
448	35	47.9	1412	1	Z462 HUMAN	Q96JN2	homo sapien							
449	35	47.9	1499	2	Q9R839	Q9R839	mycosphaere							
450	35	47.9	1559	2	Q81DC3	Q81DC3	plasmodium							
451	35	47.9	1779	2	Q9BPB6	Q9BPB6	samia cynth							
452	35	47.9	2153	2	Q97375	Q97375	strongyloce							
453	35	47.9	2403	2	Q68CP0	Q68CP0	homo sapien							
454	35	47.9	2506	2	Q63HJ5	Q63HJ5	homo sapien							
455	35	47.9	3115	2	Q9VQV1	Q9VQV1	homo sapien							
456	34.5	47.3	325	2	Q9PP25	Q9PP25	campylobact							
457	34.5	47.3	555	2	Q8H5J9	Q8H5J9	oryza sativ							
458	34	46.6	67	2	Q82548	Q82548	influenza a							
459	34	46.6	72	2	Q26942	Q26942	tribolium c							
460	34	46.6	77	2	Q7S1T4	Q7S1T4	neurospora							
461	34	46.6	78	2	Q82547	Q82547	influenza a							
462	34	46.6	85	2	Q7RTE0	Q7RTE0	oryza sativ							
463	34	46.6	87	2	Q9P224	Q9P224	homo sapien							
464	34	46.6	90	2	Q621J9	Q621J9	oryza sativ							
465	34	46.6	92	2	Q9EYK7	Q9EYK7	lactobacill							
466	34	46.6	105	2	Q7XAW8	Q7XAW8	brassicica ra							
467	34	46.6	105	2	Q7YAX1	Q7YAX1	brassicica ra							
468	34	46.6	112	2	O50739	O50739	borrelia bu							
469	34	46.6	116	2	Q50RYF3	Q50RYF3	deinococcus							

ALIGNMENTS

RESULT 1	LP3_HUMAN	STANDARD;	PRT;	311 AA.
AC	O14495; Q96GW0; Q99782;			
DT	29-MAR-2004 (Rel. 43, Created)			
DT	29-MAR-2004 (Rel. 43, Last sequence update)			
DE	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Lipid phosphate phosphohydrolase 3 (EC 3.1.3.4) (Phosphatidic acid			
DE	phosphatase 2b) (Phosphatidate phosphohydrolase type 2b) (PAP-2b)			
DE	(PAP2-beta) (Vascular endothelial growth factor and type I			
DE	collagen inducible protein) (VCIP).			
OS	Name=PPAP2B; Synonyms=LPP3;			
GN	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., CHARACTERIZATION, AND INDUCTION.			
RX	MEDLINE=97450590; PubMed=9305923; DOI=10.1074/jbc.272.39.24572;			
RA	Kai M., Wada I., Imai S.-I., Sakane F., Kanch H.;			
RT	"Cloning and characterization of two human isozymes of Mg2+-			
RT	independent phosphatidic acid phosphatase.";			
RL	J. Biol. Chem. 272:24572-24578 (1997).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.			
RX	MEDLINE=98371049; PubMed=9705349; DOI=10.1074/jbc.273.34.22059;			
RA	Roberts R., Sciorra V.A., Morris A.J.;			
RT	"Human type 2 phosphatidic acid phosphohydrolases. Substrate			
RT	specificity of the type 2a, 2b, and 2c enzymes and cell surface			
RT	activity of the 2a isoform.";			
RL	J. Biol. Chem. 273:22059-22067 (1998).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	PubMed=12660161; DOI=10.1093/emboj/cdg165;			
RA	Huntsoe J.O., Feng S., Thakker G.D., Yang J., Hong J., Wary K.K.;			
RT	"Regulation of cell-cell interactions by phosphatidic acid phosphatase			
RT	2b/VCIP.";			

RL EMBO J. 22:1539-1554 (2003).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Leung D.W., Tompkins C.K.;
 RT "Molecular cloning of and expression of an isoform of human
 RT phosphatidic acid phosphatase cDNA";
 RT Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97264341; PubMed=9110174;
 RA Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Liu W.,
 RA Ricafrente J.Y., Wentland M.A., Lennon G., Gibbs R.A.;
 RT "Large-scale concatenation cDNA sequencing";
 RL Genome Res. 7:353-358 (1997).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [7]
 RP SUBUNIT.
 RX PubMed=14725715; DOI=10.1186/1471-2091-5-2;
 RA Burnett C., Makridou P., Hewlett L., Howard K.;
 RT "Lipid phosphate phosphatases dimerise, but this interaction is not
 RT required for in vivo activity";
 RL BMC Biochem. 5:2-2 (2004).
 CC -!- FUNCTION: Catalyzes the conversion of phosphatidic acid (PA) to
 CC diacylglycerol (DG). In addition it hydrolyzes lysophosphatidic
 CC acid (LPA), ceramide-1-phosphate (C-1-P) and sphingosine-1-
 CC phosphate (S-1-P). The relative catalytic efficiency is LPA = PA >
 CC C-1-P > S-1-P. May be involved in cell adhesion and in cell-cell
 CC interactions.
 CC -!- CATALYTIC ACTIVITY: A 3-sn-phosphatidate + H(2O) = a 1,2-diacyl-
 CC sn-glycerol + phosphate.
 CC -!- ENZYME REGULATION: Inhibited by sphingosine, zinc ions and
 CC propanolol. Not inhibited by N-ethylmaleimide treatment.
 CC -!- SUBUNIT: Homodimer. This complex seems not to be involved in
 CC substrate recognition, it may confer only structural or functional
 CC stability.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Post-Golgi and
 CC plasma membrane localization.
 CC -!- TISSUE SPECIFICITY: Ubiquitously expressed. Highly expressed in
 CC heart and placenta.
 CC -!- INDUCTION: By epidermal growth factor (EGF), vascular endothelial
 CC growth factor (VEGF), basic fibroblast growth factor (bFGF) and
 CC phorbol myristate acetate (PMA).
 CC -!- PTM: N-glycosylated. Contains high-mannose oligosaccharides.
 CC -!- SIMILARITY: Belongs to the PA-phosphatase related phosphoesterase
 CC family.
 CC -!- CAUTION: Ref.5 sequence differs from that shown due to a
 CC frameshift in position 225.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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 CC -----
 DR EMBL; AB000889; BAA22594.1; -;
 DR EMBL; AF017786; AAC63433.1; -;
 DR EMBL; AF480883; AAO84481.1; -;
 DR EMBL; AF043329; AAO02271.1; -;
 DR EMBL; U79294; AAB50222.1; ALT FRAME.
 DR EMBL; BC009196; AAH09196.1; -;
 DR Genew; HGNC:9229; PPAP2B.
 DR H-InvDB; HIX0000628; -;
 DR Reactome; O14495; -;
 DR MIM; 607125; -;
 DR GO; GO:0016020; C:membrane; TAS.
 DR GO; GO:004721; P:phosphoprotein phosphatase activity; TAS.
 DR GO; GO:0008151; P:cell growth and/or maintenance; TAS.
 DR GO; GO:0008354; P:germ-cell migration; TAS.
 DR InterPro; IPR008934; ACPase_VanPerase.
 DR InterPro; IPR000326; Peptidase_PA_PTP.
 DR Pfam; PF01569; PAP2; 1.
 DR SMART; SM00014; acidppc; 1.
 KW Glycoprotein; Hydrolase; Transmembrane.
 FT DOMAIN 1 33 Cytoplasmic (Potential).
 FT TRANSMEM 34 54 Potential.
 FT DOMAIN 55 85 Lumenal (Potential).
 FT TRANSMEM 86 106 Potential.
 FT DOMAIN 107 122 Cytoplasmic (Potential).
 FT TRANSMEM 123 143 Potential.
 FT DOMAIN 144 193 Lumenal (Potential).
 FT TRANSMEM 194 214 Potential.
 FT DOMAIN 215 227 Cytoplasmic (Potential).
 FT TRANSMEM 228 248 Potential.
 FT DOMAIN 249 257 Lumenal (Potential).
 FT TRANSMEM 258 278 Potential.
 FT DOMAIN 279 311 Cytoplasmic (Potential).
 FT CARBOHYD 170 170 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 282 282 T -> M (in Ref. 6).
 SQ SEQUENCE 311 AA; 35116 MW; CB3F60189044DA31 CRC64;
 Query Match 100.0%; Score 73; DB 1; Length 311;
 Best Local Similarity 100.0%; Pred. No. 8.6e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NYRCRGDDSKVQE 13
 DB 178 NYRCRGDDSKVQE 190
 RESULT 2
 LPP3 MOUSE
 ID LPP3 MOUSE STANDARD; PRT; 312 AA.
 AC Q99YF8; QB8TB7;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Lipid phosphate phosphohydrolase 3 (EC 3.1.3.4) (Phosphatidic acid
 DE phosphatase 2b) (Phosphatidate phosphohydrolase type 2b) (PAP2b) (PAP-
 DE 2b) (PAP2-beta).
 GN Name=Ppap2b; Synonyms=Lpp3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojbori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Glissi C., Godzik A., Gough J.,
RA Grimmond S., Gustinchik S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Malcais L., Marchionni L., McKenzie L., Miki H.,
RA Nagaehima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reid J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyszynski-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zvolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sakaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP FUNCTION, AND DISEASE.
RX PubMed=12925589; DOI=10.1242/dev.00635;
RA Escalante-Alcalde D., Hernandez L., Le Stunff H., Maeda R., Lee H.-S.,
RA Cheng G. Jr., Sciorra V.A., Daar I., Spiegel S., Morris A.J.,
RA Stewart C.L.;
RT "The lipid phosphatase LPP3 regulates extra-embryonic vasculogenesis
RT and axis patterning.";
RL Development 130:4623-4637 (2003).
CC -!- FUNCTION: Catalyzes the conversion of phosphatidic acid (PA) to
CC diacylglycerol (DG). In addition it hydrolyzes lysophosphatidic
CC acid (LPA), ceramide-1-phosphate (C-1-P) and sphingosine-1-
CC phosphate (S-1-P) (By similarity). Essential to the formation of
CC the chorio-allantoic placenta and extra-embryonic vasculature.
CC Also mediates gastrulation and axis formation, probably by
CC regulating the Wnt signaling pathway.
CC -!- CATALYTIC ACTIVITY: A 3-sn-phosphatidate + H(2)O = 1,2-diacyl-
CC sn-glycerol + phosphate.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum associated (By similarity).
CC -!- DISEASE: Ppap2b deficient embryos fail to form a chorio-allantoic
CC placenta and yolk sac vasculature. A subset of embryos also show a
CC shortening of the anterior-posterior axis and frequent duplication

CC of axial structures. Loss of Ppap2b results in a marked increase
CC in beta-catenin-mediated T-cell factor (TCF) transcription.
CC -!- SIMILARITY: Belongs to the PA-phosphatase related phosphoesterase
CC family.
CC -!- CAUTION: Ref.1 sequence differs from that shown due to a
CC frameshift in position 226.
CC -----
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CC -----
CC EMBL; AK011276; BAC35327.1; ALT_FRAME.
CC EMBL; BC005558; AAH05558.1; -.
CC MGD; MGI:1915166; Ppap2b.
CC GO; GO:0042577; F:lipid phosphatase activity; IMP.
CC GO; GO:0001568; P:blood vessel development; IMP.
CC GO; GO:0010003; P:gastrulation (sensu Mammalia); IMP.
CC GO; GO:0006644; P:phospholipid metabolism; IMP.
CC GO; GO:0030111; P:regulation of Wnt receptor signaling pathway; IDA.
CC InterPro; IPR008934; AcPase_VanPerase.
CC InterPro; IPR00326; Peptidase_PA_ptp.
CC Pfam; PF01569; PAP2; 1.
CC SMART; SM00014; acidPPc; 1.
CC Developmental protein; Glycoprotein; Hydrolase; Transmembrane.
KW DOMAIN 1 33 Cytoplasmic (Potential).
FT TRANSMEM 34 54 Potential.
FT DOMAIN 55 85 Luminal (Potential).
FT TRANSMEM 86 106 Potential.
FT DOMAIN 107 123 Cytoplasmic (Potential).
FT TRANSMEM 124 144 Potential.
FT DOMAIN 145 194 Luminal (Potential).
FT TRANSMEM 195 215 Potential.
FT DOMAIN 216 226 Cytoplasmic (Potential).
FT TRANSMEM 227 247 Potential.
FT DOMAIN 248 258 Luminal (Potential).
FT TRANSMEM 259 279 Potential.
FT DOMAIN 280 312 Cytoplasmic (Potential).
FT CARBOHYD 171 171 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 312 AA; 35216 MW; D782986E04B57D7D CRC64;
Query Match 94.5%; Score 69; DB 1; Length 312;
Best Local Similarity 92.3%; Pred. No. 0.00046;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 NYRCRGDDSKVQE 13
DB 179 NYRCRGDDSKVQE 191
|||||:|||||
RESULT 3
LPP3_RAT
ID_LPP3_RAT STANDARD; PRT; 312 AA.
AC P97544;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Lipid phosphate phosphohydrolase 3 (SC 3.1.3.4) (Phosphatidic acid
DE phosphate 2b) (Phosphatidate phosphohydrolase type 2b) (PAP2b) (PAP-
DE 2b) (PAP2-beta) (Differentially expressed in rat intestine 42)
DE (Dri42).
GN Name=Ppap2b; Synonyms=Lpp3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., TOPOLOGY, AND N-GLYCOSYLATION.
RC STRAIN=Wistar; TISSUE=Small intestine;
RX MEDLINE=97094703; PubMed=8939937; DOI=10.1074/jbc.271.47.29928;

RA Barila D., Plateroti M., Nobili F., Muda A.O., Xie Y., Morimoto T.,
 RA Perozzi G.;
 RT "The Dri 42 gene, whose expression is upregulated during epithelial
 RT differentiation, encodes a novel ER resident transmembrane protein.";
 RL J. Biol. Chem. 271:29928-29936(1996).
 RN [2]
 RP TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
 RX PubMed=8055940;
 RA Barila D., Murgia C., Nobili F., Gaetani S., Perozzi G.;
 RT "Subtractive hybridization cloning of novel genes differentially
 RT expressed during intestinal development.";
 RL Eur. J. Biochem. 223:701-709(1994).
 RN [3]
 RP TISSUE SPECIFICITY.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=2155999; PubMed=11704545;
 RA Nanjundan M., Possemayer F.;
 RT "Molecular cloning and expression of pulmonary lipid phosphate
 RT phosphohydrolases";
 RL Am. J. Physiol. 281:L1484-L1493(2001).
 CC -1- FUNCTION: Catalyzes the conversion of phosphatidic acid (PA) to
 CC diacylglycerol (DG). In addition it hydrolyzes lysophosphatidic
 CC acid (LPA), ceramide-1-phosphate (C-1-P) and sphingosine-1-
 CC phosphate (S-1-P) (By similarity). Involved in the regulation of
 CC epithelial differentiation.
 CC -1- CATALYTIC ACTIVITY: A 3-sn-phosphatidate + H(2)O = a 1,2-diacyl-
 CC sn-glycerol + phosphate.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum associated.
 CC -1- TISSUE SPECIFICITY: Detected in epithelial cells of intestinal
 CC mucosa, lung, liver and brain.
 CC -1- DEVELOPMENTAL STAGE: Expression is increased during epithelial
 CC differentiation in intestinal mucosa as well as in kidney, liver
 CC and lung.
 CC -1- PTM: N-glycosylated.
 CC -1- SIMILARITY: Belongs to the PA-phosphatase related phosphoesterase
 CC family.
 CC -----
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 CC -----
 DR EMBL: Y07783; CAA69106.1; -;
 DR InterPro: IPR008934; ACPase_VanPerase.
 DR InterPro: IPR000326; Pesterase_PA_PTP.
 DR Pfam: PF01569; PAP2; 1.
 DR SMART: SM00014; acidppc; 1.
 KW Endoplasmic reticulum; Glycoprotein; Hydrolase; Transmembrane.
 FT DOMAIN 1 33 Cytoplasmic (Potential).
 FT TRANSMEM 34 54 Potential.
 FT DOMAIN 55 85 Luminal (Potential).
 FT TRANSMEM 86 106 Potential.
 FT DOMAIN 107 123 Cytoplasmic (Potential).
 FT TRANSMEM 124 144 Potential.
 FT DOMAIN 145 194 Luminal (Potential).
 FT TRANSMEM 195 215 Potential.
 FT DOMAIN 216 226 Cytoplasmic (Potential).
 FT TRANSMEM 227 247 Potential.
 FT DOMAIN 248 258 Luminal (Potential).
 FT TRANSMEM 259 279 Potential.
 FT DOMAIN 280 312 Cytoplasmic (Potential).
 FT CARBOHYD 171 171 N-linked (GLCNAC...) (Potential).
 SQ SEQUENCE 312 AA; 35318 MW; 9B447FD321DB0419 CRC64;
 Query Match 94.5%; Score 69; DB 1; Length 312;
 Best Local Similarity 92.3%; Pred. No. 0.00046;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYRCRGDDSKVOE 13
 |||||:|||||
 DB 179 NYRCRGDDSKVOE 191
 RESULT 4
 Q6IMX4 PRELIMINARY; PRT; 312 AA.
 ID Q6IMX4;
 AC Q6IMX4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE ER transmembrane protein Dri 42.
 GN Name=Dri42;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC072544; AAH72544.1; -;
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR InterPro: IPR008934; ACPase_VanPerase.
 DR InterPro: IPR000326; Pesterase_PA_PTP.
 DR Pfam: PF01569; PAP2; 1.
 DR SMART: SM00014; acidppc; 1.
 KW Transmembrane.
 SQ SEQUENCE 312 AA; 35233 MW; CDA54495C0E7D37D CRC64;
 Query Match 94.5%; Score 69; DB 2; Length 312;
 Best Local Similarity 92.3%; Pred. No. 0.00046;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYRCRGDDSKVOE 13
 |||||:|||||
 DB 179 NYRCRGDDSKVOE 191
 RESULT 5
 Q68F34 PRELIMINARY; PRT; 307 AA.
 ID Q68F34;
 AC Q68F34;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE MGC81884 protein.

GN Name=MGC81884;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Kidney;
 RC MEDLINE=22341132; PubMed=12454917; DOI=10.1002/gvdy.10174;
 RX Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Gichwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX Klein S., Gerhard D.S.;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC080011; AAH0011.1; -;
 DR InterPro; IPR008934; AcPase_VanParase.
 DR InterPro; IPR000326; Pesterase_PA_PTP.
 DR Pfam; PF01569; PAP2; 1.
 DR SMART; SM00014; acidPPc; 1.
 SQ SEQUENCE 307 AA; 34498 MW; 09666E6DA6265308 CRC64;
 Query Match 63.0%; Score 46; DB 2; Length 307;
 Best Local Similarity 61.5%; Pred. No. 6.6;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 NYRCRGDDSKVQE 13
 DB 179 NYECRGPPNKWME 191
 RESULT 6
 Q73RYO ID Q73RYO PRELIMINARY; PRT; 776 AA.
 AC Q73RYO;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=MAP4298c;
 OS Mycobacterium paratuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1770;
 [1]

RN SEQUENCE FROM N.A.
 RC STRAIN=K10;
 RA Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE017242; AAS06848.1; -;
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR003673; CAIB_BAIF.
 DR Pfam; PF02515; CoA_transf_3; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 776 AA; 82189 MW; 38A4528FCSB0B4BB CRC64;
 Query Match 63.0%; Score 46; DB 2; Length 776;
 Best Local Similarity 80.0%; Pred. No. 18;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 YRCRGDDSKV 11
 DB 615 YRCRGDDAWV 624
 RESULT 7
 Q95L84 ID Q95L84 PRELIMINARY; PRT; 167 AA.
 AC Q95L84;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Phosphatidic acid phosphatase type 2A (Fragment).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]_TaxID=9986;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22306422; PubMed=12388084;
 RA Wang D.-A., Du H., Jaggar J.H., Brindley D.N., Tigyi G.J.,
 RA Watsky M.A.;
 RT "Injury-elicited differential transcriptional regulation of
 RT phospholipid growth factor receptors in the cornea.";
 RL Am. J. Physiol. Cell Physiol. 283:C1646-C1654(2002).
 DR EMBL; AF404277; AAL01884.1; -;
 DR InterPro; IPR008934; AcPase_VanParase.
 DR InterPro; IPR000326; Pesterase_PA_PTP.
 DR Pfam; PF01569; PAP2; 1.
 DR SMART; SM00014; acidPPc; 1.
 DR NON_TER 1
 FT NON_TER 167
 SQ SEQUENCE 167 AA; 18922 MW; 5185AECB0C8B8FB CRC64;
 Query Match 60.3%; Score 44; DB 2; Length 167;
 Best Local Similarity 61.5%; Pred. No. 7.8;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 NYRCRGDDSKVQE 13
 DB 127 NYVCRGNAQVKKE 139
 RESULT 8
 Y787_METJA ID Y787_METJA STANDARD; PRT; 504 AA.
 AC Q58197;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Hypothetical protein MJ0787.
 GN OrderedLocusNames=MJ0787;
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcales; Methanocaldococcus.
 OX NCBI_TaxID=2190;
 [1]


```

RP SEQUENCE FROM N.A.
RX STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RA MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-P., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii";
RL Science 273:1058-1073 (1996).
CC -I- SIMILARITY: Strong, to M.thermoautotrophicum MTH1137.
CC
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CC -----
DR EMBL: U67523; AAB98783.1; -.
DR FIR: C64398; C64398.
DR TIGR: MJ0787; -.
DR InterPro: IPR011060; Ribp bind barrel.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 504 AA; 56128 MW; 1F6C18C2C2655EBC0 CRC64;

Query Match 60.3%; Score 44; DB 1; Length 504;
Best Local Similarity 66.7%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 YRCRGDSDSKVQE 13
DB 463 YPCNGDDKKVLE 474

RESULT 9
Q50468 ID Q50468 PRELIMINARY; PRT; 705 AA.
AC Q50468;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Pks002a.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith D.R.;
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Robison K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
CC family.
DR EMBL: U00024; AAA50930.1; -.
DR HSSP: P08659; 1LCI.
DR GO: GO:0003824; P:catalytic activity; IEA.
DR GO: GO:0048037; P:cofactor binding; IEA.
DR GO: GO:0016874; P:ligase activity; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR009081; ACP like.
DR InterPro: IPR000873; AMP-bind.
DR InterPro: IPR006163; Phspanteth_bind.
DR Pfam: PF00501; AMP-binding; 1.
DR Pfam: PF00550; PP-binding; 1.
DR PRINTS: PR00154; AMPBINDING.

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DR PROSITE; PS50075; ACP DOMAIN; 1.
SQ SEQUENCE 705 AA; 75169 MW; 9F9D4F500690BF5D CRC64;

Query Match 60.3%; Score 44; DB 2; Length 705;
Best Local Similarity 70.0%; Pred. No. 37;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YRCRGDSDSKV 11
DB 383 YRCRADDTTEV 392

RESULT 10
P96283 ID P96283 PRELIMINARY; PRT; 705 AA.
AC P96283; Q7D6D9;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE PROBABLE PARTIY-ACID-CoA LIGASE FADD22 (PARTIY-ACID-CoA SYNTHETASE)
DE (PARTIY-ACID-CoA SYNTHETASE) (EC 6.2.1.1-) (Substrate--CoA ligase).
GN Name=fadd22; OrderedLocustNames=MT3021, RV2948c;
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RA Harris D.E., Brosch R., Parkhill J., Garnier T., Churche C.M.,
RA Tekala F., Badcock K., Basham D., Brown D., Chillingworth T.,
RA Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
RA Murphy J.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
RA Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544 (1998).
[2]
RP SEQUENCE FROM N.A.
RA STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RX DOI=10.1128/JB.184.19.5479-5490.2002;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,
RA Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,
RA Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.,
RA Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
RA Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL J. Bacteriol. 184:5479-5490 (2002).
CC -I- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
CC family.
DR EMBL: BX842581; CAB06101.1; -.
DR EMBL: AE000516; AAK47347.1; -.
DR FIR: A70669; A70669.
DR HSSP: P08659; 1LCI.
DR TIGR: MT3021; -.
DR TubercuList; RV2948c; -.
DR GO: GO:0003824; P:catalytic activity; IEA.
DR GO: GO:0048037; P:cofactor binding; IEA.
DR GO: GO:0016874; P:ligase activity; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR009081; ACP like.
DR InterPro: IPR000873; AMP-bind.
DR InterPro: IPR006163; Phspanteth_bind.
DR Pfam: PF00501; AMP-binding; 1.
DR Pfam: PF00550; PP-binding; 1.
DR PRINTS: PR00154; AMPBINDING.

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DR PROSITE; PSS0075; ACP_DOMAIN; 1.
KW Ligase.
SQ SEQUENCE 705 AA; 75197 MW; 600F2D0EABFDF1DC CRC64;

Query Match 60.3%; Score 44; DB 2; Length 705;
Best Local Similarity 70.0%; Pred. No. 37;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YRCRGDDSKV 11
  ||||| :|||
DB 383 YRCRADTTEV 392

RESULT 11
Q7YXK7 PRELIMINARY; PRT; 705 AA.
AC Q7YXK7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PROBABLE FATTY-ACID-CoA LIGASE FADD22 (FATTY-ACID-CoA SYNTHETASE)
DE (FATTY-ACID-CoA SYNTHASE) (EC 6.2.1.-)
DE Names:fadd22; OrderedLocusNames=Mb2972c;
GN Mycobacterium bovis.
OS Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OC NCBI_TaxID=1765;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
RA Garnier T., Eiglmeyer K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrall B.G., Cole S.T., Gordon S.V., Hewinson R.G.,
RT "The complete genome sequence of Mycobacterium bovis."
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
DR EMBL; BX248344; CAD96659.1; -
DR GO; GO:0048037; F:cofactor binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR009081; ACP like.
DR InterPro; IPR000873; AMP-bind.
DR InterPro; IPR006163; Phspanteth_bind.
DR Pfam; PF00501; AMP-binding; 1.
DR Pfam; PF00550; PP-binding; 1.
DR PROSITE; PSS0075; ACP_DOMAIN; 1.
KW Complete proteome; Ligase.
SQ SEQUENCE 705 AA; 75197 MW; 600F2D0EABFDF1DC CRC64;

Query Match 60.3%; Score 44; DB 2; Length 705;
Best Local Similarity 70.0%; Pred. No. 37;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YRCRGDDSKV 11
  ||||| :|||
DB 383 YRCRADTTEV 392

RESULT 12
Q6AX87 PRELIMINARY; PRT; 307 AA.
AC Q6AX87;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE MGC81990 protein.
DE Name=MGC81990;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;

RN RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Klein S., Gerhard D.S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC079709; AAH79709.1; -
DR InterPro; IPR008934; ACPase_VanPerase.
DR InterPro; IPR000326; Pesterase_PA_PTP.
DR Pfam; PF01569; PAP2; 1.
DR SMART; SM00014; acidPPC; 1.
SQ SEQUENCE 307 AA; 34417 MW; 23F956E7B8FFED0D CRC64;

Query Match 58.9%; Score 43; DB 2; Length 307;
Best Local Similarity 61.5%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 NYVCRGDDSKVQ 13
  ||||| :|||
DB 179 NYVCRGPPNKWME 191

RESULT 13
Q7QP19 PRELIMINARY; PRT; 73 AA.
AC Q7QP19;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GLP 83 1716 1495.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OC NCBI_TaxID=184922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
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CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACB01000181; EAA36741.1; -.
SQ SEQUENCE 73 AA; 8125 MW; 4F866C9AEF254DDE CRC64;

Query Match 57.5%; Score 42; DB 2; Length 73;
Best Local Similarity 75.0%; Pred. No. 7.3; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 0;

Qy 1 NYRCRGDD 8
Db 27 DYRCCKGDD 34
:|||||
:|||||

RESULT 14
ID Q86KQ7 PRELIMINARY; PRT; 265 AA.
AC Q86KQ7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
RA Gloeckner G., Bichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL Nature 418:79-85(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC115584; AAO50949.1; -.
DR InterPro; IPR008997; RicinB_like.
KW Hypothetical protein.
SQ SEQUENCE 265 AA; 30503 MW; F1E238DA048F6D2 CRC64;

Query Match 57.5%; Score 42; DB 2; Length 265;
Best Local Similarity 87.5%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YRCRGDD 9
Db 45 YRCRNDD 52
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RESULT 15
Q9A731 PRELIMINARY; PRT; 513 AA.
ID Q9A731;
AC Q9A731;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anthranilate synthase component I.
GN OrderedLocusNames=CC1895;
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

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RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
RA Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
RA Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
RA Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AS005863; AAK23870.1; -.
DR PIR; B87484; B87484.
DR HSSP; P05041; 1KOG.
DR TIGR; CC1895; -.
DR GO; GO:0004049; F:anthranilate synthase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR GO; GO:0000162; P:tryptophan biosynthesis; IEA.
DR InterPro; IPR005256; Anth synth.
DR InterPro; IPR005801; Anth synth chor.
DR Pfam; PF04715; Anth synt_I_N_1_-1_N.
DR PRINTS; PR00095; Chorismate_Bind; 1.
DR PRODOM; PD000779; Anth synth chor; 1.
DR TIGRFAMs; TIGR00564; trpE_most; 1.
KW Complete proteome.
SQ SEQUENCE 513 AA; 55794 MW; A02E026E08AE30C CRC64;

Query Match 57.5%; Score 42; DB 2; Length 513;
Best Local Similarity 50.0%; Pred. No. 61;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YRCRGDDSKVQ 13
Db 73 WRCRGDQAEIAE 84
:|||||
:|||||

RESULT 16
Q8WQJ3 PRELIMINARY; PRT; 845 AA.
ID Q8WQJ3;
AC Q8WQJ3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SRCR LCCL adhesive-like protein (Fragment).
GN Name=slap;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21982590; PubMed=11985859; DOI=10.1016/S0166-6851(02)00016-6;
RA Delrieu I., Waller C.C., Mota M.M., Grainger M., Langhorne J.,
RA Holder A.A.;
RT "PSLAP, a protein with multiple adhesive motifs, is expressed in
RT Plasmodium falciparum gametocytes.";
RL Mol. Biochem. Parasitol. 121:11-20(2002).
DR EMBL; AY072023; AAL58521.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005044; F:scavenger receptor activity; IEA.
DR Pfam; PF03815; LCCL; 3.
DR Pfam; PF00530; SRCR; 2.
DR SMART; SM00202; SR; 2.
DR PROSITE; PS50820; LCCL; 2.
DR PROSITE; PS50287; SRCR_2; 2.
DR FT NON TER 1
DR FT NON TER 1
DR FT NON TER 1
SQ SEQUENCE 845 AA; 95032 MW; 06A389B4CC294477 CRC64;

Query Match 57.5%; Score 42; DB 2; Length 845;
Best Local Similarity 41.7%; Pred. No. 16+02;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NYRCRGDDSKVQ 12
Db 340 NFRCKGDEANLK 351
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:|||||

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RESULT 17
Q8WT63      PRELIMINARY;      PRT; 1304 AA.
AC Q8WT63;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Multidomain scavenger receptor protein PDSR precursor.
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2242506; PubMed=12354219;
RA Claudiano C., Dessens J.T., Trueman H.E., Arai M., Mendoza J.,
RA Butcher G.A., Crompton T., Sindén R.E.;
RT "A malaria scavenger receptor-like protein essential for parasite
RT development.";
RL Mol. Microbiol. 45:1473-1484(2002).
CC -!- SIMILARITY: Contains 1 PLAT domain.
DR EMBL; AV034780; AAK64185.1; -.
DR HSSP; O43405; 1JBI.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005044; F:scavenger receptor activity; IEA.
DR Pfam; PF03815; LCCL; 4.
DR Pfam; PF01477; PLAT; 1.
DR Pfam; PF00530; SRCR; 2.
DR SMART; SM00202; SR; 2.
DR PROSITE; PS08020; LCCL; 3.
DR PROSITE; PS00095; PLAT; 1.
DR PROSITE; PS0287; SRCR_2; 2.
KW Receptor; Signal.
FT SIGNAL 1 22 Potential.
SQ SEQUENCE 1304 AA; 148247 MW; F936CC9AE7B19F1C CRC64;

Query Match 57.5%; Score 42; DB 2; Length 1304;
Best Local Similarity 41.7%; Pred. No. 1.7e+02;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 NVYRCGDDSKVQ 12
:|:|:|:|:|:
DB 614 NFRCKGDEANLK 625

RESULT 18
Q8P0M2      PRELIMINARY;      PRT; 37 AA.
AC Q8P0M2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical phage protein.
GN OrderedLocNames=spym18_1296;
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=186103;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MGAS8232;
RA MEDLINE=2197593; PubMed=11917108; DOI=10.1073/pnas.062526099;
RA Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylvia G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks.";
RA Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
DR EMBL; AB010051; AAL97902.1; -.

KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 37 AA; 4398 MW; E7E884FEAA642342 CRC64;

Query Match 56.2%; Score 41; DB 2; Length 37;
Best Local Similarity 61.5%; Pred. No. 5.3;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 NVYRCGDDSKVQ 13
|||:|:|:|
DB 14 NYHTNGDDSKYLE 26

RESULT 19
Q69XV4      PRELIMINARY;      PRT; 226 AA.
AC Q69XV4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE DNA-binding protein-like.
GN Name=P0040H10.36-2;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
RT clone:P0040H10.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003539; BAD35373.1; -.
DR GO; GO:0003677; F:DNA binding; IEA.
KW DNA-binding.
SQ SEQUENCE 226 AA; 24068 MW; 3797E1C36CC9A244 CRC64;

Query Match 56.2%; Score 41; DB 2; Length 226;
Best Local Similarity 53.8%; Pred. No. 38;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 NVYRCGDDSKVQ 13
:|:|:|:|:|:
DB 153 DYSCGGDDSGTTE 165

RESULT 20
Q8TBF1      PRELIMINARY;      PRT; 428 AA.
AC Q8TBF1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RasGEF domain family, member 1A.
GN Name=RASGEF1A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.B.,
RA Jones S.J., Maria M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RL Sraunberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022548; AAH22548.1; -
DR GO; GO:0005085; F:guanyl-nucleotide exchange factor activity; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR000651; RasGEF_N.
DR InterPro; IPR001895; RasGEF_CDC25.
DR InterPro; IPR008937; Ras_GEF.
DR Pfam; PF00617; RasGEF; 1.
DR SMART; SM00147; RasGEF; 1.
DR PROSITE; PS50009; RASGEF_CAT; 1.
DR PROSITE; PS50212; RASGEF_NTER; 1.
SQ SEQUENCE 428 AA; 49394 MW; 2522DBF4A3D2F560 CRC64;
Query Match 56.2%; Score 41; DB 2; Length 428;
Best Local Similarity 70.0%; Pred. No. 76;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 NYRCRGDSDK 10
Db :|||||:
197 NHRCRGDLTK 206
RESULT 21
ID Q69XV5 PRELIMINARY; PRT; 461 AA.
AC Q69XV5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE DNA-binding protein-like.
GN Names=P0040H10.36-1;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC
RT clone:P0040H10.36-1;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003539; BAD35372.1; -
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001605; ARID.
DR InterPro; IPR002068; Hsp20.
DR InterPro; IPR008978; HSP20_chap.
DR Pfam; PF01388; ARID; 1.
DR SMART; SM00501; BRIGHT; 1.
DR PROSITE; PS01031; HSP20; 1.
DR DNA-binding.
SQ SEQUENCE 461 AA; 50459 MW; F6FD7A3F1B13290B CRC64;
Query Match 56.2%; Score 41; DB 2; Length 461;
Best Local Similarity 53.8%; Pred. No. 82;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 NYRCRGDSDKVQE 13

Db 153 DYSCGGDSDSGTEE 165
:|||||:
RESULT 22
ID Q8N9B8 PRELIMINARY; PRT; 489 AA.
AC Q8N9B8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ37817.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Substantia nigra;
RX PubMed=14702039; DOI=10.1038/ngl1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamiyama K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiya H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi R.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RT Nat. Genet. 36:40-45(2004).
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC
RT clone:P0040H10.36-1;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK095136; BAC04491.1; -
DR GO; GO:0005085; F:guanyl-nucleotide exchange factor activity; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR000651; RasGEF_N.
DR InterPro; IPR001895; RasGEF_CDC25.
DR InterPro; IPR008937; Ras_GEF.
DR Pfam; PF00617; RasGEF; 1.
DR SMART; SM00147; RasGEF; 1.
DR SMART; SM00229; RasGEF_N.
DR PROSITE; PS50009; RASGEF_CAT; 1.
DR PROSITE; PS50212; RASGEF_NTER; 1.
SQ SEQUENCE 489 AA; 55532 MW; 85D5986ACD2C7C76 CRC64;
Query Match 56.2%; Score 41; DB 2; Length 489;
Best Local Similarity 70.0%; Pred. No. 87;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 NYRCRGDSDK 10
Db :|||||:
258 NHRCRGDLTK 267

RESULT 23

```
Q96180
ID Q96180 PRELIMINARY; PRT; 505 AA.
AC Q96180;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PRSS12 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek A.J., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC007761; AA07761.1; -.
DR HSP; Q08380; IBY2.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005507; F:copper ion binding; IEA.
DR GO; GO:0004720; F:protein-lysine 6-oxidase activity; IEA.
DR GO; GO:0005044; F:scavenger receptor activity; IEA.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001695; Lysyl oxidase.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF00051; Kringle; 1.
DR Pfam; PF00530; SRCR; 3.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR00258; SPERACTRCPPR.
DR ProDom; PD000395; Kringle; 1.
DR ProDom; PD013887; Lysyl_oxidase; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00202; SR; 3.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00420; SRCR_1; 2.
DR PROSITE; PS00287; SRCR_2; 3.
KW Kringle.
SQ SEQUENCE 505 AA; 55658 MW; 7FF863A6246226BD CRC64;
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Query Match 56.2%; Score 41; DB 2; Length 505;

Best Local Similarity 54.5%; Pred. No. 90;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NVRCRGDSSKV 11

Db 236 NVRCRGDEINI 246

RESULT 24

```
NETR_HUMAN
ID Q96180 STANDARD; PRT; 875 AA.
AC P56730; Q9UP16;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Neurotysin precursor (EC 3.4.21.-) (Motopsin) (Leydin).
GN Name=PRSS12;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98201705; PubMed=9540828; DOI=10.1016/S0167-4781(97)00205-4;
RA Proba K., Gschwend T.P., Sonderegger P.;
RT "Cloning and sequencing of the cDNA encoding human neurotysin.";
RL Biochim. Biophys. Acta 1396:143-147(1998).
RN [2]
RP SEQUENCE OF 615-875 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=99203523; PubMed=10103056;
RA Poorafshar M., Hellman L.;
RT "Cloning and structural analysis of leydin, a novel human serine
RT protease expressed by the Leydig cells of the testis.";
RL Eur. J. Biochem. 261:244-250(1999).
RN [3]
RP DISEASE.
RX PubMed=12459588; DOI=10.1126/science.1076521;
RA Molinari F., Rio M., Meskenaitė V., Encha-Razavi F., Auge J., Bacq D.,
RA Briault S., Vekemans M., Munnich A., Attie-Bitach T., Sonderegger P.,
RA Collea L.;
RT "Truncating neurotysin mutation in autosomal recessive nonsyndromic
RT mental retardation.";
RL Science 298:1779-1781(2002).
CC -!- FUNCTION: Plays a role in neuronal plasticity and the proteolytic
CC action may subserve structural reorganizations associated with
CC learning and memory operations (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DISEASE SPECIFICITY: Brian and Leydig cells of the testis.
CC -!- DISEASE: Defects in PRSS12 are a cause of autosomal recessive
CC nonsyndromic mental retardation [MIM:249500]. Mental retardation
CC is a mental disorder characterized by significantly subaverage
CC general intellectual functioning associated with impairments in
CC adaptive behavior and manifested during the developmental
CC period.
CC -!- SIMILARITY: Belongs to the peptidase S1 family.
CC -!- SIMILARITY: Contains 1 kringle domain.
CC -!- SIMILARITY: Contains 4 SRCR domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ001531; CAA04816.1; -.
DR EMBL; AF077298; AAD25919.1; -.
DR HSP; P00760; IEZX.
DR MEROPS; S01.237; -.
DR Genew; HGNC:9477; PRSS12.
DR MIM; 249500; -.
DR MIM; 606709; -.
DR GO; GO:0008236; F:serine-type peptidase activity; TAS.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
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DR InterPro: IPR001190; Srcr_receptor.
 DR Pfam: PF00051; Kringle_1.
 DR PFam: PF00530; SRCR_4.
 DR PFam: PF00089; Trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00258; SPERACTRCPTR.
 DR ProDom: PD000395; Kringle; 1.
 DR ProDom: PD013887; Lysyl_oxidase; 2.
 DR SMART: SM00130; KR; 1.
 DR SMART: SM00202; SR; 4.
 DR SMART: SM00020; Tryp SPC; 1.
 DR PROSITE: PS00021; KRINGLE_1; 1.
 DR PROSITE: PS00720; KRINGLE_2; 1.
 DR PROSITE: PS00430; SRCR_1; 3.
 DR PROSITE: PS00420; SRCR_2; 4.
 DR PROSITE: PS00287; SRCR_3; 4.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SSR; 1.
 KW Glycoprotein; Hydrolase; Kringle; Repeat; Serine protease; Signal.
 FT SIGNAL 1 20 Potential.
 FT CHAIN 21 875 Neurotrypsin.
 FT DOMAIN 23 92 Pro-rich.
 FT DOMAIN 93 165 Kringle.
 FT DOMAIN 170 271 SRCR 1.
 FT DOMAIN 280 381 SRCR 2.
 FT DOMAIN 387 487 SRCR 3.
 FT DOMAIN 500 601 SRCR 4.
 FT DOMAIN 619 875 Serine protease.
 FT DOMAIN 619 630 Zymogen activation region.
 FT SITE 630 631 Reactive bond (Potential).
 FT ACT_SITE 676 676 Charge relay system.
 FT ACT_SITE 726 726 Charge relay system.
 FT ACT_SITE 825 825 Charge relay system.
 FT DISULFID 619 750 Potential.
 FT CARBOHYD 26 26 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 683 683 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 663 663 A -> V (in Ref. 2).
 FT CONFLICT 701 701 E -> V (in Ref. 2).
 FT CONFLICT 839 841 VVY -> AAL (in Ref. 2).
 SQ SEQUENCE 875 AA; 97011 MW; B66BC946DC208DC8 CRC64;

Query Match 56.2%; Score 41; DB 1; Length 875;
 Best Local Similarity 54.5%; Pred. No. 1.6e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 NYRCRGDSKV 11
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 Db 236 NYRCRGDENI 246

RESULT 25
 O97322 PRELIMINARY; PRT; 1334 AA.
 AC O97322; (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein MAL3P7.32.
 GN Name=MAL3P7.32; Synonyms=PF01010w;
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=36329;
 RN SEQUENCE FROM N.A.

RX MEDLINE=99376085; PubMed=10448855; DOI=10.1038/22964;
 RA Bowman S., Lawson D., Baaham D., Brown D., Chillingworth T.,
 RA Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,
 RA Gentles S., Gwilliam R., Hamlin N., Harris R., Holroyd S., Hornsby T.,
 RA Horrocks P., Jagels K., Jaseal B., Kyes S., McLean J., Moule S.,
 RA Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
 RA Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
 RA Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;
 RT "The complete nucleotide sequence of chromosome 3 of Plasmodium

RT falciparum.";
 RL Nature 400:532-538 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22255708; PubMed=12368867; DOI=10.1038/nature01095;
 RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
 RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
 RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
 RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
 RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
 RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
 RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
 RA Humphray S., Jagels K., James K.D., Johnson D., Keshornou A.,
 RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
 RA Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
 RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,
 RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
 RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
 RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
 RA Sulston J.E., Craig A., Newbold C., Barrell B.G.;
 RL "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
 RL Nature 419:527-531 (2002).
 DR EMBL; AL034559; CAB39073.2; -.
 KW Hypothetical protein.
 SQ SEQUENCE 1334 AA; 160847 MW; E3577E84C7E0C8E5 CRC64;

Query Match 56.2%; Score 41; DB 2; Length 1334;
 Best Local Similarity 60.0%; Pred. No. 2.6e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NYRCRGDSK 10
 |||||:
 Db 808 NYNCKDDNK 817

RESULT 26
 Q9RTC3 PRELIMINARY; PRT; 2736 AA.
 AC Q9RTC3; (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN Name=PY00071;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=73239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=17XNL;
 RX PubMed=12368865; DOI=10.1038/nature01099;
 RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pextea M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shallom S., van Aken S.E., Riedmiller S.B., Feidlyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
 RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 parasite Plasmodium yoelii yoelii.";
 RL Nature 419:512-519 (2002).
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; AABL01000019; EAA17884.1; -.
 DR InterPro: IPR000357; HEAT.
 DR Pfam: PF02985; HEAT; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 2736 AA; 323770 MW; C219F7662538AA00 CRC64;

Query Match 56.2%; Score 41; DB 2; Length 2736;
Best Local Similarity 46.2%; Pred. No. 5.6e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 NYRCRGDDSKVQ 13
DB 2536 NYACSTDQKIXD 2548

RESULT 27
Q9KCP2
ID Q9KCP2 PRELIMINARY; PRT; 150 AA.
AC Q9KCP2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ferric uptake regulation protein.
GN OrderedLocusNames=BHI527;
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C-125;
RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001512; BAB05246.1; -.
DR PIR; G83840; G83840.
DR HSSP; Q03456; LMZB.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002481; FUR.
DR InterPro; IPR009058; wing_hlx_DNA_bnd.
DR Pfam; PF01475; FUR; 1.
DR ProDom; PD002003; FUR; 1.
KW Complete proteome.
SQ SEQUENCE 150 AA; 17447 MW; CE4D3AC2A8B64275 CRC64;

Query Match 54.8%; Score 40; DB 2; Length 150;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDDSK 10
DB 141 HRCQGDESK 149

RESULT 28
Q20683
ID Q20683 PRELIMINARY; PRT; 179 AA.
AC Q20683;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein F52H3.5.
GN ORFNames=F52H3.5;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Gardner A.E.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z66512; CAA91325.1; -.
DR PIR; T22521; T22521.
DR WormBase; WBGene00009947; F52H3.5.
DR WormPep; F52H3.5; CE03401.
DR InterPro; IPR001440; TPR.
DR InterPro; IPR008941; TPR-like.
DR Pfam; PF00515; TPR; 1.
DR SMART; SM00028; TPR; 3.
DR PROSITE; PS00005; TPR; 1.
DR PROSITE; PS00293; TPR_REGION; 1.
KW Hypothetical protein; Repeat; TPR repeat.
SQ SEQUENCE 179 AA; 19648 MW; 6FF899837C63A18F CRC64;

Query Match 54.8%; Score 40; DB 2; Length 179;
Best Local Similarity 63.6%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 YRCRGDDSKVQ 12
DB 125 YRLRGDDDKAR 135

RESULT 29
Q95ZL6
ID Q95ZL6 PRELIMINARY; PRT; 244 AA.
AC Q95ZL6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein M01E11.4.
GN Name=M01E11.4; ORFNames=M01E11.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Pauley A., Gattung S.;
RL "The sequence of C. elegans cosmid M01E11.";
RN Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RC Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; U80450; AAK77613.1; -.
DR WormBase; WBGene00019713; M01E11.4.
DR WormPep; M01E11.4a; CE28610.
KW Hypothetical protein.


```
SQ SEQUENCE 244 AA; 27837 MW; 9AA335B0442B84C4 CRC64;
Query Match 54.8%; Score 40; DB 2; Length 244;
Best Local Similarity 70.0%; Pred. No. 62;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 CRGDDSKVOE 13
   ||| ||| |||
Db 42 CRGLDSQIQE 51

RESULT 30
Q95ZL7 PRELIMINARY; PRT; 252 AA.
AC Q95ZL7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein M01E11.4.
GN Names=M01E11.4; ORFNames=M01E11.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium. ";
RL Science 282:2012-2018 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Pauley A., Gattung S.;
RT "The sequence of C. elegans cosmid M01E11. ";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; U80450; AAK77614.1; -.
DR WormBase; WBGene00019713; M01E11.4.
DR WormPep; M01E11.4b; CE28611.
KW Hypothetical protein.
SQ SEQUENCE 252 AA; 28738 MW; FE8556D34587F3E8 CRC64;

Query Match 54.8%; Score 40; DB 2; Length 252;
Best Local Similarity 70.0%; Pred. No. 65;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 CRGDDSKVOE 13
   ||| ||| |||
Db 42 CRGLDSQIQE 51

RESULT 31
Q7R8M3 PRELIMINARY; PRT; 269 AA.
AC Q7R8M3;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
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```
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
GN Name=Yir3 protein.
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii. ";
RL Nature 419:512-519 (2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01002583; EAA19571.1; -.
DR InterPro; IPR006477; Yir_bir_cir.
DR Pfam; PF06022; Cir_Bir_Yir_I.
DR TIGRFAMs; TIGR01590; Yir-bir-cir_pla; 1.
SQ SEQUENCE 269 AA; 31732 MW; A95E52E05D6119C CRC64;

Query Match 54.8%; Score 40; DB 2; Length 269;
Best Local Similarity 54.5%; Pred. No. 69;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 NYRCRGDDSKV 11
   ||| ||| |||
Db 38 NYKCEGLDKI 48

RESULT 32
LPPI_RAT
ID LPPI_RAT STANDARD; PRT; 282 AA.
AC O08564; Q8K594;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Lipid phosphate phosphohydrolase 1 (EC 3.1.3.4) (Phosphatidic acid
DE phosphatase 2a) (Phosphatidate phosphohydrolase type 2a) (PAP2a) (PAP-
DE 2a) (PAP2-alpha).
GN Name=Pap2a; Synonym=Lpp1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
RC TISSUE=Liver;
RX PubMed=10359651; DOI=10.1042/0264-6021:3400677;
RA Jasinska R., Zhang Q.-X., Pilquil C., Singh I., Xu J., Dewald J.,
RA Dillon D.A., Berthiaume L.G., Carman G.M., Waggoner D.W.,
RA Brindley D.N.;
RT "Lipid phosphate phosphohydrolase-1 degrades exogenous glycerolipid
RT and sphingolipid phosphate esters. ";
RL Biochem. J. 340:677-686 (1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=Sprague-Dawley; TISSUE=Lung;
RX MEDLINE=21559999; PubMed=11704545;
RA Nanjundan M., Possmayer F.;
RT "Molecular cloning and expression of pulmonary lipid phosphate
```

phosphohydrolases.";
Am. J. Physiol. 281:L1484-L1493 (2001).
[3]
CHARACTERIZATION
PubMed=8663293; DOI=10.1074/jbc.271.28.15606;
Waggoner D.W., Gomez-Munoz A., Dewald J., Brindley D.N.;
"Phosphatidate phosphohydrolase catalyzes the hydrolysis of ceramide
1-phosphate, lysophosphatidate, and sphingosine 1-phosphate.";
J. Biol. Chem. 271:16506-16509(1996).
-I- FUNCTION: Broad-specificity phosphohydrolase that dephosphorylates
exogenous bioactive glycerolipids and sphingolipids. Catalyzes the
conversion of phosphatidic acid (PA) to diacylglycerol (DG). In
addition it hydrolyzes lysophosphatidic acid (LPA), diacyl
glycerol pyrophosphate (DGPP), ceramide-1-phosphate (C-1-P) and
sphingosine-1-phosphate (S-1-P). The relative catalytic efficiency
is LPA > PA > C-1-P > S-1-P.
-I- CATALYTIC ACTIVITY: A 3-sn-phosphatidate + H(2)O = a 1,2-diacyl-
sn-glycerol + phosphate.
-I- SUBUNIT: Homodimer (By similarity).
-I- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane
(By similarity).
-I- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
Name=1;
IsoId=O08564-1; Sequence=Displayed;
Name=2; Synonyms=LPPIa;
IsoId=O08564-2; Sequence=VSP_009653;
-I- SIMILARITY: Belongs to the PA-phosphatase related phosphoesterase
family.

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EMBL; U90556; AAB50246.1; --
EMBL; AF503609; AM28631.1; --
GO; GO:0005624; C:membrane fraction; ISS.
GO; GO:0008195; F:phosphatidate phosphatase activity; ISS.
GO; GO:0030521; P:androgen receptor signaling pathway; ISS.
GO; GO:0008285; P:negative regulation of cell proliferation; ISS.
GO; GO:0046839; P:phospholipid dephosphorylation; ISS.
GO; GO:0007205; P:protein kinase C activation; ISS.
GO; GO:0019216; P:regulation of lipid metabolism; ISS.
InterPro; IPR008934; ACPase_VanParase.
Pfam; PF01569; PAP2; 1.
SMART; SM00014; acidPpc; 1.
Alternative splicing; Glycoprotein; Hydrolase; Transmembrane.
DOMAIN 1 6 Cytoplasmic (Potential).
TRANSMEM 7 27 Potential.
DOMAIN 28 53 Extracellular (Potential).
TRANSMEM 54 74 Potential.
DOMAIN 75 88 Cytoplasmic (Potential).
TRANSMEM 89 109 Potential.
DOMAIN 110 164 Extracellular (Potential).
TRANSMEM 165 185 Potential.
DOMAIN 186 194 Cytoplasmic (Potential).
TRANSMEM 195 215 Potential.
DOMAIN 216 229 Extracellular (Potential).
TRANSMEM 230 250 Potential.
DOMAIN 251 282 Cytoplasmic (Potential).
CARBOHYD 142 142 N-linked (GlcNAc...) (Potential).
VARSPIC 21 70
IPVFCIIIV -> SMPMAVNGLQIYPFORGFPCSDNSVKY
PYHDSVTVTVLVGLGIPIFS (in isoform 2).
/FTID-VSP_009653.
SEQUENCE 282 AA; 31996 MW; A4ED3DEB3FD7943 CRC64;

Query Match 54.8%; Score 40; DB 1; Length 282;
Best Local Similarity 46.2%; Pred. No. 73;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 1 NYRCRGDDSKVQE 13
Db 150 NFVCCGNEQKVRE 162
|:|:|:|:|:
RESULT 33
Q6P766 PRELIMINARY; PRT; 282 AA.
ID Q6P766;
AC Q6P766;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.K., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC061815; AAH61815.1; --
DR InterPro; IPR008934; ACPase_VanParase.
DR InterPro; IPR000326; Pesterase_PA_PTP.
DR Pfam; PF01569; PAP2; 1.
DR SMART; SM00014; acidPpc; 1.
KW Hypothetical protein.
SQ SEQUENCE 282 AA; 32000 MW; 10EFD1C5F3FCB8E9 CRC64;
Query Match 54.8%; Score 40; DB 2; Length 282;
Best Local Similarity 46.2%; Pred. No. 73;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 1 NYRCRGDDSKVQE 13
Db 150 NFVCCGNEQKVRE 162
|:|:|:|:|:
RESULT 34
Q9DW23 PRELIMINARY; PRT; 288 AA.
ID Q9DW23
AC Q9DW23;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

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DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE P171.
GN Name=c171;
OS Rat cytomegalovirus (strain Maastricht).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Muromegalovirus.
OC NCBI_TaxID=79700;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Maastricht;
RX MEDLINE=96357047; PubMed=8764031;
RA Vink C., Beuken E., Bruggeman C.A.;
RT "Structure of the rat cytomegalovirus genome termini.";
RL J. Virol. 70:5221-5229(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Maastricht;
RX MEDLINE=20366325; PubMed=10906222;
RA Vink C., Beuken E., Bruggeman C.A.;
RT "Complete DNA sequence of the rat cytomegalovirus genome.";
RL J. Virol. 74:7656-7665(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Maastricht;
RX MEDLINE=20473137; PubMed=11018281; DOI=10.1016/S0168-1702(00)00208-2;
RA Gruijthuisen Y.K., Beuken E., Bruggeman C.A.;
RT "Rat cytomegalovirus R89 is a highly conserved gene which expresses a
RT spliced transcript.";
RL Virus Res. 69:119-130(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Maastricht;
RA Vink C., Beuken E., Bruggeman C.A.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP232689; AAF99267.1; -.
SQ SEQUENCE 288 AA; 32646 MW; B29EDAF6083D698B CRC64;

Query Match 54.8%; Score 40; DB 2; Length 288;
Best Local Similarity 60.0%; Pred. No. 75;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 RCRGDSKVQ 12
DB 138 RCQGEDEKVE 147
|||||:|:|:|

RESULT 35
HEM3_XANCP
ID HEM3_XANCP STANDARD; PRT; 304 AA.
AC Q8P536;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Porphobilinogen deaminase (EC 2.5.1.61) (PBG) (Hydroxymethylbilane
DE synthase) (HMB) (Pre-uroporphyrinogen synthase).
GN Name=hmc; OrderedLocusNames=XCC3511;
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12034217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavaro F., Cardozo J., Chamberg F., Chapina L.P.,
RA Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

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RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Teai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417:459-463(2002).
CC -!- FUNCTION: Tetrapolymerization of the monopyrrole PBG into the
CC hydroxymethylbilane preuroporphyrinogen in several discrete steps.
CC -!- CATALYTIC ACTIVITY: 4 porphobilinogen + H2O =
CC hydroxymethylbilane + 4 NH(3).
CC -!- COFACTOR: Covalently binds a dipyrromethane cofactor to which the
CC porphobilinogen subunits are added (By similarity).
CC -!- PATHWAY: Porphyrin biosynthesis by the C5 pathway; fourth step.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the HMB5 family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AB012470; AA042781.1; -.
DR HSSP: P06983; 1YPN.
DR HAMAP: MF_00260; -.
DR InterPro: IPR000860; Porphobil deam.
DR Pfam: PF01379; Porphobil deam; 1.
DR Pfam: PF03900; Porphobil deamC; 1.
DR PRINTS: PR00151; PORPHBDMNASE.
DR ProDom: PD002745; Porphobil deam; 1.
DR TIGRPFAMs: TIGR00212; hmc; 1.
DR PROSITE: PS00533; PORPHOBILINOGEN_DEAM; 1.
KW Complete proteome; Porphyrin biosynthesis; Transferase.
FT BINDING 240 240 Pyrromethane cofactor (By similarity).
SQ SEQUENCE 304 AA; 32460 MW; F77A49FB1932FF02 CRC64;

Query Match 54.8%; Score 40; DB 1; Length 304;
Best Local Similarity 50.0%; Pred. No. 79;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 CRGDDSKVQE 13
DB 203 CRGDDARIND 212
|||||:|:|:|

RESULT 36
PNCB_ECO57
ID PNCB_ECO57 STANDARD; PRT; 399 AA.
AC Q8XDE8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Nicotinate phosphoribosyltransferase (EC 2.4.2.11) (NAPRTase).
GN Name=pncB; OrderedLocusNames=21279, EC61014;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=0157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

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Db	38	FRCRGDD	44
RESULT 38			
PNCB_SALTI			
ID	PNCB_SALTI	STANDARD;	PRT; 399 AA.
AC	Q827Y9;		

DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Nicotinate phosphoribosyltransferase (EC 2.4.2.11) (NAPRTase).
 GN Name=ncnb; OrderedLocusNames=STV1010, t1930;
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=601;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Peltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrrell B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typhi CT18.";
 RL Nature 413:848-852(2001).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Ty2 / ATCC 700931;
 RX MEDLINE=22531367; PubMed=12644504;
 RX DOI=10.1128/JB.185.7.2330-2337.2003;
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
 RA Burland V., Kodoyanni V., Schwartz D.C., Blattner F.R.;
 RT "Comparative genomics of Salmonella enterica serovar typhi strains Ty2
 RT and CT18.";
 RL J. Bacteriol. 185:2330-2337(2003).
 CC -!- CATALYTIC ACTIVITY: Nicotinate D-ribonucleotide + diphosphate =
 CC nicotinate + 5-phospho-alpha-D-ribose 1-diphosphate.
 CC -!- PATHWAY: NAD biosynthesis; nicotinamide to NAMN; second step.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the NAPRTase family.
 CC -----
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 CC -----
 DR EMBL; AL627268; CAD05404.1; -.
 DR EMBL; AE016840; AAO69546.1; -.
 DR HAMAP; MF_00570; -; 1.
 DR InterPro; IPR007229; NAPRTase.
 DR InterPro; IPR006406; Nic Prtrans.
 DR InterPro; IPR008967; P53_like_DNA_bnd.
 DR Pfam; PF04095; NAPRTase; 1.
 DR PIRSF; PIRSF000484; Nicot_phos_ribo; 1.
 DR TIGRFAMs; TIGR01514; NAPRTase; 1.
 DR TIGRFAMs; TIGR01514; Nicot_phos_ribo; 1.
 KW Complete proteome; Glycosyltransferase;
 KW Pyridine nucleotide biosynthesis; Transferase.
 FT INIT MET 0
 FT BY similarity.
 SQ SEQUENCE 399 AA; 45562 MW; ADF38AEAE4618214 CRC64;
 Query Match 54.8%; Score 40; DB 1; Length 399;
 Best Local Similarity 85.7%; Pred. No. 1.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 YRCRGDD 8
 DB 38 FRCRGDD 44
 :|||||
 RESULT 39
 PNCB_SALTY

ID PNCB_SALTY STANDARD; PRT; 399 AA.
 AC F22253;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Nicotinate phosphoribosyltransferase (EC 2.4.2.11) (NAPRTase).
 GN Name=ncnb; OrderedLocusNames=STV1004;
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=602;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC MEDLINE=91100340; PubMed=1987148;
 RX Vinitzky A., Teng H., Grubmeyer C.T.;
 RT "Cloning and nucleic acid sequence of the Salmonella typhimurium pncB
 RT gene and structure of nicotinate phosphoribosyltransferase.";
 RL J. Bacteriol. 173:536-540(1991).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 RT LT2.";
 RL Nature 413:852-856(2001).
 CC -!- CATALYTIC ACTIVITY: Nicotinate D-ribonucleotide + diphosphate =
 CC nicotinate + 5-phospho-alpha-D-ribose 1-diphosphate.
 CC -!- PATHWAY: NAD biosynthesis; nicotinamide to NAMN; second step.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the NAPRTase family.
 CC -----
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 CC -----
 DR EMBL; M55986; AAA27190.1; -.
 DR EMBL; AE008743; AAL19938.1; -.
 DR PIR; A39130; A39130.
 DR StvGene; SG10305; pncB.
 DR HAMAP; MF_00570; -; 1.
 DR InterPro; IPR007229; NAPRTase.
 DR InterPro; IPR006406; Nic Prtrans.
 DR InterPro; IPR008967; P53_like_DNA_bnd.
 DR Pfam; PF04095; NAPRTase; 1.
 DR PIRSF; PIRSF000484; Nicot_phos_ribo; 1.
 DR TIGRFAMs; TIGR01514; NAPRTase; 1.
 DR TIGRFAMs; TIGR01514; Nicot_phos_ribo; 1.
 KW Complete proteome; Glycosyltransferase;
 KW Pyridine nucleotide biosynthesis; Transferase.
 FT INIT MET 0
 FT BY similarity.
 SQ SEQUENCE 399 AA; 45530 MW; 90D9C3EDD8C092A6 CRC64;
 Query Match 54.8%; Score 40; DB 1; Length 399;
 Best Local Similarity 85.7%; Pred. No. 1.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 YRCRGDD 8
 DB 38 FRCRGDD 44
 :|||||
 RESULT 40
 Q7UD27
 ID Q7UD27 PRELIMINARY; PRT; 400 AA.
 AC Q7UD27;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Nicotinate phosphoribosyltransferase.
 GN Name=pncB; OrderedLocusNames=S0992;
 OS Shigella flexneri.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Shigella.
 OX NCBI_TaxID=623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2457T;
 RX MEDLINE=22590274; PubMed=12704152;
 RX DOI=10.1128/IAI.71.5.2775-2786.2003;
 RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
 RA Pournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
 RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
 RA Schwartz D.C., Blattner F.R.;
 RA "Complete genome sequence and comparative genomics of Shigella
 RT flexneri serotype 2a strain 2457T.";
 RL Infect. Immun. 71:2775-2786(2003).
 DR EMBL; A5016981; AAP16443.1; -
 DR GO; GO:0004516; F:nicotinate phosphoribosyltransferase activity; IEA.
 DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
 DR GO; GO:0019357; P:nicotinate nucleotide biosynthesis; IEA.
 DR GO; GO:0019363; P:pyridine nucleotide biosynthesis; IEA.
 DR InterPro; IPR007229; NAPTase.
 DR InterPro; IPR006406; Nic_Prtase.
 DR InterPro; IPR008967; P53_like_DNA_bnd.
 DR Pfam; PF04095; NAPTase; 1.
 DR TIGRFAMs; TIGR01514; NAPTase; 1.
 DR TIGRFAMs; TIGR01514; Nicot_phos_ribo; 1.
 KW Glycosyltransferase; Transferase.
 SQ SEQUENCE 400 AA; 45911 MW; 53855BCB1A8703095 CRC64;
 Query Match 54.8%; Score 40; DB 2; Length 400;
 Best Local Similarity 85.7%; Pred. No. 1.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 YRCRGDD 8
 Db :|||||
 39 FRCRGDD 45

RESULT 41
 Q83LN3 PRELIMINARY; PRT; 416 AA.
 ID Q83LN3
 AC Q83LN3;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Nicotinate phosphoribosyltransferase.
 GN Name=pncB; OrderedLocusNames=Sf0928;
 OS Shigella flexneri.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Shigella.
 OX NCBI_TaxID=623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=301 / Serotype 2a;
 RX MEDLINE=22272406; PubMed=123844590; DOI=10.1093/nar/gkf566;
 RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
 RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
 RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
 RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
 RA Yu J.;
 RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
 RT through comparison with genomes of Escherichia coli K12 and O157.";
 RL Nucleic Acids Res. 30:4432-4441(2002).
 DR EMBL; A5015122; AAN42557.1; -
 DR GO; GO:0004516; F:nicotinate phosphoribosyltransferase activity; IEA.
 DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
 DR GO; GO:0019357; P:nicotinate nucleotide biosynthesis; IEA.

DR GO; GO:0019363; P:pyridine nucleotide biosynthesis; IEA.
 DR InterPro; IPR007229; NAPTase.
 DR InterPro; IPR006406; Nic_Prtase.
 DR InterPro; IPR008967; P53_like_DNA_bnd.
 DR Pfam; PF04095; NAPTase; 1.
 DR TIGRFAMs; TIGR000484; Nicot_phos_ribo; 1.
 DR TIGRFAMs; TIGR01514; NAPTase; 1.
 KW Complete proteome; Glycosyltransferase; Transferase.
 SQ SEQUENCE 416 AA; 47700 MW; E43D723542AF2DD5 CRC64;
 Query Match 54.8%; Score 40; DB 2; Length 416;
 Best Local Similarity 85.7%; Pred. No. 1.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 YRCRGDD 8
 Db :|||||
 55 FRCRGDD 61

RESULT 42
 Q8FJ98 PRELIMINARY; PRT; 416 AA.
 ID Q8FJ98
 AC Q8FJ98;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Nicotinate phosphoribosyltransferase (EC 2.4.2.11).
 GN Name=pncB; OrderedLocusNames=c1073;
 OS Escherichia coli O6.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=217992;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C6:HI / CFT073 / ATCC 700928 / UPEC;
 RX MEDLINE=23388234; PubMed=12471157; DOI=10.1073/pnas.252597999;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
 RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
 RA "Extensive mosaic structure revealed by the complete genome sequence
 RT of uropathogenic Escherichia coli.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
 DR EMBL; A5016758; AAN79541.1; -
 DR GO; GO:0004516; F:nicotinate phosphoribosyltransferase activity; IEA.
 DR GO; GO:0019357; P:nicotinate nucleotide biosynthesis; IEA.
 DR GO; GO:0019363; P:pyridine nucleotide biosynthesis; IEA.
 DR InterPro; IPR007229; NAPTase.
 DR InterPro; IPR006406; Nic_Prtase.
 DR InterPro; IPR008967; P53_like_DNA_bnd.
 DR Pfam; PF04095; NAPTase; 1.
 DR TIGRFAMs; TIGR000484; Nicot_phos_ribo; 1.
 DR TIGRFAMs; TIGR01514; NAPTase; 1.
 KW Complete proteome.
 SQ SEQUENCE 416 AA; 47722 MW; F00AFC07B04B1E23 CRC64;
 Query Match 54.8%; Score 40; DB 2; Length 416;
 Best Local Similarity 85.7%; Pred. No. 1.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 YRCRGDD 8
 Db :|||||
 55 FRCRGDD 61

RESULT 43
 QY4B CAEL STANDARD; PRT; 577 AA.
 ID YQ4B CAEL
 AC Q17426;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Hypothetical pseudouridine synthase in chromosome V (EC 4.2.1.70).

GN ORPNames=B0024.11;
OC Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology.";
RL Science 282:2012-2018(1998).
CC -1- CATALYTIC ACTIVITY: Uracil + D-ribose 5-phosphate = pseudouridine
+ 5'-phosphate + H(2)O.
CC -1- SIMILARITY: Belongs to the pseudouridine synthase truD family.
CC -1- SIMILARITY: Contains 1 TRUD domain.
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CC -----
DR EMBL; Z71178; CAA94883.1; -.
DR PIR; T18646; T18646.
DR WormBase; WBGene00007101; B0024.11.
DR WormPep; B0024.11; CE05155.
DR InterPro; IPR001656; Pfam_synch_truD.
DR Pfam; PF01142; Trud; 1.
DR PROSITE; PS50984; TRUD; 1.
DR PROSITE; PS01268; UPF0024; 1.
DR DOMAIN 265 472
KW Hypothetical protein; Lyase; TRUD.
FT ACT_SITE 188 188 By similarity.
SQ SEQUENCE 577 AA; 64631 MW; A1F3BC06481CD281 CRC64;

Query Match 54.8%; Score 40; DB 1; Length 577;
Best Local Similarity 46.2%; Pred. No. 1.6e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 NYRCRGDDSKVQ 13
Db :: ||||| :
544 SFKTRGDDKTEE 556

RESULT 44
Q62YB1 PRELIMINARY; PRT; 586 AA.
AC Q62YB1; 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Alpha amylase, catalytic subdomain.
GN Names=yvdf; ORFNames=BL00497;
OS Bacillus licheniformis DSM 13.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=279010;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14580;
RX Simpson A.J.G., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
Rey M.W., Ramaiya P., Xiang H., Gusti V., Clausen I.G., Olsen P.B.,
Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B.,
Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,
Sorokin A., Bolotin A., Lapidus A., Gallon N., Ehrlich S.D.,
Berka R.M.;
RT "Complete genome sequence of the industrial bacterium Bacillus
licheniformis and comparisons with closely related Bacillus species.";
RL Genome Biol. 5:R77-R77(2004).
DR EMBL; CP000002; AAU22447.1; -.
SQ SEQUENCE 586 AA; 67330 MW; 03070D1F57DEDFD2 CRC64;

Query Match 54.8%; Score 40; DB 2; Length 586;
Best Local Similarity 70.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RCRGDDSKVQ 12
Db ||||| :
431 RCGDDKKVR 440

RESULT 45
Q65MW8 PRELIMINARY; PRT; 587 AA.
AC Q65MW8; 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Maltogenic alpha-amylase (EC 3.2.1.133).
GN ORFNames=BLi0658;
OS Bacillus licheniformis DSM 13.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=279010;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 13;
RX PubMed=15383718;
RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
Ehrenreich P., Baumer S., Henne A., Liesegang H., Merkl R.,
Ehrenreich A., Gottschalk G.;
RT "The Complete Genome Sequence of Bacillus licheniformis DSM13, an
Organism with Great Industrial Potential.";
RL J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
DR EMBL; AE017333; AAU39596.1; -.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 587 AA; 67461 MW; 7F3C26DA8C994309 CRC64;

Query Match 54.8%; Score 40; DB 2; Length 587;
Best Local Similarity 70.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RCRGDDSKVQ 12
Db ||||| :
432 RCGDDKKVR 441

RESULT 46
Q9PA43 PRELIMINARY; PRT; 721 AA.
AC Q9PA43; 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE L-ascorbate oxidase.
GN OrderedLocusNames=Xf2677;
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OX Xanthomonadaceae; Xylella.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9a5C;
RX MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
RA Simpson A.J.G., Reinach P.C., Arruda P., Abreu F.A., Acencio M.,
Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
Ho P.L., Hohnsael J.D., Junqueira M.L., Kemper E.L., Leite J.C.P.,
Krieger J.E., Kuramae E.E., Laigret P., Lambais M.R., Leite L.C.C.,

RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuchioka M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Weidman J., Stetubal J.C.;
RT "The genome sequence of the plant pathogen *Xylella fastidiosa*.";
RL Nature 406:151-159(2000).
DR EMBL; AB004073; AAF85474.1; -.
DR FTR; H82528; H82528.
DR HSSP; Q51883; 1BAW.
DR GO; GO:0005507; F:copper ion binding; IEA.
DR InterPro; IPR001117; Cu-oxidase.
DR InterPro; IPR008972; Cupredoxin.
DR InterPro; IPR002355; Cu_ox_copper_BS.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
KW Complete proteome.
SQ SEQUENCE 721 AA; 80882 MW; 847E513614FB1955 CRC64;

Query Match 54.8%; Score 40; DB 2; Length 721;
Best Local Similarity 54.5%; Pred. No. 2e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 YRCRGDSKVQ 12
DB 282 YACRGNDGKLK 292

RESULT 47
Q7UKD4 PRELIMINARY; PRT; 1129 AA.
ID Q7UKD4
AC Q7UKD4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similar to serine/threonine protein kinase related protein-putative
DE PQQ-dependent oxidoreductase.
GN OrderedLocusNames=RB10706;
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete *Pirellula* sp.
RT strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294152; CAD76947.1; -.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006118; F:electron transport; IEA.
DR InterPro; IPR002372; PQQ repeat.
DR InterPro; IPR011047; Quin_alc_DH like.
DR SMART; SM00564; PQQ; 3.
KW Complete proteome; Kinase; Serine/threonine-protein kinase.
SQ SEQUENCE 1129 AA; 122926 MW; A5AC5DF164BE06F1 CRC64;

Query Match 54.8%; Score 40; DB 2; Length 1129;

Best Local Similarity 60.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 RCRGDSKVQ 12
DB 500 RCRGEDGEVE 509

RESULT 48
Q7RQM4 PRELIMINARY; PRT; 1615 AA.
ID Q7RQM4;
AC Q7RQM4;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Multidomain scavenger receptor protein PDSR precursor.
GN Name=PY01071;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabli A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite *Plasmodium yoelii* yoelii.";
RL Nature 419:512-519(2002).
CC -!- SIMILARITY: Contains 1 PLAT domain.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBB whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AABL01000281; EAA20072.1; -.
DR HSSP; O57811; 1G8A.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0005044; F:scavenger receptor activity; IEA.
DR GO; GO:0006364; F:rRNA processing; IEA.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR000692; Fibrillarin.
DR InterPro; IPR004043; LCCL.
DR InterPro; IPR001024; Lipoxigenase_LH2.
DR InterPro; IPR008976; PLAT_LH2.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF01269; Fibrillarin; 1.
DR Pfam; PF03815; LCCL; 4.
DR Pfam; PF03477; PLAT; 1.
DR Pfam; PF00530; SRCR; 2.
DR PRINTS; PR00052; FIBRILLARIN.
DR ProDom; PD004637; Fibrillarin; 1.
DR PROSITE; PS00566; FIBRILLARIN; 1.
DR PROSITE; PS0820; LCCL; 4.
DR PROSITE; PS50095; PLAT; 1.
DR PROSITE; PS50287; SRCR_2; 2.
KW Receptor.
SQ SEQUENCE 1615 AA; 180943 MW; 94053C4C9AC93505 CRC64;

Query Match 54.8%; Score 40; DB 2; Length 1615;
Best Local Similarity 41.7%; Pred. No. 4.8e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 NYRCRGDSKVQ 12

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 7, 2005, 19:49:10 ; Search time 7.67442 Seconds
(without alignments)
125.373 Million cell updates/sec

Title: US-10-812-238B-20

Perfect score: 59

Sequence: 1 NYRCRGDDSK 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

PIR 79:*

1: Pirl:*

2: Pirl:*

3: Pirl:*

4: Pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	67.8	150	2 G83840	ferric uptake regu
2	40	67.8	400	1 A39130	nicotinate phospho
3	40	67.8	400	1 JQ0756	nicotinate phospho
4	40	67.8	400	2 AB0617	nicotinate phospho
5	40	67.8	400	2 F90755	nicotinate phospho
6	40	67.8	400	2 D85619	nicotinate phospho
7	40	67.8	705	2 A70669	probable acid-CoA
8	39	66.1	179	2 T22521	hypothetical prote
9	38	64.4	389	2 T27085	hypothetical prote
10	38	64.4	721	2 H82528	L-ascorbate oxidas
11	38	64.4	1267	1 MWXR31	lambda 3 protein -
12	38	64.4	1267	1 MWXR32	lambda 3 protein -
13	38	64.4	1267	1 MWXR33	lambda 3 protein -
14	37	62.7	430	2 S75313	serine-tRNA ligase
15	37	62.7	504	2 C64398	hypothetical prote
16	37	62.7	1268	2 T31420	C-terminal domain-
17	36	61.0	347	2 T35013	probable membrane
18	36	61.0	461	1 E69360	4-hydroxyphenylace
19	36	61.0	470	2 E72376	hypothetical prote
20	36	61.0	507	2 AD3382	ABC transporter-as
21	36	61.0	1812	2 I49350	breast/ovarian can
22	35	59.3	138	2 C90460	hypothetical prote
23	35	59.3	187	2 A10520	Ampd protein (anhy
24	35	59.3	269	2 A46506	leukocyte activati
25	35	59.3	374	2 T32736	hypothetical prote
26	35	59.3	329	2 T20546	hypothetical prote
27	35	59.3	453	2 T24127	probable chitinase
28	35	59.3	513	2 B87484	anthranilate synth
29	35	59.3	656	2 T10664	serine/threonine-s

30	35	59.3	662	2 I37892	IL12 receptor comp
31	35	59.3	1323	2 T37533	coronin-like prote
32	34.5	58.5	325	2 B81364	probable periplasm
33	34	57.6	112	2 H70232	hypothetical prote
34	34	57.6	122	2 T04118	mitochondrial proc
35	34	57.6	172	2 F81439	translation initia
36	34	57.6	180	2 AC3270	hypothetical expor
37	34	57.6	255	2 G84320	hypothetical prote
38	34	57.6	259	2 E84427	hypothetical prote
39	34	57.6	270	2 C96731	unknown protein F5
40	34	57.6	273	2 T10610	hypothetical prote
41	34	57.6	296	2 A95408	hypothetical prote
42	34	57.6	344	2 T05437	hypothetical prote
43	34	57.6	348	2 H85256	hypothetical prote
44	34	57.6	375	2 B96551	hypothetical prote
45	34	57.6	393	2 B86189	protein T25N20.9 [
46	34	57.6	407	2 C36786	hypothetical prote
47	34	57.6	413	2 F96743	probable C2H2-type
48	34	57.6	482	2 H71400	hypothetical prote
49	34	57.6	596	2 B41627	furin (EC 3.4.21.7
50	34	57.6	783	2 A1627	furin (EC 3.4.21.7
51	34	57.6	801	2 A89862	Na+/H+ antiporter
52	34	57.6	850	2 S54553	SIN3 protein-bindi
53	34	57.6	988	2 F86315	protein T10022.13
54	34	57.6	1030	2 F96763	hypothetical prote
55	34	57.6	1036	2 T18530	phospholipase D (E
56	33	55.9	152	2 A10448	probable ribonucle
57	33	55.9	167	2 B84536	hypothetical prote
58	33	55.9	185	2 H87107	ribosome recycling
59	33	55.9	200	2 T02826	ribosomal protein
60	33	55.9	214	2 S46476	cysteine proteinas
61	33	55.9	226	2 AD2198	hypothetical prote
62	33	55.9	238	2 T11718	hypothetical prote
63	33	55.9	248	2 F64908	probable dehydroge
64	33	55.9	248	2 D90897	probable oxidoredu
65	33	55.9	248	2 C85720	probable oxidoredu
66	33	55.9	273	2 D81878	probable oxidoredu
67	33	55.9	336	2 G82228	formiminoglutamase
68	33	55.9	352	2 C96643	hypothetical prote
69	33	55.9	370	2 F84550	hypothetical prote
70	33	55.9	389	1 A48329	histidinol-phospha
71	33	55.9	421	2 A83467	glutamate dehydrog
72	33	55.9	489	2 C87480	conserved hypothet
73	33	55.9	521	2 T18896	glypican 1 precurs
74	33	55.9	569	2 D85354	hypothetical prote
75	33	55.9	577	2 T18646	hypothetical prote
76	33	55.9	600	2 E87665	arginyl-tRNA synth
77	33	55.9	675	2 S74399	sensory transducti
78	33	55.9	680	2 G82526	ATP-dependent DNA
79	33	55.9	707	2 F86925	probable acyl-CoA
80	33	55.9	725	2 J80100	neural cell adhesi
81	33	55.9	730	2 JH0798	fasciclin IV precu
82	33	55.9	842	2 C83177	probable phosphotr
83	33	55.9	955	2 T18435	hypothetical prote
84	33	55.9	1035	2 T42093	phospholipase D (E
85	33	55.9	1036	2 T13732	phospholipase D (E
86	33	55.9	1037	2 T13943	phospholipase D (E
87	33	55.9	1041	2 P00442	polyprotein - barl
88	33	55.9	1074	2 T17203	phospholipase (EC
89	33	55.9	1074	2 T13725	phospholipase D (E
90	33	55.9	1075	2 T46635	phospholipase D (E
91	33	55.9	1092	1 UN0635	neural cell adhesi
92	33	55.9	1202	2 P00440	polyprotein - barl
93	33	55.9	1231	1 NBH0H	complement factor
94	33	55.9	1470	2 S45323	genome polyprotein
95	33	55.9	2212	2 T28157	erythrocyte membra
96	33	55.9	2410	1 JQ1948	genome polyprotein
97	33	55.9	2412	1 JQ1537	hypothetical prote
98	33	55.9	2647	2 T28161	LDL-receptor-relat
99	33	55.9	4753	1 A47437	syringomycin synth
100	33	55.9	9376	2 T14593	probable sulfatase
101	32.5	55.1	571	2 A10506	DNA-binding protei
102	32	54.2	66	1 DNVFB	

103	32	54.2	74	1	DNPVAS	DNA-binding protei	176	31	52.5	129	2	S48902	hypothetical prote
104	32	54.2	97	2	A82158	hypothetical prote	177	31	52.5	145	2	F82133	hypothetical prote
105	32	54.2	111	2	C71401	hypothetical prote	178	31	52.5	147	2	T18586	hypothetical prote
106	32	54.2	129	2	AF0527	conserved hypotet	179	31	52.5	161	2	AC0883	conserved hypotet
107	32	54.2	145	2	A83010	conserved hypotet	180	31	52.5	170	2	AG2479	aminoglycoside N6'
108	32	54.2	154	2	A60998	replication protei	181	31	52.5	182	2	A25468	T-cell surface gly
109	32	54.2	158	2	AB0426	transcription elon	182	31	52.5	222	2	S26994	cellulose 1,4-beta
110	32	54.2	161	1	TPHUC2	troponin C, cardia	183	31	52.5	228	2	S26995	cellulose 1,4-beta
111	32	54.2	161	1	TPBOCC	troponin C, cardia	184	31	52.5	228	2	T47425	NAC domain-like pr
112	32	54.2	161	1	TPBRCC	troponin C, cardia	185	31	52.5	236	2	S26993	cellulose 1,4-beta
113	32	54.2	161	2	S07450	troponin C - quail	186	31	52.5	240	2	E86418	probable eukaryoti
114	32	54.2	161	2	A27204	troponin C, cardia	187	31	52.5	245	2	G82175	hypothetical prote
115	32	54.2	161	2	JU0035	troponin C, cardia	188	31	52.5	268	2	T31699	hypothetical prote
116	32	54.2	161	2	JW0064	slow cardiac tropo	189	31	52.5	274	2	T10270	protein kinase (EC
117	32	54.2	161	2	A32620	troponin C, cardia	190	31	52.5	280	2	T43011	suppressor protein
118	32	54.2	171	1	RWHD1	T-cell surface gly	191	31	52.5	284	2	AG3231	conjugal transfer
119	32	54.2	183	2	AF0904	probable exported	192	31	52.5	285	2	G85016	probable myb-relat
120	32	54.2	190	2	T46053	ADP-ribosylation f	193	31	52.5	286	2	S50855	neurotrophin-6 - s
121	32	54.2	204	2	E84173	hypothetical prote	194	31	52.5	292	2	T10106	chitinase (EC 3.2.
122	32	54.2	221	2	T26921	hypothetical prote	195	31	52.5	314	2	C90256	conserved hypotet
123	32	54.2	229	2	I46614	nerve growth facto	196	31	52.5	317	2	T18695	hypothetical prote
124	32	54.2	241	2	JL0097	nerve growth facto	197	31	52.5	323	2	T27640	hypothetical prote
125	32	54.2	245	2	I56570	beta-nerve growth	198	31	52.5	338	2	H83228	hypothetical prote
126	32	54.2	289	1	NGHUBM	nerve growth facto	199	31	52.5	344	2	T27664	hypothetical prote
127	32	54.2	289	2	T44599	oligopeptide trans	200	31	52.5	346	2	T49085	hypothetical prote
128	32	54.2	303	1	NGRTBA	nerve growth facto	201	31	52.5	347	2	JC7828	glucuronyltransfer
129	32	54.2	305	2	E84261	glycosyl transfera	202	31	52.5	359	2	AF3184	beta-lactamase [im
130	32	54.2	307	1	NGMSMG	nerve growth facto	203	31	52.5	370	2	T22082	hypothetical prote
131	32	54.2	324	2	H86244	lysophospholipase	204	31	52.5	422	2	S34199	polygalacturonase
132	32	54.2	350	2	T25451	transforming growt	205	31	52.5	435	2	T32195	hypothetical prote
133	32	54.2	357	2	AG1072	conserved hypotet	206	31	52.5	460	2	JC4214	translation elonga
134	32	54.2	363	2	G95937	probable mureinpep	207	31	52.5	461	2	T33747	hypothetical prote
135	32	54.2	383	2	A96704	hypothetical prote	208	31	52.5	497	2	B97555	hypothetical prote
136	32	54.2	387	2	JL0101	methane monooxygen	209	31	52.5	497	2	AD2775	fumarate hydratase
137	32	54.2	427	2	G02034	Killer cell inhibi	210	31	52.5	501	2	T37747	hypothetical prote
138	32	54.2	435	2	G69194	L-asparaginase I -	211	31	52.5	510	2	S41943	cellulose 1,4-beta
139	32	54.2	444	2	G01924	KIR (cl-2) NK rece	212	31	52.5	511	2	S44716	cellulose 1,4-beta
140	32	54.2	444	2	G01925	KIR (cl-11) NK rec	213	31	52.5	530	2	S65773	glutamyl-tRNA redu
141	32	54.2	455	2	G01923	KIR (cl-5) NK rece	214	31	52.5	530	2	G86233	hypothetical prote
142	32	54.2	457	2	T48036	hypothetical prote	215	31	52.5	540	2	S41942	cellulose 1,4-beta
143	32	54.2	462	2	H95914	hypothetical membr	216	31	52.5	542	2	T10245	glutamyl-tRNA redu
144	32	54.2	474	1	OMHU1B	alpha-1-B-glycopro	217	31	52.5	548	2	T22137	hypothetical prote
145	32	54.2	486	2	A83284	probable oxidoredu	218	31	52.5	551	2	S58238	HR38 protein - fr
146	32	54.2	502	2	S38139	LAS1 protein - yea	219	31	52.5	557	2	T16696	hypothetical prote
147	32	54.2	509	2	T19106	probable serine ca	220	31	52.5	567	2	E95901	conserved hypotet
148	32	54.2	509	2	T02864	probable Zn finger	221	31	52.5	576	2	T41587	probable carbon ca
149	32	54.2	516	2	D96682	protein F1822.18 [222	31	52.5	577	2	T02401	probable beta-gluc
150	32	54.2	536	2	T20736	hypothetical prote	223	31	52.5	587	2	F84475	hypothetical prote
151	32	54.2	539	2	A54294	cell division cont	224	31	52.5	594	2	I58386	receptor tyrosine
152	32	54.2	562	2	AF0852	secretory protein i	225	31	52.5	597	2	E85090	probable transposo
153	32	54.2	563	2	S54420	invasion protein i	226	31	52.5	612	2	T02414	probable protein k
154	32	54.2	589	2	F70033	glucan 1,4-alpha-m	227	31	52.5	615	2	S54468	AIPI protein - yea
155	32	54.2	607	2	S77092	hypothetical prote	228	31	52.5	629	2	H86383	probable wall-asso
156	32	54.2	664	2	E70770	probable atp-depen	229	31	52.5	651	2	F90111	DNA primase [impor
157	32	54.2	729	2	T45951	hypothetical prote	230	31	52.5	662	2	T41442	omnipotent nonsens
158	32	54.2	731	2	T29129	probable ATP/GTP b	231	31	52.5	662	2	T51948	omnipotent nonsens
159	32	54.2	864	2	T30441	probable capsid-as	232	31	52.5	710	1	I51283	hepatocyte growth
160	32	54.2	1095	2	T00329	hypothetical prote	233	31	52.5	728	1	S59553	arginine decarboxy
161	32	54.2	1116	2	T38073	serine/threonine-p	234	31	52.5	729	2	T23972	hypothetical prote
162	32	54.2	1283	2	T13799	neurexin iv - frui	235	31	52.5	778	2	B70667	hypothetical prote
163	32	54.2	1331	2	S05011	calcium channel al	236	31	52.5	838	2	T20125	hypothetical prote
164	32	54.2	1429	2	JU0609	nitric-oxide synth	237	31	52.5	878	2	H83184	phosphoenolpyruvat
165	32	54.2	1429	2	S16233	nitric-oxide synth	238	31	52.5	888	2	H88085	protein T11F1.8 li
166	32	54.2	1433	2	G01946	nitric-oxide synth	239	31	52.5	1150	2	T18303	DNA binding regula
167	32	54.2	2042	2	T18399	variant-specific s	240	31	52.5	1162	2	T18199	reverse transcript
168	32	54.2	2166	2	S11339	calcium channel pr	241	31	52.5	1330	2	S49010	embryonic receptor
169	32	54.2	2171	2	S05054	calcium channel al	242	31	52.5	1333	2	I78875	receptor tyrosine
170	32	54.2	2204	1	RRNZNV	genome polyprotein	243	31	52.5	1336	2	I60598	Fit-1 tyrosine kin
171	32	54.2	2657	2	T18497	hypothetical prote	244	31	52.5	1364	2	T00250	MEGF2 protein - hu
172	32	54.2	2911	2	T20566	hypothetical prote	245	31	52.5	1390	2	S51364	sperm tail-specifi
173	32	54.2	3228	2	T21281	hypothetical prote	246	31	52.5	1475	2	T29809	hypothetical prote
174	31.5	53.4	189	2	G96514	hypothetical prote	247	31	52.5	1489	2	T38842	probable RAS GTPas
175	31	52.5	125	2	T32471	hypothetical prote	248	31	52.5	1580	2	T26204	hypothetical prote

249	31	52.5	1750	2	H64403	ribonucleoside-tri	322	30	50.8	376	2	T32837	hypothetical prote
250	31	52.5	1763	2	T19183	hypothetical prote	323	30	50.8	377	2	B72275	probable aspartate
251	31	52.5	1769	2	T19184	hypothetical prote	324	30	50.8	382	2	G85234	hypothetical prote
252	31	52.5	2051	2	T30938	receptor tyrosine	325	30	50.8	384	1	S41584	histidinol-phospha
253	31	52.5	3328	2	T30835	breast cancer tumo	326	30	50.8	385	1	S48456	hypothetical prote
254	31	52.5	3329	2	T42205	breast cancer susc	327	30	50.8	392	2	A86252	probable nicotinat
255	31	52.5	3329	2	T30904	breast cancer tumo	328	30	50.8	401	2	AG0172	hypothetical prote
256	31	52.5	3432	1	GNWVJS	genome polyprotein	329	30	50.8	408	2	D46335	hypothetical prote
257	31	52.5	3432	1	GNWVJE	genome polyprotein	330	30	50.8	414	2	T24563	hypothetical prote
258	31	52.5	4549	2	T20771	hypothetical prote	331	30	50.8	416	2	B55649	TNFR-associated pr
259	31	52.5	4667	2	T20774	hypothetical prote	332	30	50.8	423	2	B84751	hypothetical prote
260	30.5	51.7	732	2	T16422	hypothetical prote	333	30	50.8	428	2	S10013	alpha-amylase (EC
261	30.5	51.7	1140	2	B97820	hypothetical prote	334	30	50.8	434	1	DESBHT	histidinol dehydro
262	30	50.8	36	2	A06002	annexin II - golde	335	30	50.8	434	2	AD0764	histidinol dehydro
263	30	50.8	39	2	A36453	decorsin - leech (336	30	50.8	434	2	S12775	alpha-amylase (EC
264	30	50.8	57	1	T1FHPB	proteinase inhibit	337	30	50.8	462	2	AH1130	glutamate decarbox
265	30	50.8	85	2	T10571	hypothetical prote	338	30	50.8	465	2	T05734	glutamyl-tRNA redu
266	30	50.8	89	2	B91173	phosphotransferase	339	30	50.8	465	2	T00090	glycosyltransferas
267	30	50.8	89	2	B86019	probable phosphoca	340	30	50.8	467	2	A47388	serine/threonine p
268	30	50.8	112	2	B86263	F13K23.19 protei	341	30	50.8	468	2	T10595	hypothetical prote
269	30	50.8	116	2	H75591	hypothetical prote	342	30	50.8	470	2	F85164	hypothetical prote
270	30	50.8	133	2	I45927	membrane-bound inm	343	30	50.8	470	2	S54089	hypothetical prote
271	30	50.8	135	2	I49275	protein kinase Sry	344	30	50.8	483	2	A39676	protein kinase Sry
272	30	50.8	141	2	A40463	integrin alpha-6 c	345	30	50.8	484	2	E64432	spore coat polysac
273	30	50.8	147	1	LZDK	lysozyme (EC 3.2.1	346	30	50.8	485	2	T32144	hypothetical prote
274	30	50.8	149	2	B40463	integrin alpha-6 c	347	30	50.8	491	2	E87452	ankyrin-related pr
275	30	50.8	163	2	D83883	hypothetical prote	348	30	50.8	499	2	H83148	AMP nucleosidase p
276	30	50.8	183	2	S05569	signaling protein	349	30	50.8	503	2	T46852	anthranilate synth
277	30	50.8	183	2	B90643	Ampb protein [impo	350	30	50.8	514	2	F64899	nitrate reductase
278	30	50.8	183	2	B85494	regulates ampC [im	351	30	50.8	514	2	C85730	cryptic nitrate re
279	30	50.8	183	2	C65110	hypothetical prote	352	30	50.8	514	2	F90887	cryptic nitrate re
280	30	50.8	183	2	C85983	hypothetical prote	353	30	50.8	528	2	T05732	probable glutamyl-
281	30	50.8	183	2	H91137	hypothetical prote	354	30	50.8	529	2	S18453	variant surface gl
282	30	50.8	188	2	H90255	hypothetical prote	355	30	50.8	543	2	E96616	hypothetical prote
283	30	50.8	195	2	B85364	adenylate kinase r	356	30	50.8	546	1	S13757	RNA helicase DBP2
284	30	50.8	211	2	S55129	hypothetical prote	357	30	50.8	548	2	T28910	hypothetical prote
285	30	50.8	219	2	AH2353	transcription fact	358	30	50.8	549	2	H96944	arginine degradati
286	30	50.8	226	2	H84237	conserved hypothet	359	30	50.8	552	2	T10186	glutamyl-tRNA redu
287	30	50.8	231	2	T32146	hypothetical prote	360	30	50.8	566	2	F84903	probable ubiquitin
288	30	50.8	254	2	E98329	hypothetical prote	361	30	50.8	573	2	S00661	hypothetical prote
289	30	50.8	255	2	A84723	hypothetical prote	362	30	50.8	573	2	JC4335	anti-mullerian hor
290	30	50.8	264	2	T47183	hypothetical prote	363	30	50.8	586	2	T20353	hypothetical prote
291	30	50.8	266	2	T10609	hypothetical prote	364	30	50.8	602	1	S46676	probable phosphoe
292	30	50.8	270	1	ICMS1	interleukin-1 alph	365	30	50.8	633	2	T04835	probable serine/th
293	30	50.8	270	1	JX0064	interleukin-1 alph	366	30	50.8	634	2	S77096	icfG protein sir18
294	30	50.8	270	1	F86177	protein F19p19.1 [367	30	50.8	665	2	E86775	ribonuclease [impo
295	30	50.8	273	2	H81140	oxidoreductase, sh	368	30	50.8	673	2	S36336	probable transcrip
296	30	50.8	285	2	A86419	probable eukaryoti	369	30	50.8	738	1	TFHUM	melanotransferrin
297	30	50.8	288	2	C83518	hypothetical prote	370	30	50.8	738	2	T27289	hypothetical prote
298	30	50.8	297	2	H44020	hypothetical prote	371	30	50.8	752	1	PLIVBC	RNA-directed RNA p
299	30	50.8	303	2	B84744	hypothetical prote	372	30	50.8	752	1	PLIVBL	RNA-directed RNA p
300	30	50.8	306	2	I49068	protein kinase Sry	373	30	50.8	752	1	PLIVBW	RNA-directed RNA p
301	30	50.8	309	1	KIECRB	ribokinase (EC 2.7	374	30	50.8	830	2	T04848	protein kinase hom
302	30	50.8	309	2	F91215	ribokinase [import	375	30	50.8	862	2	I49583	differentiation an
303	30	50.8	309	2	G86061	ribokinase [import	376	30	50.8	868	2	A46512	CD22 homolog/B lym
304	30	50.8	312	2	T35940	probable transport	377	30	50.8	931	2	AFJ276	ATP-dependent clp
305	30	50.8	315	2	S13550	hypothetical prote	378	30	50.8	932	2	F84465	hypothetical prote
306	30	50.8	321	2	S13550	anther-specific pr	379	30	50.8	964	2	E71460	probable outer mem
307	30	50.8	326	2	AE2466	acetyl-CoA carboxy	380	30	50.8	976	2	F81722	polymorphic membra
308	30	50.8	336	2	E69845	thiamin biosynthes	381	30	50.8	1030	2	C86189	unknown protein. 2
309	30	50.8	339	1	LUBO36	annexin II - bovin	382	30	50.8	1048	2	C86189	protein T5N20.11
310	30	50.8	339	1	LUBO36	annexin II - human	383	30	50.8	1073	2	B36429	integrin alpha-6 c
311	30	50.8	339	1	LUMS36	annexin II - mouse	384	30	50.8	1091	2	A41543	integrin alpha-6 c
312	30	50.8	339	2	S33700	annexin II - rat	385	30	50.8	1132	2	A35089	myosin-binding pro
313	30	50.8	339	2	B34895	transcription fact	386	30	50.8	1205	2	T18517	procollagen N-endo
314	30	50.8	341	2	S55277	annexin II - rat	387	30	50.8	1207	2	T23754	hypothetical prote
315	30	50.8	342	2	T45577	protein kinase-lik	388	30	50.8	1372	2	A49634	aldehyde oxidase (
316	30	50.8	344	1	FWXL3	transcription fact	389	30	50.8	1372	2	T25933	hypothetical prote
317	30	50.8	352	2	C98170	hypothetical prote	390	30	50.8	1375	2	T13822	frazzled gene prot
318	30	50.8	373	2	T47115	probable 4-carboxy	391	30	50.8	1385	2	S34230	156K protein - Pla
319	30	50.8	375	2	I60125	PDGF receptor beta	392	30	50.8	1419	2	A41182	collagen alpha 1(I
320	30	50.8	375	2	AC1350	N-acetylmuramoyl-L	393	30	50.8	1433	1	GNVUBW	M polyprotein prec
321	30	50.8	375	2	AF1720	N-acetylmuramoyl-L	394	30	50.8	1526	2	T13823	frazzled gene prot

395	30	50.8	1535	2	T49042	hypothetical prote	468	29	49.2	243	2	A26311	nerve growth facto
396	30	50.8	1806	2	T23298	hypothetical prote	469	29	49.2	243	2	I51193	nerve growth facto
397	30	50.8	1847	2	T18308	probable vitellog	470	29	49.2	244	1	VCCVSV	coat protein - mai
398	30	50.8	2515	2	A41519	posterior-group pr	471	29	49.2	244	2	T10112	capsid protein - m
399	30	50.8	3005	2	S33642	homeotic protein z	472	29	49.2	247	2	T02253	chlorophyll a/b-bi
400	30	50.8	3433	1	GNWVKV	genome polyprotein	473	29	49.2	249	2	AI3401	arginyltransferase
401	30	50.8	3434	1	GNWVMV	genome polyprotein	474	29	49.2	252	2	C83837	hypothetical prote
402	30	50.8	3924	2	S37431	ankyrin 2, neurona	475	29	49.2	252	2	T46247	hypothetical prote
403	30	50.8	4543	1	A53102	alpha-2-macroglobu	476	29	49.2	264	2	F91017	hypothetical prote
404	30	50.8	4544	1	S02392	alpha-2-macroglobu	477	29	49.2	264	2	H85861	hypothetical prote
405	30	50.8	4545	1	S25111	alpha-2-macroglobu	478	29	49.2	265	2	D83577	conserved hypothet
406	30	50.8	4660	2	T42737	gp330 protein prec	479	29	49.2	270	2	G96686	hypothetical prote
407	30	50.8	4687	1	A39638	plectin - rat	480	29	49.2	271	2	H97230	alpha/beta superfa
408	29.5	50.0	83	2	T23366	hypothetical prote	481	29	49.2	273	2	T39405	hypothetical prote
409	29.5	50.0	343	2	T02071	glyceraldehyde-3-p	482	29	49.2	280	2	T27758	hypothetical prote
410	29.5	50.0	373	2	T34126	hypothetical prote	483	29	49.2	282	2	C95181	degv family protei
411	29.5	50.0	430	2	S50604	AST2 protein - yea	484	29	49.2	282	2	F98048	conserved hypothet
412	29.5	50.0	442	2	S50062	cell wall glycopro	485	29	49.2	284	2	G96660	protein F2k11.8 [i
413	29.5	50.0	1367	2	H82874	conserved hypothet	486	29	49.2	287	2	T25064	hypothetical prote
414	29.5	50.0	7962	2	I38346	elastic titin - hu	487	29	49.2	287	2	C97546	hypothetical prote
415	29	49.2	30	2	PQ0444	hypothetical prote	488	29	49.2	287	2	AE2765	cytochrome-c oxida
416	29	49.2	57	2	D81152	hypothetical prote	489	29	49.2	288	2	G59387	conserved hypothet
417	29	49.2	60	2	A54369	fibrinogen recepto	490	29	49.2	292	2	A97034	transcription regu
418	29	49.2	83	2	AE1851	hypothetical prote	491	29	49.2	296	2	T14672	hypothetical prote
419	29	49.2	86	2	AI3131	hypothetical prote	492	29	49.2	296	2	T36437	probable ABC-type
420	29	49.2	110	2	E85547	probable transcrip	493	29	49.2	297	1	S49348	cytochrome-c oxida
421	29	49.2	117	2	S28161	nerve growth facto	494	29	49.2	297	2	T27584	hypothetical prote
422	29	49.2	120	2	T07765	disease resistance	495	29	49.2	299	2	A10188	ATP phosphoribosyl
423	29	49.2	124	2	S24696	Ig heavy chain V6	496	29	49.2	299	2	T14943	hypothetical prote
424	29	49.2	125	2	A26312	nerve growth facto	497	29	49.2	300	2	AF3092	conserved hypothet
425	29	49.2	132	2	AB1757	hypothetical prote	498	29	49.2	300	2	D98194	hypothetical prote
426	29	49.2	134	2	AF3482	hypothetical prote	499	29	49.2	301	2	T27585	hypothetical prote
427	29	49.2	135	2	P64779	probable transcrip	500	29	49.2	302	2	A96661	unknown protein, 8
428	29	49.2	135	2	A90697	probable transcrip							
429	29	49.2	138	2	AF0564	copper efflux regu							
430	29	49.2	142	2	A47142	cystatin D precurs							
431	29	49.2	142	2	D84300	bacterio-opsin lin							
432	29	49.2	145	2	A55932	galectin-5 - rat							
433	29	49.2	145	2	AD1215	hypothetical prote							
434	29	49.2	145	2	AH1568	hypothetical prote							
435	29	49.2	149	2	S12913	cystatin - fruit f							
436	29	49.2	151	2	A50333	rpoc protein homol							
437	29	49.2	157	1	EDXF3	immediate-early pr							
438	29	49.2	161	2	T10853	V4iR protein - Rhi							
439	29	49.2	164	2	S63995	peptidylprolyl iso							
440	29	49.2	165	2	B38388	peptidylprolyl iso							
441	29	49.2	171	2	T50770	peptidylprolyl iso							
442	29	49.2	172	2	T07950	peptidylprolyl iso							
443	29	49.2	172	2	T06073	peptidylprolyl iso							
444	29	49.2	172	2	S54833	peptidylprolyl iso							
445	29	49.2	173	2	H69079	conserved hypothet							
446	29	49.2	173	2	AD0718	probable lipoprote							
447	29	49.2	174	2	E84597	cyclophilin (CYP2)							
448	29	49.2	174	2	T50772	peptidylprolyl iso							
449	29	49.2	174	2	JE0323	gammaS-crySTALLIN							
450	29	49.2	178	2	AB3279	invasion protein A							
451	29	49.2	179	2	S48018	peptidylprolyl iso							
452	29	49.2	182	2	I67436	interleukin-1-beta							
453	29	49.2	191	2	A71814	hypothetical prote							
454	29	49.2	200	2	T42678	hypothetical prote							
455	29	49.2	201	2	A30833	ribosomal protein							
456	29	49.2	205	2	B97584	30S ribosomal prot							
457	29	49.2	205	2	AB2805	30S ribosomal prot							
458	29	49.2	205	2	F87560	ribosomal protein							
459	29	49.2	208	2	E95338	hypothetical prote							
460	29	49.2	213	2	S43723	lactase (EC 3.2.1.							
461	29	49.2	213	2	S43722	lactase (EC 3.2.1.							
462	29	49.2	214	2	S65052	pistil-specific pr							
463	29	49.2	216	2	E84450	hypothetical prote							
464	29	49.2	218	2	T08737	hypothetical prote							
465	29	49.2	227	2	T47186	hypothetical prote							
466	29	49.2	229	2	T09215	H+-exporting ATPas							
467	29	49.2	235	2	S14481	nerve growth facto							

R;Vinitsky, A.; Teng, H.; Grubmeyer, C.T.

J. Bacteriol. 173, 536-540, 1991

A;Title: Cloning and nucleic acid sequence of the *Salmonella typhimurium* pncB gene and

A;Reference number: A39130; MUID:91100340; PMID:1987148

A;Accession: A39130

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-400 <VIN>

A;Cross-references: UNIPROT:P22253; GB:M55986; NID:g154268; PIDN:AAA27190.1; PID:g154269

C;Genetics:

A;Gene: pncB

C;Function:

A;Pathway: nicotinate and nicotinamide metabolism

C;Superfamily: nicotinate phosphoribosyltransferase

C;Keywords: glycosyltransferase; pentosyltransferase

Query Match 67.8%; Score 40; DB 1; Length 400;

Best Local Similarity 85.7%; Pred. No. 11;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8

Db 39 FRCRGDD 45

RESULT 3

JQ0756

nicotinate phosphoribosyltransferase (EC 2.4.2.11) - *Escherichia coli* (strain K-12)

C;Species: *Escherichia coli*

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: JQ0756; B64833

R;Wubolts, M.G.; Terpstra, P.; van Beilen, J.B.; Kingma, J.; Meesters, H.A.R.; Witholt,

J. Biol. Chem. 265, 17665-17672, 1990

A;Title: Variation of cofactor levels in *Escherichia coli*; sequence analysis and expres

A;Reference number: JQ0756; MUID:91009224; PMID:2211655

A;Accession: JQ0756

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-400 <WUB>

A;Cross-references: UNIPROT:P18133; GB:J05568; NID:g147306; PIDN:AAA24400.1; PID:g147307

A;Experimental source: strain GEC70

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of *Escherichia coli* K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: B64833

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-400 <BLAT>

A;Cross-references: GB:AE000195; GB:U00096; NID:g1787156; PIDN:AAC74017.1; PID:g1787162;

A;Experimental source: strain K-12, substrain MG1655

C;Genetics:

A;Gene: pncB

C;Function:

A;Pathway: nicotinate and nicotinamide metabolism

C;Superfamily: nicotinate phosphoribosyltransferase

C;Keywords: glycosyltransferase; pentosyltransferase

Query Match 67.8%; Score 40; DB 1; Length 400;

Best Local Similarity 85.7%; Pred. No. 11;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8

Db 39 FRCRGDD 45

RESULT 4

AB0617

nicotinate phosphoribosyltransferase [imported] - *Salmonella enterica* subsp. *enterica* se

C;Species: *Salmonella enterica* subsp. *enterica* serovar Typhi

A;Note: this species has also been called *Salmonella typhi*

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C;Accession: AB0617

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerston, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, . S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AB0617

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-400 <PAR>

A;Cross-references: GB:AL513382; PIDN:CAD05404.1; PID:g16502165; GSPDB:GN00176

C;Genetics:

A;Gene: STY1010

C;Superfamily: nicotinate phosphoribosyltransferase

Query Match 67.8%; Score 40; DB 2; Length 400;

Best Local Similarity 85.7%; Pred. No. 11;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8

Db 39 FRCRGDD 45

RESULT 5

F90755

nicotinate phosphoribosyltransferase [imported] - *Escherichia coli* (strain O157:H7, subsp

C;Species: *Escherichia coli*

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C;Accession: F90755

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;

gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genom

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: F90755

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-400 <HAY>

A;Cross-references: UNIPROT:Q8XDE8; GB:BA000007; PIDN:BAE34437.1; PID:g13360473; GSPDB:GP

A;Experimental source: strain O157:H7, substrain RIMD 0509952

C;Genetics:

A;Gene: ECs1014

C;Superfamily: nicotinate phosphoribosyltransferase

Query Match 67.8%; Score 40; DB 2; Length 400;

Best Local Similarity 85.7%; Pred. No. 11;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8

Db 39 FRCRGDD 45

RESULT 6

D85619

nicotinate phosphoribosyltransferase [imported] - *Escherichia coli* (strain O157:H7, subsp

C;Species: *Escherichia coli*

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C;Accession: D85619

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A;Reference number: AB5480; MUID:21074935; PMID:11206551

A;Accession: D85619

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-400 <STO>

A;Cross-references: UNIPROT:Q8XDE8; GB:AE005174; NID:g12514106; PIDN:AGS55416.1; GSPDB:GP

A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: pncB
C:Superfamily: nicotinate phosphoribosyltransferase

Query Match 67.8%; Score 40; DB 2; Length 400;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
:|||||
Db 39 FRCRGDD 45

RESULT 7
A70669
Probable acid-CoA ligase (EC 6.2.1.1.-) fadD22 [similarity] - Mycobacterium tuberculosis
N:Alternate names: hypothetical protein pks002a
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: A70669; S73073
R:Coles, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: A70669
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-705 <COL>
A:Cross-references: UNIPROT:P96283; GB:Z83858; GB:AL123456; NID:G3261675; PIDN:CAB06101.
A:Experimental source: strain H37Rv
R:Smith, D.R.; Robinson, K.
submitted to the EMBL Data Library, September 1994
A:Description: Mycobacterium tuberculosis cosmid tbc2.
A:Reference number: S73053
A:Accession: S73073
A:Molecule type: DNA
A:Residues: 1-486, 'QQ', 489-705 <SMI>
A:Cross-references: EMBL:U00024; NID:G560506; PIDN:AAA50930.1; PID:G560509

C:Genetics:
A:Gene: fadD22
C:Keywords: acid-thiol ligase; carrier protein; phosphopantetheine; phosphoprotein
F:51-486/Domain: acetate-CoA ligase homology <ACI>
F:544-615/Domain: acyl carrier protein homology <ACPI>
F:579/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

Query Match 67.8%; Score 40; DB 2; Length 705;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YRCRGDDSK 10
|||||
Db 383 YRCRADDTTE 391

RESULT 8
T22521
Hypothetical protein F52H3.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22521

R:Gardner, A.
submitted to the EMBL Data Library, October 1995
A:Reference number: Z19575
A:Accession: T22521
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-179 <WIL>
A:Cross-references: UNIPROT:Q20683; EMBL:Z66512; PIDN:CAA91325.1; GSPDB:GN000020; CESP:F5
A:Experimental source: clone F52H3

C:Genetics:
A:Gene: CESP:F52H3.5
A:Map position: 2
A:Introns: 68/2; 95/1; 135/3

Query Match 66.1%; Score 39; DB 2; Length 179;
Best Local Similarity 77.8%; Pred. No. 7.8;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YRCRGDDSK 10
|||||
Db 125 YRLRGDDDK 133

RESULT 9
T27085
Hypothetical protein Y51A2D.17 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004
C:Accession: T27085; T27320
R:McMurray, A.
submitted to the EMBL Data Library, January 1998
A:Reference number: Z20307
A:Accession: T27085
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-389 <WIL>
A:Cross-references: UNIPROT:Q9XTG0; UNIPROT:Q9GTD6; EMBL:AL021497; PIDN:CAA16413.1; GSPDE
A:Experimental source: clone Y51A2D
R:McMurray, A.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z20343
A:Accession: T27320
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-389 <WIL>
A:Cross-references: EMBL:Z98877; PIDN:CAB11571.1; GSPDB:GN00023; CESP:Y51A2D.17
A:Experimental source: clone Y69H2

C:Genetics:
A:Gene: CESP:Y51A2D.17
A:Map position: 5
A:Introns: 29/2; 58/1; 80/1; 162/3; 204/3; 228/1; 305/1; 356/3
C:Superfamily: erba transforming protein homology

Query Match 64.4%; Score 38; DB 2; Length 389;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGD 7
|||||
Db 45 YRCRGD 50

RESULT 10
H82528
L-ascorbate oxidase XP2677 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: H82528
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: H82528
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-721 <SIM>
A:Cross-references: UNIPROT:Q9PA43; GB:AE003849; NID:G9107904; PIDN:AAF85474
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; AJ
Briones, M.R.S.; Bueno, M.R.F.; Camargo, A.A.; Camargo, D.M.; Carrer, H.
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.S.; Laigh Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawaak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A;Contents: annotation
C;Genetics:
A;Gene: XF2677

Query Match 64.4%; Score 38; DB 2; Length 721;
Best Local Similarity 66.7%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YRCRGDDSK 10
|||:|
Db 282 YACRGNDGK 290

RESULT 11

MMXR31
lambda 3 protein - reovirus type 1 (strain Lang)
N;Alternate names: minor core protein
C;Species: reovirus type 1
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: A30121
R;Wiener, J.R.; Joklik, W.K.
Virology 169, 194-203, 1989
A;Title: The sequences of the reovirus serotype 1, 2, and 3 L1 genome segments and analysis
A;Reference number: A94390; MUID:89163254; PMID:2922925
A;Accession: A30121
A;Molecule type: Genomic RNA
A;Residues: 1-1267 <WIE>
A;Cross-references: UNIPROT:P17376; GB:M24734; NID:G499863
A;Note: This sequence, which matches the sequence attributed to type 1 in Fig. 2, matches he translations in entries REO1LAM3P and REO3LAM3P now differ only by the sequence correction
C;Comment: See also PIR:MMXR33.
C;Genetics:
A;Map position: segment L1
C;Superfamily: reovirus lambda 3 protein
C;Keywords: core protein

Query Match 64.4%; Score 38; DB 1; Length 1267;
Best Local Similarity 75.0%; Pred. No. 71;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
|||:|
Db 728 NYVCGDD 735

RESULT 12

MMXR32
lambda 3 protein - reovirus type 2 (strain D5/Jones)
N;Alternate names: minor core protein
C;Species: reovirus type 2
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: B30121
R;Wiener, J.R.; Joklik, W.K.
Virology 169, 194-203, 1989
A;Title: The sequences of the reovirus serotype 1, 2, and 3 L1 genome segments and analysis
A;Reference number: A94390; MUID:89163254; PMID:2922925
A;Accession: B30121
A;Molecule type: Genomic RNA
A;Residues: 1-1267 <WIE>
A;Cross-references: UNIPROT:P17377; GB:M31057; NID:G499865; PIDN:AAA47245.1; PID:G499866
C;Genetics:
A;Map position: segment L1

C;Superfamily: reovirus lambda 3 protein
C;Keywords: core protein

Query Match 64.4%; Score 38; DB 1; Length 1267;
Best Local Similarity 75.0%; Pred. No. 71;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
|||:|
Db 728 NYVCGDD 735

RESULT 13

MMXR33
lambda 3 protein - reovirus type 3 (strain Dearing)
N;Alternate names: minor core protein
C;Species: reovirus type 3
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: C30121
R;Wiener, J.R.; Joklik, W.K.
Virology 169, 194-203, 1989
A;Title: The sequences of the reovirus serotype 1, 2, and 3 L1 genome segments and analysis
A;Reference number: A94390; MUID:89163254; PMID:2922925
A;Accession: C30121
A;Molecule type: Genomic RNA
A;Residues: 1-1267 <WIE>
A;Cross-references: UNIPROT:P17378; GB:M31058; NID:G499867; GB:M24734; NID:G499863; PIDN: A;Note: This sequence, which matches the sequence attributed to type 3 in Fig. 2, matches nries REO1LAM3P and REO3LAM3P now differ only by the sequence correction apparently made
C;Comment: See also PIR:MMXR31.
C;Genetics:
A;Map position: segment L1
C;Superfamily: reovirus lambda 3 protein
C;Keywords: core protein

Query Match 64.4%; Score 38; DB 1; Length 1267;
Best Local Similarity 75.0%; Pred. No. 71;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
|||:|
Db 728 NYVCGDD 735

RESULT 14

S75313
serine-tRNA ligase (EC 6.1.1.11) - Synecocystis sp. (strain PCC 6803)
N;Alternate names: protein slr1703; seryl-tRNA synthetase
C;Species: Synecocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S75313
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O.K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S75313
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-430 <KAN>
A;Cross-references: UNIPROT:P73201; EMBL:D90904; GB:AB001339; NID:g1652225; PIDN:BAAL1722; A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Gene: serS
A;Start codon: GTG
C;Function:
A;Description: charges tRNA(Ser) with serine
A;Pathway: protein biosynthesis
C;Superfamily: serine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ATP; ligase; protein biosynthesis

```

Query Match      62.7%; Score 37; DB 2; Length 430;
Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
DB 225 SFQCRGDD 232

RESULT 15
C64398
hypothetical protein homolog MJ0787 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: C64398
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: C64398
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-504 <BUL>
A:Cross-references: UNIPROT:Q58197; GB:U67523; GB:L77117; NID:g2826319; PIDN:AAB98783.1;
C:Genetics:
A:Map position: FOR710775-712289

Query Match      62.7%; Score 37; DB 2; Length 504;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YRCRGDDSK 10
DB 463 YPCNGDDKK 471

RESULT 16
T31420
C-terminal domain-binding protein rA8 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31420
R:Yuryev, A.; Patturajan, M.; Liyingtung, Y.; Joshi, R.V.; Gentile, C.; Gebara, M.; Cord
Proc. Natl. Acad. Sci. U.S.A. 93, 6975-6980, 1996
A:Title: The C-terminal domain of the largest subunit of RNA polymerase II interacts wit
A:Reference number: Z21024; MUID:96293459; PMID:8692929
A:Accession: T31420
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1268 <YUR>
A:Cross-references: UNIPROT:Q63623; EMBL:U49055; NID:g1438529; PID:g1438530; PIDN:AA526
A:Experimental source: hippocampus

Query Match      62.7%; Score 37; DB 2; Length 1268;
Best Local Similarity 85.7%; Pred. No. 11e-02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
DB 100 YRCPGDD 106

RESULT 17
T35013
probable membrane protein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C:Accession: T35013
R:Seeger, S.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999

A:Reference number: Z21565
A:Accession: T35013
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-347 <SEE>
A:Cross-references: UNIPROT:Q9XAN5; EMBL:AL079355; PIDN:CAB45569.1; GSPDB:GN00070; SCODEI
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCORDB:SC4C6.05C
C:Superfamily: Streptomyces coelicolor probable membrane protein SC4C6.05C

Query Match      61.0%; Score 36; DB 2; Length 347;
Best Local Similarity 66.7%; Pred. No. 51;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YRCRGDDSK 10
DB 206 YKCPGDTSK 214

RESULT 18
E93360
4-hydroxyphenylacetate 3-monooxygenase (EC 1.14.13.3) hpaA-2 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: E93360
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson,
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Uitterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.A
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: E93360
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-461 <KLE>
A:Cross-references: UNIPROT:O29377; GB:AE001043; GB:AE000782; NID:g2689366; PIDN:AAB9035f
C:Superfamily: Escherichia coli 4-hydroxyphenylacetate 3-monooxygenase large chain
C:Keywords: FAD; NAD; oxidoreductase

Query Match      61.0%; Score 36; DB 1; Length 461;
Best Local Similarity 66.7%; Pred. No. 66;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NYRCRGDD 9
DB 94 NYRCTGCDA 102

RESULT 19
E72376
hypothetical protein TM0434 - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: E72376; F72298
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: E72376
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-470 <ARN>
A:Cross-references: UNIPROT:Q9WYR5; GB:AE001722; GB:AE000512; NID:g4980938; PIDN:AAD3551f
A:Experimental source: strain MSB8
A:Accession: F72298
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-415,'A',417-464,'GS' <AR2>

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A;Cross-references: GB:AE001767; GB:AE000512; NID:g4981611; PIDN:AAD36145.1; PID:g4981611
A;Experimental source: strain MS8
C;Genetics:
A;Gene: TW0434; TM1068
C;Superfamily: melibiose-specific alpha-galactosidase

Query Match 61.0%; Score 36; DB 2; Length 470;
Best Local Similarity 71.4%; Pred. No. 67;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
:|||||
Db 214 FRCRGED 220

RESULT 20
ADJ382
ABC transporter-associated protein BME11042 [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: ADJ382
R;DeiVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujaer, C.; Los, T.; Ivanova, M.; Mazur, M.; Goldsman, E.; Salkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A;Reference number: ADJ252; PMID:11756688
A;Accession: ADJ382
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-507 <KUR>
A;Cross-references: UNIPROT:Q8YGM3; GB:AE008917; PIDN:AAL52223.1; PID:g17983006; GSPDB:GADJ382
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BME11042
A;Map position: 1
C;Superfamily: conserved hypothetical protein b1683

Query Match 61.0%; Score 36; DB 2; Length 507;
Best Local Similarity 85.7%; Pred. No. 72;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 CRGDDSK 10
|||||
Db 319 CRGDNK 325

RESULT 21
I49350
breast/ovarian cancer susceptibility protein BRCA1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-May-2004
C;Accession: I49350
R;Marquis, S.T.; Rajan, J.V.; Wynshaw-Boris, A.; Xu, J.; Yin, G.Y.; Abel, K.J.; Weber, E. Nature Genet. 11, 17-26, 1995
A;Title: The developmental pattern of Brcal expression implies a role in differentiation
A;Reference number: I49350; MUID:96021028; PMID:7550308
A;Accession: I49350
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1812 <RES>
A;Cross-references: EMBL:U31625; NID:g988213; PIDN:AAB17114.1; PID:g988214
C;Genetics:
A;Gene: Brcal
C;Superfamily: transcriptional regulator, BRCA1 type; RING finger homology
C;Keywords: zinc
F;20-70/Domain: RING finger homology <RNG>

Query Match 61.0%; Score 36; DB 2; Length 1812;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDS 9
:|||||

Db 1786 SYRCRGLDA 1794

RESULT 22
C90460
hypothetical protein SSO2828 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: C90460
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-yong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.; arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: C90460
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-138 <KUR>
A;Cross-references: UNIPROT:Q97V09; GB:AE006641; NID:gl3816183; PIDN:AAK42938.1; GSPDB:GN0460
C;Genetics:
A;Gene: SSO2828

Query Match 59.3%; Score 35; DB 2; Length 138;
Best Local Similarity 66.7%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YRCRGDDSK 10
|||||
Db 45 YRCGDIGK 53

RESULT 23
AI0520
AmpD protein (anhydro-N-acetylmuramyl-tripeptide amidase) [imported] - Salmonella enterica
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Dec-2002
C;Accession: AI0520
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AI0520
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-187 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD01305.1; PID:g16501433; GSPDB:GN00176
C;Genetics:
A;Gene: STY0168
C;Superfamily: AmpD protein

Query Match 59.3%; Score 35; DB 2; Length 187;
Best Local Similarity 60.0%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
:|||||
Db 18 HYDCRPDDEK 27

RESULT 24
A46506
leukocyte activation antigen M6 - human
N;Alternate names: basigin; collagenase stimulatory factor, tumor-derived
C;Species: Homo sapiens (man)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
A;Accession: A46506; S13906; I52729; I55194; S19203
R;Kasinrark, W.; Fiebigler, E.; Stefanova, I.; Baumruker, T.; Knapp, W.; Stockinger, H. J. Immunol. 149, 847-854, 1992

A;Title: Human leukocyte activation antigen M6, a member of the Ig superfamily, is the s
A;Reference number: A46506; MUID:92340888; PMID:1634773
A;Accession: A46506
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-269 <RAS>
A;Cross-references: UNIPROT:P35613; EMBL:X64364; NID:G34448; PIDN:CAA45716.1; PID:G34449
A;Note: sequence extracted from NCBI backbone (NCBIP:109314)
R;Nabeshima, K.; Lane, W.S.; Biswas, C.
Arch. Biochem. Biophys. 285, 90-96, 1991
A;Title: Partial sequencing and characterization of the tumor cell-derived collagenase s
A;Reference number: S13906; MUID:91119430; PMID:1846736
A;Accession: S13906
A;Status: preliminary
A;Molecule type: protein
A;Residues: 22-36 <NAB>
R;Biswas, C.; Zhang, Y.; DeCastro, R.; Guo, H.; Nakamura, T.; Kataoka, H.; Nabeshima, K.
Cancer Res. 55, 434-439, 1995
A;Title: The human tumor cell-derived collagenase stimulatory factor (renamed EMMPRIN) i
A;Reference number: I52729; MUID:95112304; PMID:7812975
A;Accession: I52729
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-269 <RES>
A;Cross-references: GB:I10240; NID:G409356; PIDN:AAA68936.1; PID:G409357
R;Miyauchi, T.; Masuzawa, Y.; Muramatsu, T.
J. Biochem. 110, 770-774, 1991
A;Title: The basigin group of the immunoglobulin superfamily: complete conservation of a
A;Reference number: I55194; MUID:92147596; PMID:1783610
A;Accession: I55194
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-269 <RE2>
A;Cross-references: GB:D45131; NID:gl304103; PIDN:BAA08109.1; PID:G633069
C;Genetics:
A;Gene: GDB:BSG
A;Cross-references: GDB:228978; OMIM:109480
A;Map position: 19p13.3-19p13.3
C;Superfamily: cell surface glycoprotein HT7; immunoglobulin homology
C;Keywords: transmembrane protein

Query Match 59.3%; Score 35; DB 2; Length 269;
Best Local Similarity 66.7%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YRCRGDSK 10
||| |||
DB 183 YRCNGTSSK 191

RESULT 25
T32736
hypothetical protein F54D7.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T32736
R;Dante, M.; Twyman, B.
submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid F54D7.
A;Reference number: Z21218
A;Accession: T32736
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-274 <DAN>
A;Cross-references: EMBL:AF039712; PIDN:AAB96718.1; GSPDB:GN00019; CESP:F54D7.4
A;Experimental source: strain Bristol N2; clone F54D7
C;Genetics:
A;Gene: CESP:F54D7.4
A;Map position: 1
A;Introns: 10/1; 54/2; 78/3; 124/1; 203/1; 258/2

Query Match 59.3%; Score 35; DB 2; Length 274;
Best Local Similarity 75.0%; Pred. No. 62;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YRCRGDS 9
||| |||
DB 228 YRCIGDNS 235

RESULT 26
T20546
hypothetical protein F07C6.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20546
R;Steward, C.
submitted to the EMBL Data Library, February 1996
A;Reference number: Z19290
A;Accession: T20546
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-329 <WIL>
A;Cross-references: UNIPROT:O19157; EMBL:Z69659; PIDN:CAA93483.1; GSPDB:GN00022; CESP:F0;
A;Experimental source: clone F07C6
C;Genetics:
A;Gene: CESP:F07C6.1
A;Map position: 4
A;Introns: 14/2; 47/2; 85/1; 146/1; 226/3; 299/2

Query Match 59.3%; Score 35; DB 2; Length 329;
Best Local Similarity 85.7%; Pred. No. 74;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
||| |||
DB 287 YRCRGCD 293

RESULT 27
T24127
probable chitinase (EC 3.2.1.14) precursor R10D12.15 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24127; T25316; T25318
R;Percy, C.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19842
A;Accession: T24127
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-453 <WIL>
A;Cross-references: UNIPROT:P92013; EMBL:Z81109; PIDN:CAB03255.1; GSPDB:GN00023; CESP:R1
A;Experimental source: clone R10D12
R;Percy, C.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z20014
A;Accession: T25316
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-453 <W12>
A;Cross-references: EMBL:Z82054; PIDN:CAB04840.1; GSPDB:GN00023; CESP:T26F2.1
A;Experimental source: clone T26F2
A;Accession: T25318
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-453 <W13>
A;Cross-references: EMBL:Z82054; PIDN:CAB04842.1; GSPDB:GN00023; CESP:R10D12.15
A;Experimental source: clone T26F2
C;Genetics:
A;Gene: CESP:R10D12.15; CESP:T26F2.1
A;Map position: 5
A;Introns: 23/1; 118/3; 150/2; 237/3; 369/1
C;Keywords: glycosidase; hydrolase

Query Match 59.3%; Score 35; DB 2; Length 453;

Best Local Similarity 60.0%; Pred. No. 99;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
| | | | |
Db 325 NNECSGDSK 334

RESULT 28
B87484
anthranilate synthase component I [imported] - Caulobacter crescentus
C/Species: Caulobacter crescentus
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C/Accession: B87484
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A/Title: Complete Genome Sequence of Caulobacter crescentus.
A/Reference number: A87249; MUID:21173698; PMID:11259647
A/Accession: B87484
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-513 <STO>
A/Cross-references: UNIPROT:Q9A731; GB:AE005673; NID:gl3423344; PIDN:AAK23870.1; GSPDB:G
C/Genetics:
A/Gene: CCI895
C/Superfamily: anthranilate synthase component I

Query Match 59.3%; Score 35; DB 2; Length 513;
Best Local Similarity 55.8%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 YRCRGDDSK 10
: | | | | :
Db 73 WRCRGDQAE 81

RESULT 29
T10664
serine/threonine-specific protein kinase homolog F6E21.20 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T10664
R;Revan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancro
submitted to the Protein Sequence Database, June 1999
A/Reference number: Z16533
A/Accession: T10664
A/Molecule type: DNA
A/Residues: 1-656 <BEV>
A/Cross-references: UNIPROT:Q9M092; EMBL:AL049914; GSPDB:GN00062; ATSP:F6E21.20
A/Experimental source: cultivar Columbia; BAC clone F6E21
C/Genetics:
A/Gene: ATSP:F6E21.20
A/Map position: 4
A/Intons: 206/1; 243/1
C/Superfamily: Arabidopsis probable serine/threonine-specific protein kinase PRO25; prob

Query Match 59.3%; Score 35; DB 2; Length 656;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YRCRGDDSK 10
| | | | |
Db 230 YRCVGDKTK 238

RESULT 30
I37892
IL12 receptor component - human
C/Species: Homo sapiens (man)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I37892

R;Chua, A.O.; Chizzonite, R.; Desai, B.B.; Truitt, T.P.; Nunes, P.; Minetti, L.J.; Warric
J. Immunol. 153, 128-136, 1994
A/Title: Expression cloning of a human IL-12 receptor component. A new member of the cytc
A/Reference number: I37892; MUID:94267217; PMID:7911493
A/Accession: I37892
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-662 <RES>
A/Cross-references: UNIPROT:P42701; EMBL:U03187; NID:G507150; PIDN:AAA21340.1; PID:G50715

Query Match 59.3%; Score 35; DB 2; Length 662;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 RCRGDDSK 10
| | | | |
Db 484 RCRDEDSK 491

RESULT 31
T37533
coronin-like protein - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T37533
R;Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, August 1997
A/Reference number: Z21721
A/Accession: T37533
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1323 <MUR>
A/Cross-references: UNIPROT:O13686; EMBL:Z98595; PIDN:CAB11184.1; GSPDB:GN00066; SPDB:SP
A/Experimental source: strain 972h; cosmid c11E3
C/Genetics:
A/Gene: SPDB:SPAC11E3.05
A/Map position: 1

Query Match 59.3%; Score 35; DB 2; Length 1323;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
: | | | | :
Db 512 WRCRGED 518

RESULT 32
B81364
probable periplasmic protein Cj0906c [imported] - Campylobacter jejuni (strain NCTC 1116f
C/Species: Campylobacter jejuni
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C/Accession: B81364
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A/Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals h
A/Reference number: A81250; MUID:20150912; PMID:10688204
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-325 <PAR>
A/Cross-references: UNIPROT:Q9PP25; GB:AL139076; GB:AL111168; NID:G6968128; PIDN:CAB73164
A/Experimental source: serotype O2, strain NCTC 11168
C/Genetics:
A/Gene: Cj0906c
C/Superfamily: Helicobacter pylori hypothetical protein jhp0467

Query Match 58.5%; Score 34.5; DB 2; Length 325;
Best Local Similarity 52.9%; Pred. No. 90;
Matches 9; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 1 NYRCRGD-----DSK 10

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DB      300 NVRFRGDKILYVKIDSK 316
|||||
|||||
RESULT 33
H70232
hypothetical protein BBG16 - Lyme disease spirochete plasmid G/lp28-2
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C>Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: H70232
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White-
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: H70232
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-112 <KLE>
A:Cross-references: UNIPROT:O50739; GB:AE000786; NID:g2690008; PIDN:AAC66064.1; PID:g269
A:Experimental source: strain B31
C:Genetics:
A:Superfamily: Lyme disease spirochete plasmid G/lp28-2 hypothetical protein BBG16

Query Match      57.6%; Score 34; DB 2; Length 112;
Best Local Similarity 50.0%; Pred. No. 42;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 NVRCRGDDSK 10
      |||||
DB      77 NTRCKGDQKE 86
      |||||

RESULT 34
T04118
mitochondrial processing peptidase homolog - rice (fragment)
C:Species: Oryza sativa (rice)
A:Reference number: Z14944
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T04118
R:Uchimiya, H.
submitted to the EMBL Data Library, November 1993
A:Reference number: Z14944
A:Accession: T04118
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-122 <UCH>
A:Cross-references: UNIPROT:Q40738; EMBL:D25241; PIDN:BAA04964.1
C:Genetics:
A:Gene: SS656
C:Superfamily: mitochondrial processing peptidase alpha chain
C:Keywords: mitochondrion

Query Match      57.6%; Score 34; DB 2; Length 122;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 NVRCRGDDSK 10
      :|||:|
DB      48 DYRCQADSK 57
      :|||:|

RESULT 35
F81439
translation initiation factor IF-3 Cj0207 [imported] - Campylobacter jejuni (strain NCTC
C:Species: Campylobacter jejuni
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: F81439
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kerley, J.M.; Churcher, C.; Baeham, D.; Chillin
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000

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A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype
A:Reference number: A81250; MUID:20150912; PMID:1068204
A:Accession: F81439
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-172 <PAR>
A:Cross-references: UNIPROT:Q9PIS2; GB:AL139074; GB:AL111168; NID:g6967505; PIDN:CAB7269
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: infC; Cj0207
C:Superfamily: translation initiation factor IF-3

Query Match      57.6%; Score 34; DB 2; Length 172;
Best Local Similarity 75.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 RCRGDDSK 10
      |||||
DB      19 RCVGDDGK 26
      |||||

RESULT 36
AC3270
hypothetical exported protein BMEI0144 [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AC3270
R:DelVecchio, V.G.; Kaputral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Loeb, T.; Ivanova, I
; Mazur, M.; Goltzman, E.; Selkov, E.; Elzei, P.H.; Hagius, S.; O'Callaghan, D.; Letessc
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AC3270
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-180 <KUR>
A:Cross-references: UNIPROT:Q8YJ22; UNIPROT:Q8FYG1; GB:AE008917; PIDN:AAL51326.1; PID:g1
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI0144
A:Map position: 1

Query Match      57.6%; Score 34; DB 2; Length 180;
Best Local Similarity 55.6%; Pred. No. 65;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 YRCRGDDSK 10
      |||||
DB      97 YNCKGDGSE 105
      |||||

RESULT 37
G64320
hypothetical protein MJ0166 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: G64320
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, J
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: G64320
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-255 <BUL>
A:Cross-references: UNIPROT:Q57630; GB:U67473; GB:L77117; NID:g2826256; PIDN:AAB98148.1;
C:Genetics:
A:Map position: REV170194-169427
C:Superfamily: Pyrococcus horikoshii hypothetical protein PH0006

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Query Match          57.6%; Score 34; DB 2; Length 255;
Best Local Similarity 71.4%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CRGDDSK 10
    |||||
Db 233 CRGDDKR 239

RESULT 38
E84427
hypothetical protein At2g01660 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: E84427
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: E84427
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-259 <STO>
A:Cross-references: UNIPROT:Q9ZU94; GB:AE002093; NID:94220482; PIDN:AAD12705.1; GSPDB:GN
C:Genetics:
A:Gene: At2g01660
A:Map position: 2

Query Match          57.6%; Score 34; DB 2; Length 259;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGD 7
    |:|||
Db 82 YQCRGD 87

RESULT 39
C96731
unknown protein F5A18.13 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: C96731
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.E.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: C96731
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-270 <STO>
A:Cross-references: UNIPROT:Q9CAB9; GB:AE005173; NID:96453891; PIDN:AAF09074.1; GSPDB:GN
C:Genetics:
A:Gene: F5A18.13
A:Map position: 1

Query Match          57.6%; Score 34; DB 2; Length 270;
Best Local Similarity 83.3%; Pred. No. 94;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGD 7
    |:|||
Db 87 YQCRGD 92

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RESULT 40
T10610
hypothetical protein F21C20.30 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10610
R:Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Lemcke,
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z16991
A:Accession: T10610
A:Molecule type: DNA
A:Residues: 1-273 <BEV>
A:Cross-references: UNIPROT:Q9SVH9; EMBL:AL080254; GSPDB:GN00062; ATSP:F21C20.30
A:Experimental source: cultivar Columbia; BAC clone F21C20
C:Genetics:
A:Gene: ATSP:F21C20.30
A:Map position: 4
A:Introns: 114/3

Query Match          57.6%; Score 34; DB 2; Length 273;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGD 7
    |:|||
Db 93 YQCRGD 98

RESULT 41
A95408
hypothetical protein Sma2147 [imported] - Sinorhizobium meliloti (strain 1021) magaplaemf
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: A95408
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.;
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: A95408
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-296 <KUR>
A:Cross-references: UNIPROT:Q92XS2; GB:AE006469; PIDN:AAK65827.1; PID:gl4524331; GSPDB:GN
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, P.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.
A:title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: Sma2147
A:Genome: plasmid

Query Match          57.6%; Score 34; DB 2; Length 296;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 NYRCRGDQSK 10
    |:|||
Db 2 NEECKGDGGE 11

RESULT 42
T05437
hypothetical protein F7K2.10 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999

```


C:Accession: T05437
 R:Bevan, M.; Wedler, H.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schueller submitted to the Protein Sequence Database, November 1998
 A:Reference number: Z15416
 A:Accession: T05437
 A:Molecule type: DNA
 A:Residues: 1-344 <BEV>
 A:Cross-references: EMBL:AL033545
 A:Experimental source: cultivar Columbia; BAC clone F7K2
 C:Genetics:
 A:Map position: 4
 A:Note: F7K2.10

Query Match 57.6%; Score 34; DB 2; Length 344;
 Best Local Similarity 60.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
 ||: ||: ||
 Db 267 NYKIFGDESK 276

RESULT 43
 H85256
 hypothetical protein AT4g22430 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C:Accession: H85256
 R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999
 A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
 A:Reference number: A85001; MUID:20083488; PMID:10617198
 A:Accession: H85256
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-348 <STO>
 A:Cross-references: UNIPROT:Q9SUX6; GB:NC_001268; NID:g7269089; PIDN:CAB79198.1; GSPDB:G
 C:Genetics:
 A:Gene: AT4g22430
 A:Map position: 4

Query Match 57.6%; Score 34; DB 2; Length 348;
 Best Local Similarity 60.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
 ||: ||: ||
 Db 271 NYKIFGDESK 280

RESULT 44
 B96551
 hypothetical protein F11M15.18 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: B96551
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: B96551
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-375 <STO>
 A:Cross-references: UNIPROT:Q9SYD4; GB:AE005173; NID:g4836941; PIDN:AAD30643.1; GSPDB:GN
 C:Genetics:
 A:Gene: F7K2.10

A:Gene: F11M15.18
 A:Map position: 1
 C:Superfamily: Arabidopsis thaliana hypothetical protein F24M12.210

Query Match 57.6%; Score 34; DB 2; Length 375;
 Best Local Similarity 62.5%; Pred. No. 1.3e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YRCRGDSS 9
 ||: ||: ||
 Db 152 YKCEGDSS 159

RESULT 45
 B96189
 protein T25N20.9 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: B96189
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: B96189
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-393 <STO>
 A:Cross-references: UNIPROT:Q9ZVZ4; GB:AE005172; NID:g8778729; PIDN:AAF79737.1; GSPDB:GN
 C:Genetics:
 A:Gene: T25N20.9
 A:Map position: 1

Query Match 57.6%; Score 34; DB 2; Length 393;
 Best Local Similarity 75.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 RCRGDDSK 10
 ||: ||: ||
 Db 234 RCTGSDSK 241

RESULT 46
 C36786
 hypothetical protein 2 - ictalurid herpesvirus 1 (strain auburn 1)
 C:Species: ictalurid herpesvirus 1
 A:Note: host Ictalurus punctatus (channel catfish)
 C:Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 09-Jul-2004
 C:Accession: C36786
 R:Davidson, A.J.
 submitted to GenBank, January 1992
 A:Description: Channel catfish virus: a new type of herpesvirus.
 A:Reference number: A36804
 A:Accession: C36786
 A:Molecule type: DNA
 A:Residues: 1-407 <DAV>
 A:Cross-references: UNIPROT:Q00126; GB:M75136; NID:g331209; PIDN:AAA88105.1; PID:g331212
 R:Davidson, A.J.
 Virology 186, 9-14, 1992
 A:Title: Channel catfish virus: a new type of herpesvirus.
 A:Reference number: A39447; MUID:92087490; PMID:1727613
 A:Contents: annotation
 A:Note: neither protein nor nucleic acid sequence is given
 C:Genetics:
 A:Gene: 2
 C:Superfamily: ictalurid herpesvirus 1 hypothetical protein 2

Query Match 57.6%; Score 34; DB 2; Length 407;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RCRGDDDS 9
|||
DB 270 RCLGDDDS 276

RESULT 47

F96743
probable C2H2-type zinc finger protein F28P5.6 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: F96743
R:Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: F96743
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-413 <STO>
A:Cross-references: UNIPROT:Q9C7G8; GB:AEO05173; NID:gl1054410; PIDN:AAG27797.1; GSPDB:C
C:Genetics:
A:Gene: F28P5.6
A:Map position: 1

Query Match 57.6%; Score 34; DB 2; Length 413;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CRGDDSK 10
|:|:|
DB 191 CKGDDDK 197

RESULT 48

H71400
hypothetical protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
A:Variety: columbia
C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
C:Accession: H71400
R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenecker, T.; Pohl, T.M.; Terry, N.; Giel
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998
A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; And
C.; Chludzinski, N.
A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal
A:Reference number: A71400; MUID:98121113; PMID:9461215
A:Accession: H71400
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-482 <BEV>
A:Cross-references: UNIPROT:O23260; GB:297335; NID:g2244747; PID:g2244755
C:Genetics:
A:Map position: 4COP9-4C3845
C:Superfamily: Arabidopsis thaliana hypothetical protein At2g32740

Query Match 57.6%; Score 34; DB 2; Length 482;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NYRCRGDDDS 9
|||
DB 163 NYRCCLTNDSD 171

RESULT 49

B41627
furin (EC 3.4.21.75) 18 precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 26-May-2000
C:Accession: B41627
R:Korner, J.; Chun, J.; O'Bryan, L.; Axel, R.
Proc. Natl. Acad. Sci. U.S.A. 88, 11393-11397, 1991
A:Title: Prohormone processing in Xenopus oocytes: characterization of cleavage signals
A:Reference number: A41627; MUID:92107956; PMID:1722329
A:Accession: B41627
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-596 <KOR>
A:Cross-references: GB:M80471
C:Superfamily: Kexin; subtilisin homology
C:Keywords: hydrolase; serine proteinase
F:142-380/Domain: subtilisin homology <SBT>
F:151,192,366/Active site: Asp, His, Ser #status predicted

Query Match 57.6%; Score 34; DB 2; Length 596;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGD 7
:|:|
DB 492 SYNCRGD 498

RESULT 50

A41627
furin (EC 3.4.21.75) 1 precursor - African clawed frog
N:Alternate names: furin homolog 14
C:Species: Xenopus laevis (African clawed frog)
C:Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 09-Jul-2004
C:Accession: A41627
R:Korner, J.; Chun, J.; O'Bryan, L.; Axel, R.
Proc. Natl. Acad. Sci. U.S.A. 88, 11393-11397, 1991
A:Title: Prohormone processing in Xenopus oocytes: characterization of cleavage signals
A:Reference number: A41627; MUID:92107956; PMID:1722329
A:Accession: A41627
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-783 <KOR>
A:Cross-references: UNIPROT:P29119; GB:M80471; NID:g214158; PIDN:AAA49717.1; PID:g214159
C:Superfamily: Kexin; subtilisin homology
C:Keywords: hydrolase; serine proteinase; transmembrane protein
F:142-380/Domain: subtilisin homology <SBT>
F:151,192,366/Active site: Asp, His, Ser #status predicted

Query Match 57.6%; Score 34; DB 2; Length 783;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGD 7
:|:|
DB 492 SYNCRGD 498

Search completed: September 7, 2005, 20:03:56
Job time : 19.674 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 7, 2005, 19:43:14 ; Search time 35.1163 Seconds
(without alignments)
145.824 Million cell updates/sec

Title: US-10-812-238B-20

Perfect score: 59

Sequence: 1 NYRCRGDDSK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Maximum Match 0%
Listing first 500 summaries

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Uniprot_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	311	1 LPP3_HUMAN	O14495 h lipid pho
2	55	93.2	312	1 LPP3_MOUSE	Q99JY8 mus musculus
3	55	93.2	312	1 LPP3_RAT	P97544 rattus norv
4	55	93.2	312	2 Q6IMX4	Q6IMX4 rattus norv
5	45	76.3	776	2 Q73RY0	Q73RY0 mycobacteri
6	42	71.2	73	2 Q7OP19	Q7OP19 giardia lam
7	42	71.2	265	2 Q85KQ7	Q85KQ7 dictyosteli
8	41	69.5	428	2 Q8TBF1	Q8TBF1 homo sapien
9	41	69.5	489	2 Q8N9B8	Q8N9B8 homo sapien
10	41	69.5	1334	2 Q97322	Q97322 plasmodium
11	40	67.8	150	2 Q9KCP2	Q9KCP2 bacillus ha
12	40	67.8	399	1 PNCB_ECO57	Q8XDE8 escherichia
13	40	67.8	399	1 PNCB_ECOLI	F18133 escherichia
14	40	67.8	399	1 PNCB_SALTI	Q8Z7Y9 salmonella
15	40	67.8	399	1 PNCB_SALTY	P22253 salmonella
16	40	67.8	400	2 Q7UD27	Q7UD27 shigella fl
17	40	67.8	416	2 Q83LN3	Q83LN3 shigella fl
18	40	67.8	416	2 Q8FJ98	Q8FJ98 escherichia
19	40	67.8	705	2 Q50468	Q50468 mycobacteri
20	40	67.8	705	2 P96283	P96283 mycobacteri
21	40	67.8	705	2 Q7TXK7	Q7TXK7 mycobacteri
22	40	67.8	845	2 Q8WQJ3	Q8WQJ3 plasmodium
23	40	67.8	1304	2 Q8WT63	Q8WT63 plasmodium
24	39	66.1	37	2 Q8POM2	Q8POM2 streptococc
25	39	66.1	46	2 Q848W4	Q848W4 bacillus me
26	39	66.1	154	2 Q8BUS2	Q8BUS2 mus musculus
27	39	66.1	179	2 Q20683	Q20683 caenorhabdi
28	39	66.1	588	2 Q70681	Q70681 sugarcane s
29	39	66.1	1420	2 Q9YBN1	Q9YBN1 sugarcane s
30	39	66.1	1615	2 Q7RQM4	Q7RQM4 plasmodium
31	38	64.4	121	2 Q8V163	Q8V163 reovirus sp

32	38	64.4	121	2	Q8V164	Q8V164 reovirus sp
33	38	64.4	121	2	Q8V165	Q8V165 reovirus sp
34	38	64.4	121	2	Q8V166	Q8V166 reovirus sp
35	38	64.4	121	2	Q8V167	Q8V167 reovirus sp
36	38	64.4	121	2	Q8V168	Q8V168 reovirus sp
37	38	64.4	121	2	Q8V169	Q8V169 reovirus sp
38	38	64.4	121	2	Q8V170	Q8V170 reovirus sp
39	38	64.4	121	2	Q8V171	Q8V171 reovirus sp
40	38	64.4	121	2	Q8V172	Q8V172 reovirus sp
41	38	64.4	121	2	Q8V173	Q8V173 reovirus sp
42	38	64.4	121	2	Q8V174	Q8V174 reovirus sp
43	38	64.4	121	2	Q8V175	Q8V175 reovirus sp
44	38	64.4	121	2	Q8V176	Q8V176 reovirus sp
45	38	64.4	121	2	Q8V177	Q8V177 reovirus sp
46	38	64.4	121	2	Q8V178	Q8V178 reovirus sp
47	38	64.4	121	2	Q8V179	Q8V179 reovirus sp
48	38	64.4	121	2	Q8V180	Q8V180 reovirus sp
49	38	64.4	121	2	Q8V181	Q8V181 reovirus sp
50	38	64.4	121	2	Q8V182	Q8V182 reovirus sp
51	38	64.4	121	2	Q8V183	Q8V183 reovirus sp
52	38	64.4	121	2	Q8V184	Q8V184 reovirus sp
53	38	64.4	121	2	Q8V185	Q8V185 reovirus sp
54	38	64.4	121	2	Q8V186	Q8V186 reovirus sp
55	38	64.4	121	2	Q8V187	Q8V187 reovirus sp
56	38	64.4	121	2	Q8V188	Q8V188 reovirus sp
57	38	64.4	121	2	Q8V189	Q8V189 reovirus sp
58	38	64.4	121	2	Q8V190	Q8V190 reovirus sp
59	38	64.4	121	2	Q8V191	Q8V191 reovirus sp
60	38	64.4	121	2	Q8V192	Q8V192 reovirus sp
61	38	64.4	121	2	Q8V193	Q8V193 reovirus sp
62	38	64.4	121	2	Q8V194	Q8V194 reovirus sp
63	38	64.4	121	2	Q8V195	Q8V195 reovirus sp
64	38	64.4	121	2	Q8V196	Q8V196 reovirus sp
65	38	64.4	121	2	Q8V197	Q8V197 reovirus sp
66	38	64.4	121	2	Q8V198	Q8V198 reovirus sp
67	38	64.4	121	2	Q8V199	Q8V199 reovirus sp
68	38	64.4	121	2	Q8V1A0	Q8V1A0 reovirus sp
69	38	64.4	121	2	Q8V1A1	Q8V1A1 reovirus sp
70	38	64.4	121	2	Q8V1A2	Q8V1A2 reovirus sp
71	38	64.4	121	2	Q8V1A3	Q8V1A3 reovirus sp
72	38	64.4	121	2	Q8RJU0	Q8RJU0 reovirus sp
73	38	64.4	130	2	Q9VHG0	Q9VHG0 ginglymosto
74	38	64.4	191	2	Q9AY18	Q9AY18 funaria apo
75	38	64.4	193	2	Q9AY16	Q9AY16 entosthodon
76	38	64.4	298	2	Q7Q232	Q7Q232 anopheles g
77	38	64.4	383	2	Q9GTD8	Q9GTD8 caenorhabdi
78	38	64.4	387	2	Q9GTD7	Q9GTD7 caenorhabdi
79	38	64.4	388	2	Q9GTD6	Q9GTD6 caenorhabdi
80	38	64.4	389	2	Q9XTG0	Q9XTG0 caenorhabdi
81	38	64.4	435	2	Q8UTB2	Q8UTB2 golden ide
82	38	64.4	505	2	Q96180	Q96180 homo sapien
83	38	64.4	661	2	Q8JTB6	Q8JTB6 striped fas
84	38	64.4	721	2	Q9PA43	Q9PA43 xylella fas
85	38	64.4	875	1	NETR_HUMAN	P56730 homo sapien
86	38	64.4	1240	2	Q8VA42	Q8VA42 chum salmon
87	38	64.4	1267	1	VL3_REOVD	P17378 reovirus ty
88	38	64.4	1267	1	VL3_REOVJ	P17377 reovirus ty
89	38	64.4	1267	1	VL3_REOVL	P17376 reovirus ty
90	38	64.4	1267	2	Q8V5E5	Q8V5E5 ndelle viru
91	38	64.4	1267	2	Q85665	Q85665 reovirus ty
92	38	64.4	1274	2	Q8JU61	Q8JU61 golden shin
93	38	64.4	1274	2	Q6ETU2	Q6ETU2 oryza sativ
94	37	62.7	59	2	Q8HU07	Q8HU07 rhodobryum
95	37	62.7	269	2	Q7R8M3	Q7R8M3 plasmodium
96	37	62.7	307	2	Q8F34	Q8F34 xenopus lae
97	37	62.7	330	2	Q82MF0	Q82MF0 streptomyce
98	37	62.7	430	1	SYS_SYNY3	P73201 synchocyst
99	37	62.7	504	1	Y787_METJA	Q68197 methanococc
100	37	62.7	1268	2	Q63623	Q63623 rattus norv
101	37	62.7	1268	2	Q6DID3	Q6DID3 mus musculu
102	37	62.7	1271	1	RBMG_HUMAN	Q9upn6 homo sapien
103	37	62.7	1271	2	Q6NSK3	Q6NSK3 homo sapien
104	37	62.7	1271	2	Q6NSK3	Q6NSK3 homo sapien

105	37	62.7	1362	2	Q80TJ3	Q80ctj3 mus musculus	178	35	59.3	476	2	Q6B8Q6	Q6b8q6 gracilaria
106	37	62.7	4569	2	Q7PS35	Q7ps35 anopheles g	179	35	59.3	503	2	Q6BK51	Q6bk51 debaryomyce
107	36	61.0	63	2	Q9BS83	Q9bs83 homo sapien	180	35	59.3	513	2	Q9A731	Q9a731 caulobacter
108	36	61.0	188	2	Q63XE8	Q63xe8 burkholderi	181	35	59.3	562	2	Q6ZMG3	Q6zmg3 homo sapien
109	36	61.0	226	2	Q69XV4	Q69xv4 oryza sativ	182	35	59.3	575	2	Q8WTU2	Q8wtu2 homo sapien
110	36	61.0	248	2	Q62115	Q62115 burkholderi	183	35	59.3	586	2	Q62YB1	Q62yb1 bacillus li
111	36	61.0	248	2	Q63RB3	Q63rb3 burkholderi	184	35	59.3	587	2	Q65MW8	Q65mw8 bacillus li
112	36	61.0	266	2	Q8EJ20	Q8ej20 shewanella	185	35	59.3	656	2	Q9M092	Q9m092 arabidopsis
113	36	61.0	306	2	Q7RIN6	Q7rin6 plasmodium	186	35	59.3	662	1	I12R_HUMAN	P42701 homo sapien
114	36	61.0	340	2	Q8V286	Q8v286 helicoverpa	187	35	59.3	757	2	Q6LTA6	Q6lta6 photobacter
115	36	61.0	340	2	Q77LV8	Q77lv8 helicoverpa	188	35	59.3	782	2	Q8PP65	Q8pp65 xanthomonas
116	36	61.0	340	2	Q9E219	Q9e219 helicoverpa	189	35	59.3	849	2	Q8ISV7	Q8isv7 plasmodium
117	36	61.0	340	2	Q91FJ4	Q91fj4 helicoverpa	190	35	59.3	915	2	Q7UV66	Q7uv66 rhodospirell
118	36	61.0	347	2	Q9XAN5	Q9xan5 streptomyce	191	35	59.3	1019	2	Q6CV73	Q6cv73 kluyveromyc
119	36	61.0	401	2	Q6D454	Q6d454 erwinia car	192	35	59.3	1323	2	O13686	O13686 schizosacch
120	36	61.0	404	2	Q7N621	Q7n621 photorhabdi	193	35	59.3	1402	2	Q7RBQ6	Q7rbq6 plasmodium
121	36	61.0	461	2	Q29377	Q29377 archaeoglob	194	35	59.3	1499	2	Q9Y839	Q9y839 mycosphaere
122	36	61.0	461	2	Q69XV5	Q69xv5 oryza sativ	195	35	59.3	1559	2	Q8IDC3	Q8idc3 plasmodium
123	36	61.0	466	2	Q9S5X4	Q9s5x4 thermotoga	196	35	59.3	2736	2	Q7RTC3	Q7rtc3 plasmodium
124	36	61.0	470	2	Q9WYR5	Q9wyr5 thermotoga	197	34.5	58.5	325	2	Q9PP25	Q9pp25 campylobact
125	36	61.0	485	2	Q8CFK1	Q8cfk1 mus musculu	198	34.5	58.5	555	2	Q8H5J9	Q8h5j9 oryza sativ
126	36	61.0	488	2	Q75DX4	Q75dx4 ashbya goss	199	34	57.6	72	2	Q26942	Q26942 triboolium c
127	36	61.0	498	1	NMT2_HUMAN	Q60551 homo sapien	200	34	57.6	87	2	Q9P2Z4	Q9p2z4 homo sapien
128	36	61.0	503	2	Q6FZW1	Q6fzw1 bartonella	201	34	57.6	108	2	Q6ESN2	Q6esn2 oryza sativ
129	36	61.0	503	2	Q6G3B9	Q6g3b9 bartonella	202	34	57.6	112	2	O50739	O50739 borrelia bu
130	36	61.0	507	2	Q8YGM3	Q8ygm3 brucella me	203	34	57.6	122	2	Q40738	Q40738 oryza sativ
131	36	61.0	507	2	Q8G100	Q8g100 brucella su	204	34	57.6	137	2	Q8NAF9	Q8naf9 homo sapien
132	36	61.0	523	2	Q6K632	Q6k632 oryza sativ	205	34	57.6	146	2	Q9CTI3	Q9cti3 mus musculu
133	36	61.0	529	1	NMT2_MOUSE	Q70031 mus musculu	206	34	57.6	164	2	Q7Q0D5	Q7q0d5 anopheles g
134	36	61.0	529	1	Q700Q7	Q700q7 rattus norv	207	34	57.6	164	2	Q8HRE9	Q8hre9 bryum gemmi
135	36	61.0	609	2	Q8IER1	Q8ier1 plasmodium	208	34	57.6	167	2	Q95L84	Q95l84 cryptotolagus
136	36	61.0	808	2	Q7O4C6	Q7o4c6 anopheles g	209	34	57.6	172	1	IF3_CAMJEE	Q9pis2 campylobact
137	36	61.0	897	2	Q93Y95	Q93y95 zea mays (m	210	34	57.6	180	2	O8YJE2	O8yje2 brucella me
138	36	61.0	1022	2	Q8XN34	Q8xn34 clostridium	211	34	57.6	180	2	Q8FYG1	Q8fyg1 brucella su
139	36	61.0	1168	2	Q7RH99	Q7rh99 plasmodium	212	34	57.6	186	2	Q8HRF4	Q8hrf4 anomobryum
140	36	61.0	1363	2	Q8IAM5	Q8iam5 plasmodium	213	34	57.6	187	2	Q8MG46	Q8mg46 rosulabryum
141	36	61.0	1450	2	Q815X9	Q815x9 plasmodium	214	34	57.6	188	2	O63005	O63005 bryum alpin
142	36	61.0	2209	2	Q9U0G6	Q9u0g6 plasmodium	215	34	57.6	188	2	Q9AY14	Q9ay14 physcomitri
143	35.5	60.2	459	2	Q7QJN6	Q7qjn6 anopheles g	216	34	57.6	188	2	O9LRL9	O9lrl9 arabidopsis
144	35.5	60.2	468	2	Q72WL4	Q72wl4 desulfovibr	217	34	57.6	189	2	O63006	O63006 bryum caesp
145	35	59.3	55	2	Q6SA81	Q6sa81 salmonella	218	34	57.6	189	2	O63011	O63011 rhodobryum
146	35	59.3	128	2	Q74FF9	Q74ff9 geobacter s	219	34	57.6	189	2	O6JE74	O6je74 splachnum w
147	35	59.3	137	2	Q88JY2	Q88jy2 pseudomonas	220	34	57.6	190	2	O62998	O62998 funaria hyg
148	35	59.3	138	2	Q97V09	Q97v09 sulfolobus	221	34	57.6	190	2	O63009	O63009 bryum steno
149	35	59.3	140	2	Q6JLB3	Q6jlb3 francisella	222	34	57.6	190	2	Q8HU00	Q8hu00 bryum palie
150	35	59.3	141	2	O7WUA2	Q7wua2 porphyromon	223	34	57.6	190	2	Q8MCT1	Q8mct1 haplodontiu
151	35	59.3	172	2	Q897T4	Q897t4 clostridium	224	34	57.6	190	2	Q9AY13	Q9ay13 aphanorizneg
152	35	59.3	179	2	Q67BF6	Q67bf6 haemophilus	225	34	57.6	191	2	Q9AY15	Q9ay15 physcomitri
153	35	59.3	179	2	Q7VN40	Q7vn40 haemophilus	226	34	57.6	194	2	O63008	O63008 anomobryum
154	35	59.3	187	1	AMPD_SALTY	P30013 salmonella	227	34	57.6	194	2	Q8MU05	Q8mu05 bryum russa
155	35	59.3	187	2	Q8Z9F5	Q8z9f5 salmonella	228	34	57.6	194	2	Q8MCU1	Q8mcu1 bryum capil
156	35	59.3	190	2	Q9GBF5	Q9gbf5 homo sapien	229	34	57.6	194	2	Q8HRE7	Q8hre7 bryum ortho
157	35	59.3	195	2	Q9VRN5	Q9vrn5 drosophila	230	34	57.6	194	2	Q8BCF4	Q8bcf4 physcomitre
158	35	59.3	205	1	BASI_BOVIN	Q865r3 bos taurus	231	34	57.6	195	2	Q8MCU2	Q8mcu2 bryum bicol
159	35	59.3	221	2	Q9ALZ8	Q9alz8 fremyella d	232	34	57.6	195	2	Q8MCU6	Q8mcu6 brachymeni
160	35	59.3	239	2	O44730	Q44730 caenorhabdi	233	34	57.6	196	2	Q8HTZ5	Q8htz5 brachymeni
161	35	59.3	255	2	O86KQ6	Q86kq6 dictyosteli	234	34	57.6	196	2	Q8HU06	Q8hu06 rhodobryum
162	35	59.3	256	2	O86KQ8	Q86kq8 dictyosteli	235	34	57.6	196	2	O8HU13	O8hu13 bryum bland
163	35	59.3	259	2	O6LGM9	Q6lgm9 photobacter	236	34	57.6	196	2	Q8MCT4	Q8mct4 bryum pseud
164	35	59.3	283	2	Q9W057	Q9w057 drosophila	237	34	57.6	196	2	Q8MCU8	Q8mcu8 acidodontiu
165	35	59.3	293	2	O8RYM8	Q8rym8 oryza sativ	238	34	57.6	197	2	Q8HTZ7	Q8htz7 bryum gemmi
166	35	59.3	304	1	HEN3_XANAC	Q8ppr3 xanthomonas	239	34	57.6	197	2	Q8MCT8	Q8mct8 bryum pachy
167	35	59.3	304	1	HEM3_XANCP	Q8p536 xanthomonas	240	34	57.6	197	2	Q8MCT6	Q8mct6 bryum pachy
168	35	59.3	321	2	O9GRJ9	Q9grj9 leishmania	241	34	57.6	197	2	Q8MCT8	Q8mct8 bryum lisae
169	35	59.3	321	2	O8RYK1	Q8ryk1 oryza sativ	242	34	57.6	197	2	Q8MCU0	Q8mcu0 bryum cyath
170	35	59.3	329	1	PIN2_CABEL	Q19157 caenorhabdi	243	34	57.6	197	2	Q8MCU3	Q8mcu3 bryum archa
171	35	59.3	362	2	Q61L91	Q61l91 drosophila	244	34	57.6	197	2	Q8MCU4	Q8mcu4 bryum arach
172	35	59.3	385	1	BASI_HUMAN	P35613 h basigin p	245	34	57.6	197	2	Q8MCU9	Q8mcu9 acidodontiu
173	35	59.3	401	2	Q82N33	Q82n33 streptomyce	246	34	57.6	197	2	O8MCV0	O8mcv0 acidodontiu
174	35	59.3	422	2	O9K426	Q9k426 streptomyce	247	34	57.6	197	2	O8HRF0	O8hrf0 bryum clava
175	35	59.3	439	1	LIA3_HUMAN	Q8nc68 homo sapien	248	34	57.6	197	2	Q8HRF2	Q8hrf2 brachymeni
176	35	59.3	453	2	P92013	P92013 caenorhabdi	249	34	57.6	197	2	O8HRV8	O8hrv8 bryum radic
177	35	59.3	467	1	VE2_HP24	P50770 human papil	250	34	57.6	197	2	O8HRV9	O8hrv9 bryum rudr

251	34	57.6	198	2	Q8HU04	Q8hu04 bryum purpu	324	34	57.6	447	2	Q9FDM8	Q9fdm8 streptococc
252	34	57.6	198	2	Q8HU08	Q8hu08 brachymeniu	325	34	57.6	447	2	Q9RPL5	Q9rpl5 streptococc
253	34	57.6	198	2	Q8HU09	Q8hu09 brachymeniu	326	34	57.6	461	2	Q6COC6	Q6coc6 yarrowia li
254	34	57.6	198	2	Q8MCS7	Q8mcs7 rhodobryum	327	34	57.6	470	2	Q755U1	Q755u1 ashbya goss
255	34	57.6	198	2	Q8MCS9	Q8mcs9 bryum cauca	328	34	57.6	482	2	O23260	O23260 arabidopsis
256	34	57.6	198	2	Q8MCU5	Q8mcu5 bryum algov	329	34	57.6	490	2	O82137	O82137 streptomyc
257	34	57.6	198	2	Q8MCU7	Q8mcu7 anomobryum	330	34	57.6	491	2	Q7PDP6	Q7ppd6 anopheles g
258	34	57.6	198	2	Q8HRE8	Q8hre8 bryum coron	331	34	57.6	497	2	Q75KY5	Q75ky5 oryza sativ
259	34	57.6	199	2	Q63007	Q63007 bryum donia	332	34	57.6	521	2	O64R16	O64r16 arabidopsis
260	34	57.6	199	2	O63010	Q63010 brachymeniu	333	34	57.6	522	2	Q6XQ95	Q6xq95 enterobacte
261	34	57.6	199	2	Q8HTZ6	Q8htz6 bryum muehl	334	34	57.6	530	2	Q6BQJ5	Q6bqj5 debaryomyce
262	34	57.6	199	2	Q8HU01	Q8hu01 bryum funck	335	34	57.6	533	2	O86J09	O86j09 dictyosteli
263	34	57.6	199	2	Q8HU02	Q8hu02 bryum cellu	336	34	57.6	595	2	O91751	O91751 xenopus lae
264	34	57.6	199	2	Q8HU10	Q8hu10 brachymeniu	337	34	57.6	622	2	Q653D2	Q653d2 oryza sativ
265	34	57.6	199	2	Q8HU11	Q8hu11 brachymeniu	338	34	57.6	639	2	Q8D1D1	Q8dd1d synecococc
266	34	57.6	199	2	Q8HU12	Q8hu12 brachymeniu	339	34	57.6	644	2	Q7MYZ2	Q7myz2 photorhabdu
267	34	57.6	199	2	Q8HU14	Q8hu14 bryum argen	340	34	57.6	770	2	Q653D1	Q653d1 oryza sativ
268	34	57.6	199	2	Q8HRF1	Q8hrf1 brachymeniu	341	34	57.6	783	1	FUR1_XENLA	P29119 xenopus lae
269	34	57.6	199	2	Q8HRF3	Q8hrf3 anomobryum	342	34	57.6	783	2	Q6DE77	Q6de77 xenopus lae
270	34	57.6	199	2	Q9GGF1	Q9gff1 bryum billa	343	34	57.6	801	1	MNHA_STAAM	P60874 staphylococ
271	34	57.6	201	1	RR4_FUNHY	Q9smg1 funaria hyg	344	34	57.6	801	1	MNHA_STAAN	P60875 staphylococ
272	34	57.6	201	1	RR4_PHYPA	Q6yxp3 physcomitre	345	34	57.6	801	1	MNHA_STAAN	Q92ng6 staphylococ
273	34	57.6	202	1	RR4_BRVCA	P59135 bryum capil	346	34	57.6	801	1	MNHA_STAAN	Q8nxf6 staphylococ
274	34	57.6	202	1	Q9LRL0	Q9lrl0 arabidopsis	347	34	57.6	801	2	O6GAX4	O6gax4 staphylococ
275	34	57.6	203	2	Q6QPD0	Q6qp00 simian aden	348	34	57.6	801	2	Q6GID6	Q6gid6 staphylococ
276	34	57.6	204	2	Q6QPD9	Q6qp94 simian aden	349	34	57.6	808	2	Q8N270	Q8n270 homo sapien
277	34	57.6	204	2	Q6QPD6	Q6qp96 simian aden	350	34	57.6	850	1	STB2_YEAST	P46679 saccharomyc
278	34	57.6	250	2	Q6AY82	Q6ay82 rattus norv	351	34	57.6	884	2	Q94J11	Q94j11 oryza sativ
279	34	57.6	254	2	Q7W386	Q7w386 bordetella	352	34	57.6	908	2	Q9FNN3	Q9fnf3 arabidopsis
280	34	57.6	254	2	Q7WEK5	Q7wek5 bordetella	353	34	57.6	966	2	Q9LMS1	Q9lml1 arabidopsis
281	34	57.6	255	1	Y166_METJA	Q57830 methanococc	354	34	57.6	970	2	Q7X8K7	Q7x8k7 brassica ju
282	34	57.6	262	2	Q9LRK9	Q9lkr9 arabidopsis	355	34	57.6	973	2	Q7XNC89	Q7xnc89 strongyloce
283	34	57.6	269	2	Q759L0	Q759l0 ashbya goss	356	34	57.6	988	2	Q9LM32	Q9lm32 arabidopsis
284	34	57.6	270	2	Q9CAB9	Q9cab9 arabidopsis	357	34	57.6	992	2	Q8LPH3	Q8lph3 arabidopsis
285	34	57.6	273	2	Q7XU16	Q7xu16 oryza sativ	358	34	57.6	1030	2	O8L625	O8l625 arabidopsis
286	34	57.6	273	2	Q9SVH9	Q9svh9 arabidopsis	359	34	57.6	1030	2	Q9C9U5	Q9c9u5 arabidopsis
287	34	57.6	278	2	Q6DRF1	Q6drf1 brachydanio	360	34	57.6	1036	1	PLD1_CRIGR	O08884 cricetus
288	34	57.6	279	2	Q80V15	Q80v15 mus musculu	361	34	57.6	1074	1	PLD1_HUMAN	Q13393 homo sapien
289	34	57.6	280	2	O95698	Q95698 homo sapien	362	34	57.6	1075	2	Q9NC90	Q9nc90 strongyloce
290	34	57.6	280	2	Q9H160	Q9hi60 homo sapien	363	34	57.6	1129	2	Q7UKD4	Q7ukd4 rhodopirell
291	34	57.6	281	2	O856E2	Q856e2 mycobacteri	364	34	57.6	1164	2	O6SLC8	Q6slc8 cochlidiobol
292	34	57.6	281	2	Q8BGU8	Q8bgu8 m mus muscu	365	34	57.6	1233	1	RGY2_SULTO	Q975p6 sulfolobus
293	34	57.6	281	2	Q9ESK4	Q9esk4 mus musculu	366	34	57.6	1245	2	Q9Y7V5	Q9y7v5 trichoderma
294	34	57.6	288	2	Q9ZU94	Q9zu94 arabidopsis	367	34	57.6	1247	2	Q8I7Z6	Q8i7z6 toxoplasma
295	34	57.6	288	2	Q9DW23	Q9dw23 rat cytomeg	368	34	57.6	1335	2	Q8VI17	Q8vi17 mus musculu
296	34	57.6	289	2	Q8LDG0	Q8ldg0 arabidopsis	369	34	57.6	1336	2	Q9ES55	Q9es55 mus musculu
297	34	57.6	296	2	Q92XS2	Q92xs2 rhizobium m	370	34	57.6	2020	2	Q7RQO6	Q7rgq6 plasmodium
298	34	57.6	297	2	Q6H663	Q6h663 oryza sativ	371	34	57.6	2443	2	Q96J17	Q96j17 homo sapien
299	34	57.6	299	2	Q8LA52	Q8la52 arabidopsis	372	34	57.6	2798	2	Q7RPL8	Q7rpl8 plasmodium
300	34	57.6	299	2	Q8GUJ2	Q8guj2 arabidopsis	373	34	57.6	4699	2	Q9V383	Q9v383 drosophila
301	34	57.6	307	2	Q6AXH7	Q6axh7 xenopus lae	374	33	55.9	82	2	Q8MVZ2	Q8mvz2 ornithodor
302	34	57.6	307	2	Q9CQ18	Q9cg18 m mus muscu	375	33	55.9	82	2	Q8MVZ3	Q8mvz3 ornithodor
303	34	57.6	308	2	Q8R220	Q8r220 mus musculu	376	33	55.9	93	2	Q89U57	Q89us7 bradyrhizob
304	34	57.6	308	2	Q7R2D9	Q7r2d9 giardia lam	377	33	55.9	110	2	Q9DWM8	Q9dwm8 hepatitis c
305	34	57.6	323	2	Q940P2	Q940p2 arabidopsis	378	33	55.9	113	2	Q8H6L0	Q8h6l0 brassica ra
306	34	57.6	333	2	Q6A898	Q6a898 propionibac	379	33	55.9	118	2	Q6T399	Q6t399 tomato leaf
307	34	57.6	333	2	Q6A898	Q6a898 propionibac	380	33	55.9	118	2	Q6T886	Q6t886 tomato leaf
308	34	57.6	348	2	Q9SUX6	Q9sux6 arabidopsis	381	33	55.9	127	2	Q8AW35	Q8aw35 brachydanio
309	34	57.6	350	1	SNY_MYCGA	Q7nat8 mycoplasma	382	33	55.9	140	2	Q70K60	Q70k60 gordonia we
310	34	57.6	362	1	CY25_HUMAN	Q7z5m8 homo sapien	383	33	55.9	152	2	Q8ZAU7	Q8zau7 versinia pe
311	34	57.6	373	2	Q9PYT1	Q9pyt1 xestia c-ni	384	33	55.9	154	2	Q7N040	Q7n040 photorhabdu
312	34	57.6	375	2	Q9SYD4	Q9syd4 arabidopsis	385	33	55.9	157	2	Q665H4	Q665h4 versinia pe
313	34	57.6	381	2	Q98C19	Q98c19 rhizobium l	386	33	55.9	157	2	Q8D1Q1	Q8dd1q1 versinia pe
314	34	57.6	386	2	Q8XOR8	Q8x0r8 neurospora	387	33	55.9	159	2	Q8TTR5	Q8ttr5 methanocarc
315	34	57.6	392	2	Q86AD7	Q86ad7 dictyosteli	388	33	55.9	167	2	Q9X1I2	Q9x1i2 arabidopsis
316	34	57.6	393	2	Q9ZVZ4	Q9zvz4 arabidopsis	389	33	55.9	173	2	Q8EIH1	Q8eih1 shewanella
317	34	57.6	407	1	VG02_ICHV1	Q00126 ictalurid h	390	33	55.9	182	2	Q7UST8	Q7ust8 rhodopirell
318	34	57.6	412	2	Q84M24	Q84m24 arabidopsis	391	33	55.9	185	1	RRF_MYCLE	Q33046 mycobacteri
319	34	57.6	413	2	Q9C7G8	Q9c7g8 arabidopsis	392	33	55.9	187	2	Q68IK5	Q68ik5 helicobacte
320	34	57.6	421	2	O44635	O44635 caenorhabdi	393	33	55.9	196	2	Q8MCS8	Q8mcs8 rhodobryum
321	34	57.6	429	1	SYS_GLOVI	Q7nmp9 gloeobacter	394	33	55.9	200	2	O02498	O02498 leishmania
322	34	57.6	437	2	Q6FQ58	Q6fq58 candida gla	395	33	55.9	204	2	Q7M5K8	Q7m5k8 simian aden
323	34	57.6	447	2	Q9F0G1	Q9f0g1 streptococc	396	33	55.9	217	2	Q8L5E8	Q8l5e8 hordeum vul

397	33	55.9	226	1	YV39_ANASP	Q8yee9 anabaena sp	470	33	55.9	559	2	Q9E7C0	Q9e7c0 cucumber ve
398	33	55.9	226	2	Q73222	Q73222 mycobacteri	471	33	55.9	566	2	Q8S313	Q8s313 phytophthor
399	33	55.9	228	2	Q33530	Q33530 rhizobium l	472	33	55.9	567	2	Q8SRV0	Q8srvo encephalito
400	33	55.9	238	2	Q74551	Q74551 schizosacch	473	33	55.9	569	2	Q9M0C9	Q9m0c9 arabidopsis
401	33	55.9	244	2	Q93WH5	Q93wh5 oryza sativ	474	33	55.9	571	2	Q9M0C3	Q9m0c3 arabidopsis
402	33	55.9	248	1	YDFG_ECOLI	P39831 escherichia	475	33	55.9	574	2	Q8X003	Q8x003 neurospora
403	33	55.9	248	2	Q65S85	Q65s85 mannheimia	476	33	55.9	576	2	Q73MU5	Q73mu5 neurospora
404	33	55.9	248	2	Q7UCH2	Q7uch2 shigella fl	477	33	55.9	577	1	Q7RVN7	Q7rvn7 neurospora
405	33	55.9	248	2	Q8X505	Q8x505 escherichia	478	33	55.9	579	2	Y04B_CAEEL	Q17426 caenorhabdi
406	33	55.9	253	2	Q83RE8	Q83re8 shigella fl	479	33	55.9	581	2	Q6Y5M8	Q6y5m8 mus musculu
407	33	55.9	253	2	Q8FHD2	Q8fhd2 escherichia	480	33	55.9	581	2	Q8Y5M8	Q8y5m8 mus musculu
408	33	55.9	255	2	Q8MI30	Q8mi30 equus caball	481	33	55.9	582	2	Q8S660	Q8s660 barley mild
409	33	55.9	257	2	Q91RK3	Q91rk3 arabidopsis	482	33	55.9	584	2	Q51717	Q51717 pseudomonas
410	33	55.9	259	2	Q7V949	Q7v949 prochloroco	483	33	55.9	600	1	SVR_CAUCR	Q9a347 caulobacter
411	33	55.9	270	2	Q70H83	Q70h83 fowlpox vir	484	33	55.9	605	2	Q6BK98	Q6bk98 debaryomyce
412	33	55.9	270	2	Q9J5E2	Q9j5e2 fowlpox vir	485	33	55.9	608	2	Q73JW5	Q73jw5 treponema d
413	33	55.9	273	2	Q9JUV3	Q9juv3 neisseria m	486	33	55.9	625	2	Q9D3V8	Q9d3v8 mus musculu
414	33	55.9	287	2	P72287	P72287 rhizobium l	487	33	55.9	640	2	Q8Q561	Q8q561 pongine her
415	33	55.9	295	2	Q7NGY7	Q7ngy7 gloeobacter	488	33	55.9	644	2	Q8A3E1	Q8a3e1 bacteroides
416	33	55.9	299	2	Q6GL93	Q6gl93 xenopus tro	489	33	55.9	657	2	Q14006	Q14006 homo sapien
417	33	55.9	307	2	Q6ZLA2	Q6zla2 oryza sativ	490	33	55.9	658	2	Q8P3D2	Q8p3d2 xanthomonas
418	33	55.9	309	2	Q6LNT6	Q6lnt6 xenopus lae	491	33	55.9	658	2	Q8PEQ9	Q8peq9 xanthomonas
419	33	55.9	310	2	Q8DIT7	Q8dit7 synechococc	492	33	55.9	658	2	Q87928	Q87928 xylella fas
420	33	55.9	312	2	Q66KV0	Q66kv0 xenopus lae	493	33	55.9	667	2	Q6FWT7	Q6fwt7 candida gla
421	33	55.9	323	2	Q8EM66	Q8em66 oceanobacil	494	33	55.9	675	2	Q55177	Q55177 synechocyst
422	33	55.9	329	2	Q9NHE0	Q9nhe0 meloidogyne	495	33	55.9	678	2	Q9QBG6	Q9qbg6 wheat yello
423	33	55.9	336	1	HUTG_VIBCH	Q9ksq2 vibrio chol	496	33	55.9	680	2	Q9PA40	Q9pa40 xylella fas
424	33	55.9	347	1	CORT_VIBPA	Q87q46 vibrio para	497	33	55.9	707	2	Q8CD82	Q8cd82 mycobacteri
425	33	55.9	352	2	Q9SYB1	Q9syb1 arabidopsis	498	33	55.9	719	2	P87541	P87541 barley mild
426	33	55.9	360	2	Q9LKY3	Q9lky3 glycine max	499	33	55.9	725	2	Q73634	Q73634 xenopus lae
427	33	55.9	360	2	Q9LKY4	Q9lky4 glycine max	500	33	55.9	727	2	Q6RKB2	Q6rkb2 rattus norv
428	33	55.9	370	2	Q8LL17	Q8lll17 arabidopsis							
429	33	55.9	389	1	HIS8_CANMA	P56099 candida mal							
430	33	55.9	399	2	Q90BG5	Q9qbg5 wheat yello							
431	33	55.9	401	2	Q7S9U6	Q7s9u6 neurospora							
432	33	55.9	403	2	Q6BMG0	Q6bm90 debaryomyce							
433	33	55.9	411	2	Q8SXG0	Q8sxg0 drosophila							
434	33	55.9	411	2	Q9VX69	Q9vx69 anopheles g							
435	33	55.9	412	2	Q7Q1R5	Q7qlr5 anopheles g							
436	33	55.9	413	2	Q6REL5	Q6rel5 rhodococcus							
437	33	55.9	419	2	Q6GLS6	Q6glr6 xenopus lae							
438	33	55.9	420	2	Q6LNB3	Q6lnb3 photobacter							
439	33	55.9	421	2	Q8YF04	Q8yf04 bruceella me							
440	33	55.9	421	2	Q8G2T7	Q8g2t7 bruceella su							
441	33	55.9	421	2	Q41898	Q41898 rice necros							
442	33	55.9	432	2	Q98LP4	Q98lp4 rhizobium l							
443	33	55.9	448	2	Q91BP9	Q91bp9 oat mosaic							
444	33	55.9	460	2	Q9N8R2	Q9n8r2 trypanosoma							
445	33	55.9	469	2	Q6Z4U6	Q6z4u6 oryza sativ							
446	33	55.9	481	2	Q7MXE2	Q7mxe2 porphyromon							
447	33	55.9	485	2	Q8P748	Q8p748 xanthomonas							
448	33	55.9	488	2	Q8X0T4	Q8x0t4 mus musculu							
449	33	55.9	488	2	Q91QR6	Q91qr6 wheat yello							
450	33	55.9	489	2	Q9A762	Q9a762 caulobacter							
451	33	55.9	490	2	Q9BM62	Q9bw62 homo sapien							
452	33	55.9	494	2	Q9Z012	Q9z012 wheat spin							
453	33	55.9	498	2	Q89M54	Q89m54 bradyrhizob							
454	33	55.9	505	2	Q98NR7	Q98nr7 rhizobium l							
455	33	55.9	508	2	Q78617	Q78617 neurospora							
456	33	55.9	510	2	Q6M0Z3	Q6m0z3 methanococc							
457	33	55.9	513	2	Q83869	Q83869 narcisus l							
458	33	55.9	514	2	Q80BV2	Q80bv2 alpina mos							
459	33	55.9	528	2	Q97379	Q97379 strongyloce							
460	33	55.9	528	2	Q6J0M7	Q6jom7 indian card							
461	33	55.9	528	2	Q9QD49	Q9qd49 cardanom mo							
462	33	55.9	540	2	Q76771	Q76771 dictyosteli							
463	33	55.9	543	2	Q17900	Q17900 caenorhabdi							
464	33	55.9	544	2	Q77810	Q77810 wheat strea							
465	33	55.9	545	2	Q9U3Z2	Q9u3z2 hydra atten							
466	33	55.9	546	2	Q29111	Q29111 sus scrofa							
467	33	55.9	554	2	Q77F98	Q7tf98 cucumber ve							
468	33	55.9	555	2	Q9QB93	Q9qb93 wheat yello							
469	33	55.9	557	2	Q91DH6	Q91dh6 chinese yam							

ALIGNMENTS

RESULT 1	
LPP3_HUMAN	
ID_LPP3_HUMAN	STANDARD; PRT; 311 AA.
AC	O14495; Q96GW0; Q99782;
DT	29-MAR-2004 (Rel. 43, Created)
DT	29-MAR-2004 (Rel. 43, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Lipid phosphate phosphohydrolase 3 (SC 3.1.3.4) (Phosphatidic acid
DE	phosphatase 2b) (Phosphatidate phosphohydrolase type 2b) (PAP2b) (PAP-
DE	2b) (PAP2-beta) (Vascular endothelial growth factor and type I
DE	collagen inducible protein) (VCIP).
GN	Name=PAP2b; Synonyms=LPP3;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A., CHARACTERIZATION, AND INDUCTION.
RX	MEDLINE=97450990; PubMed=9305923; DOI=10.1074/jbc.272.39.24572;
RA	Kai M., Wada I., Imai S.-I., Sakane F., Kanoh H.;
RT	"Cloning and characterization of two human isozymes of Mg2+-
RT	independent phosphatidic acid phosphatase.";
RL	J. Biol. Chem. 272:24572-24578(1997).
RN	[2]
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX	MEDLINE=98371049; PubMed=9705349; DOI=10.1074/jbc.273.34.22059;
RA	Roberts R., Sciorra V.A., Morris A.J.;
RT	"Human type 2 phosphatidic acid phosphohydrolases. Substrate
RT	specificity of the type 2a, 2b, and 2c enzymes and cell surface
RT	activity of the 2a isoform.";
RL	J. Biol. Chem. 273:22059-22067(1998).
RN	[3]
RP	SEQUENCE FROM N.A.
RX	PubMed=12660161; DOI=10.1093/emboj/cdg165;
RA	Huntsue J.O., Feng S., Thakker G.D., Yang J., Hong J., Wary K.K.;
RT	"Regulation of cell-cell interactions by phosphatidic acid phosphatase
RT	2b/VCIP.";

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EMBL; AB000889; BAA22594.1; -;
 DR EMBL; AF017786; AAC63433.1; -;
 DR EMBL; AF480883; AAO84481.1; -;
 DR EMBL; AF043329; AAD02271.1; -;
 DR EMBL; U79294; AAB50222.1; ALT_FRAME.
 DR EMBL; BC009196; AAH09196.1; -;
 DR GENE; HGNC:9229; PPAP2B.
 DR H-InvDB; HIX000628; -;
 DR Reactome; O14495; -;
 DR MIM; 607125; -;
 DR GO; GO:0016020; C-membrane; TAS.
 DR GO; GO:0004721; P:phosphoprotein phosphatase activity; TAS.
 DR GO; GO:0008151; P:cell growth and/or maintenance; TAS.
 DR GO; GO:0008354; P:germ-cell migration; TAS.
 DR InterPro; IPR008934; AcPase VanParase.
 DR InterPro; IPR000326; Pesterase_PA_PTP.
 DR Pfam; PF01569; PAP2; 1.
 DR SMART; SM00014; acidppc; 1.
 KW Glycoprotein; Hydrolase; Transmembrane.
 FT DOMAIN 1 33 Cytoplasmic (Potential).
 FT TRANSMEM 34 54 Potential.
 FT DOMAIN 55 85 Luminal (Potential).
 FT TRANSMEM 86 106 Potential.
 FT DOMAIN 107 122 Cytoplasmic (Potential).
 FT TRANSMEM 123 143 Potential.
 FT DOMAIN 144 193 Luminal (Potential).
 FT FT TRANSMEM 194 214 Potential.
 FT FT TRANSMEM 215 227 Cytoplasmic (Potential).
 FT FT TRANSMEM 228 248 Potential.
 FT DOMAIN 249 257 Luminal (Potential).
 FT TRANSMEM 258 278 Potential.
 FT DOMAIN 279 311 Cytoplasmic (Potential).
 FT FT CARBOHYD 170 170 N-linked (GlcNAc...) (Potential).
 FT FT CONFLICT 282 282 T -> M (in Ref. 6).
 SQ SEQUENCE 311 AA; 35116 MW; CB3F60189044DA31 CRC64;

Query Match 100.0%; Score 59; DB 1; Length 311;
 Best Local Similarity 100.0%; Pred. No. 0.0084;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NTRCRGDDSK 10
 |||||||
 DB 178 NTRCRGDDSK 187

RESULT 2
 LPP3_MOUSE STANDARD; PRT; 312 AA.
 AC Q99JY8; Q8BTB7;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Lipid phosphate phosphohydrolase 3 (EC 3.1.3.4) (Phosphatidic acid
 DE phosphatase 2b) (Phosphatidate phosphohydrolase type 2b) (PAP-
 DE 2b) (PAP2-beta).
 GN Name=Ppap2b; Synonym=Lpp3;
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN {1}
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaïdo I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nocchi A., Schonbach C., Gotobori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Lee Y., Lenhard B., Lyons P.A.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlee G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reid D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirose-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sakaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zengerg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murzyn D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP FUNCTION, AND DISEASE.
RX PubMed=12925589; DOI=10.1242/dev.00635;
RA Escalante-Alcalde D., Hernandez L., Le Stunff H., Maeda R., Lee H.-S.,
RA Cheng G. Jr., Sciorra V.A., Daar I., Spiegel S., Morris A.J.,
RA Stewart C.L.;
RT "The lipid phosphatase LPP3 regulates extra-embryonic vasculogenesis
RT and axis patterning.";
RL Development 130:4623-4637 (2003).
CC -1- FUNCTION: Catalyzes the conversion of phosphatidic acid (PA) to
CC diacylglycerol (DG). In addition it hydrolyzes lysophosphatidic
CC acid (LPA), ceramide-1-phosphate (C-1-P) and sphingosine-1-
CC phosphate (S-1-P) (By similarity). Essential to the formation of
CC the chorio-allantoic placenta and extra-embryonic vasculature.
CC Also mediates gastrulation and axis formation, probably by
CC regulating the Wnt signaling pathway.
CC -1- CATALYTIC ACTIVITY: A 3-sn-phosphatidate + H(2)O = 1,2-diacyl-
CC sn-glycerol + phosphate.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum associated (By similarity).
CC -1- DISEASE: Ppap2b deficient embryos fail to form a chorio-allantoic
CC placenta and yolk sac vasculature. A subset of embryos also show a
CC shortening of the anterior-posterior axis and frequent duplication

CC of axial structures. Loss of Ppap2b results in a marked increase
CC in beta-catenin-mediated T-cell factor (TCF) transcription.
CC -1- SIMILARITY: Belongs to the PA-phosphatase related phosphoesterase
CC family.
CC -1- CAUTION: Ref.1 sequence differs from that shown due to a
CC frameshift in position 226.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AK011276; BAC35327.1; ALT_FRAME.
CC EMBL: BC005559; AAH05558.1; --.
CC MGD: MGI:1915166; Ppap2b.
CC GO: GO:0042577; F:lipid phosphatase activity; IMP.
CC GO: GO:0001569; P:blood vessel development; IMP.
CC GO: GO:0010003; P:gastrulation (sensu Mammalia); IMP.
CC GO: GO:0006644; P:phospholipid metabolism; IMP.
CC GO: GO:0030111; P:regulation of Wnt receptor signaling pathway; IDA.
CC InterPro: IPR008934; Acpase_Vanperase.
CC InterPro: IPR000326; Pesterase_PA_PTP.
CC Pfam: PF01569; PAP2; 1.
CC SMART: SM00014; acidPPc; 1.
CC Developmental protein; Glycoprotein; Hydrolase; Transmembrane.
CC DOMAIN 1 33 Cytoplasmic (Potential).
CC TRANSMEM 34 54 Potential.
CC DOMAIN 55 85 Luminal (Potential).
CC TRANSMEM 86 106 Potential.
CC DOMAIN 107 123 Cytoplasmic (Potential).
CC TRANSMEM 124 144 Potential.
CC DOMAIN 145 194 Luminal (Potential).
CC TRANSMEM 195 215 Potential.
CC DOMAIN 216 226 Cytoplasmic (Potential).
CC TRANSMEM 227 247 Potential.
CC DOMAIN 248 258 Luminal (Potential).
CC TRANSMEM 259 279 Potential.
CC DOMAIN 280 312 Cytoplasmic (Potential).
CC CARBOHYD 171 171 N-linked (GlcNAc...) (Potential).
CC SEQUENCE 312 AA; 35216 MW; D782986E04B57D7D CRC64;
SQ
Query Match 93.12%; Score 55; DB 1; Length 312;
Best Local Similarity 90.0%; Pred. No. 0.048;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYRCRGDSK 10
Db 179 NYRCRGDSK 188
|||||:||||
RESULT 3
LPP3 RAT
ID LPP3 RAT STANDARD; PRT; 312 AA.
AC P97544;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Lipid phosphate phosphohydrolase 3 (EC 3.1.3.4) (Phosphatidic acid
DE phosphate 2b) (Phosphatidate phosphohydrolase type 2b) (PAP2b) (PAP-
DE 2b) (PAP2-beta) (Differentially expressed in rat intestine 42)
DE (Dri42).
GN Name=Ppap2b; Synonyms=Lpp3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., TOPOLOGY, AND N-GLYCOSYLATION.
RC STRAIN=Wistar; TISSUE=Small intestine;
RX MEDLINE=97094703; PubMed=8939937; DOI=10.1074/jbc.271.47.29928;

RA Barila D., Plateroti M., Nobili F., Muda A.O., Xie Y., Morimoto T.,
RA Perozzi G.;
RT "The Dri 42 gene, whose expression is upregulated during epithelial
RT differentiation, encodes a novel ER resident transmembrane protein.";
RL J. Biol. Chem. 271:29928-29936(1996).
RN [2]
RP TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
RX PubMed=8055940;
RA Barila D., Murgia C., Nobili F., Gaetani S., Perozzi G.;
RT "Subtractive hybridization cloning of novel genes differentially
RT expressed during intestinal development.";
RL Eur. J. Biochem. 223:701-709(1994).
RN [3]
RP TISSUE SPECIFICITY.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=2155999; PubMed=11704545;
RA Nanjundan M., Possmayer F.;
RT "Molecular cloning and expression of pulmonary lipid phosphate
RT phosphohydrolases";
RL Am. J. Physiol. 281:L1484-L1493(2001).
CC -1- FUNCTION: Catalyzes the conversion of phosphatidic acid (PA) to
CC diacylglycerol (DG). In addition it hydrolyzes lysophosphatidic
CC acid (LPA), ceramide-1-phosphate (C-1-P) and sphingosine-1-
CC phosphate (S-1-P) (By similarity). Involved in the regulation of
CC epithelial differentiation.
CC -1- CATALYTIC ACTIVITY: A 3-sn-phosphatidate + H(2)O = a 1,2-diacyl-
CC sn-glycerol + phosphate.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum associated.
CC -1- TISSUE SPECIFICITY: Detected in epithelial cells of intestinal
CC mucosa, lung, liver and brain.
CC -1- DEVELOPMENTAL STAGE: Expression is increased during epithelial
CC differentiation in intestinal mucosa as well as in kidney, liver
CC and lung.
CC -1- PTM: N-glycosylated.
CC -1- SIMILARITY: Belongs to the PA-phosphatase related phosphoesterase
CC family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: Y07783; CAA69106.1; --
CC InterPro: IPR008934; ACPase_VanPerase.
CC InterPro: IPR000326; Pesterase_PA_PTP.
CC Pfam: PF01569; PAP2; 1.
CC SMART: SM00014; acidppc; 1.
CC DR Endoplasmic reticulum; Glycoprotein; Hydrolase; Transmembrane.
CC FT DOMAIN 1 33 Cytoplasmic (Potential).
CC TRANSMEM 34 54 Potential.
CC FT DOMAIN 55 85 Luminal (Potential).
CC TRANSMEM 86 106 Potential.
CC FT DOMAIN 107 123 Cytoplasmic (Potential).
CC TRANSMEM 124 144 Potential.
CC FT DOMAIN 145 194 Luminal (Potential).
CC TRANSMEM 195 215 Potential.
CC FT DOMAIN 216 226 Cytoplasmic (Potential).
CC TRANSMEM 227 247 Potential.
CC FT DOMAIN 248 258 Luminal (Potential).
CC TRANSMEM 259 279 Potential.
CC FT DOMAIN 280 312 Cytoplasmic (Potential).
CC CARBOHYD 171 171 N-linked (GlcNAc...) (Potential).
CC SQ SEQUENCE 312 AA; 35318 MW; 9B447FD321DB0419 CRC64;
CC -----
CC Query Match 93.2%; Score 55; DB 1; Length 312;
CC Best Local Similarity 90.0%; Pred. No. 0.048;
CC Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYRCRGDSDK 10
Db 179 NYRCRGEDSK 188
|||||:||||
RESULT 4
Q6IMX4 PRELIMINARY; PRT; 312 AA.
ID Q6IMX4
AC Q6IMX4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ER transmembrane protein Dri 42.
GN Name=Dri42;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC072544; AAH72544.1; --
DR GO: GO:0016021; C:integral to membrane; IEA.
DR InterPro: IPR008934; ACPase_VanPerase.
DR InterPro: IPR000326; Pesterase_PA_PTP.
DR Pfam: PF01569; PAP2; 1.
DR SMART: SM00014; acidppc; 1.
CC Transmembrane
CC SQ SEQUENCE 312 AA; 35233 MW; CDA54495C0E7D37D CRC64;
CC -----
CC Query Match 93.2%; Score 55; DB 2; Length 312;
CC Best Local Similarity 90.0%; Pred. No. 0.048;
CC Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYRCRGDSDK 10
Db 179 NYRCRGEDSK 188
|||||:||||
RESULT 5
Q73RY0 PRELIMINARY; PRT; 776 AA.
ID Q73RY0
AC Q73RY0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.

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GN OrderedLocusNames=MAP4298c;
OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1770;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=k10;
RA Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AS017242; AAS06848.1; -.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR003673; CAIB_BAIF.
DR Pfam; PF02515; CoA_transf_3; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 776 AA; 82189 MW; 38A4528FC5B0B4BB CRC64;

Query Match 76.3%; Score 45; DB 2; Length 776;
Best Local Similarity 87.5%; Pred. No. 9.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 9
DB 615 YRCRGDDA 622
|||||:

RESULT 6
Q7QP19 PRELIMINARY; PRT; 73 AA.
ID Q7QP19
AC Q7QP19
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GLP 83 1716 1495.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RL "Draft sequence of the Giardia lamblia genome.";
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACB01000181; EAA36741.1; -.
SQ SEQUENCE 73 AA; 8125 MW; 4F866C8ABF254DDE CRC64;

Query Match 71.2%; Score 42; DB 2; Length 73;
Best Local Similarity 75.0%; Pred. No. 3;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
DB 27 DYRCRGDD 34
|||||:

RESULT 7
Q86KQ7 PRELIMINARY; PRT; 265 AA.
ID Q86KQ7
AC Q86KQ7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;

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RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Leemann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL Nature 418:79-85(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC115584; AAO50949.1; -.
DR InterPro; IPR008997; RicinB_like.
KW Hypothetical protein.
SQ SEQUENCE 265 AA; 30503 MW; F1E238D4A048F6D2 CRC64;

Query Match 71.2%; Score 42; DB 2; Length 265;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YRCRGDD 9
DB 45 YRCRGDD 52
|||||:

RESULT 8
Q8TBF1 PRELIMINARY; PRT; 428 AA.
ID Q8TBF1
AC Q8TBF1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RasGEF domain family, member 1A.
DE Name=RASGEF1A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022548; AAH22548.1; -.
DR GO; GO:0005085; P:guanylyl-nucleotide exchange factor activity; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR000651; RasGef_N.
DR InterPro; IPR001895; RasGRF_CDC25.
DR InterPro; IPR008937; Ras_GEF.

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DR Pfam; PF00617; RasGEF; 1.
DR SMART; SM00147; RasGEF; 1.
DR PROSITE; PSS0009; RasGEF_CAT; 1.
DR PROSITE; PSS0212; RasGEF_NTER; 1.
SQ SEQUENCE 428 AA; 49394 MW; 2522DBF4A3D2F560 CRC64;

Query Match 69.5%; Score 41; DB 2; Length 428;
Best Local Similarity 70.0%; Pred. No. 28;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
Db 197 NHRCRGDLTK 206
|:|||||:|

RESULT 9
Q8N9B8 PRELIMINARY; PRT; 489 AA.
AC Q8N9B8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ37817.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX TSSUE=Substantia nigra;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Oeuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto K., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuma T., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ihibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Iehida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara K., Takeuchi K., Arita N., Imose N.,
RA Yoshino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Mouriya S., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Takamura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama H., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamaehita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RA "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs";
RL Nat. Genet. 36:40-45(2004).
DR EMBL; AK095136; BAC04491.1; -.
DR GO; GO:0005085; P:guanylnucleotide exchange factor activity; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR000651; RasGEF_N.
DR InterPro; IPR001895; RasGEF_CDC25.
DR InterPro; IPR008937; Ras_GEF.
DR Pfam; PF00617; RasGEF; 1.
DR SMART; SM00147; RasGEF; 1.
DR PROSITE; PSS0009; RasGEF_CAT; 1.
DR PROSITE; PSS0212; RasGEF_NTER; 1.

SQ SEQUENCE 489 AA; 55532 MW; 85D5986ACD2C7C76 CRC64;

Query Match 69.5%; Score 41; DB 2; Length 489;
Best Local Similarity 70.0%; Pred. No. 32;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
Db 258 NHRCRGDLTK 267
|:|||||:|

RESULT 10
Q97322 PRELIMINARY; PRT; 1334 AA.
AC Q97322;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein MAL3P7.32
GN Name=MAL3P7.32; Synonyms=PFCl01010w;
OS Plasmodium falciparum (Isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99376085; PubMed=10448855; DOI=10.1038/22964;
RA Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
RA Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,
RA Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T.,
RA Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S.,
RA Mungall K., Murphy L., Oliver K., Quail M.A., Rajadream M.-A.,
RA Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
RA Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;
RT "The complete nucleotide sequence of chromosome 3 of Plasmodium
RT falciparum.";
RN Nature 400:532-538(1999).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22255708; PubMed=12369867; DOI=10.1038/nature01095;
RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C., Corton C.,
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitch E.,
RA Rajadream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA Sulston J.E., Craig A., Newbold C., Barrell B.G.;
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
RL Nature 419:527-531(2002).
DR EMBL; AL034559; CAB39073.2; -.
KW Hypothetical protein.
SQ SEQUENCE 1334 AA; 160847 MW; E3577E84C7E0C8E5 CRC64;

Query Match 69.5%; Score 41; DB 2; Length 1334;
Best Local Similarity 60.0%; Pred. No. 91;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
Db 808 NTNCKDDDNK 817
|:|||||:|

RESULT 11
Q9KCP2 PRELIMINARY; PRT; 150 AA.
AC Q9KCP2;

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DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Ferric uptake regulation protein.
GN OrderedLocusNames=BH1527;
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125;
RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331 (2000).
DR EMBL; AF001512; BAB05246.1; -.
DR PIR; G83840; G83840.
DR HSSP; O03456; 1M2B.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002481; FUR.
DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
DR Pfam; PF01475; FUR; 1.
DR ProDom; PD002003; FUR; 1.
KW Complete proteome.
SQ SEQUENCE 150 AA; 17447 MW; CE4D3AC2A8B64275 CRC64;

Query Match 67.8%; Score 40; DB 2; Length 150;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDSSK 10
DB 141 HRCQGDSSK 149

RESULT 12
PNCB_ECO57
ID PNCB_ECO57 STANDARD; PRT; 399 AA.
AC Q8XDE8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Nicotinate phosphoribosyltransferase (EC 2.4.2.11) (NAPRTase).
GN Escherichia coli O157:H7.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dinalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / Sakai / RIMD 050952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT "Complete genome sequence of Escherichia coli K-12.";

RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22 (2001).
CC -|- CATALYTIC ACTIVITY: Nicotinate D-ribose 1-diphosphate + diphosphate =
CC nicotinate + 5-phospho-alpha-D-ribose 1-diphosphate.
CC -|- PATHWAY: NAD biosynthesis; nicotinamide to NAMN; second step.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -|- SIMILARITY: Belongs to the NAPRTase family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AE005283; AAG55416.1; -.
CC EMBL; AP002553; BAB34437.1; -.
CC PIR; D85619; D85619.
CC PIR; F90755; F90755.
CC HAMAP; MF 00570; -. 1.
CC InterPro; IPR007229; NAPRTase.
CC InterPro; IPR006406; Nic_Prtans.
CC InterPro; IPR008967; P53_like_DNA_bnd.
CC Pfam; PF04095; NAPRTase; 1.
CC PIRSF; PIRSF000484; Nicot_phos_ribo; 1.
CC TIGRFAMs; TIGR01514; NAPRTase; 1.
KW Complete proteome; Glycosyltransferase;
KW Pyridine nucleotide biosynthesis; Transferase.
FT INIT MET 0 By similarity.
SQ SEQUENCE 399 AA; 45838 MW; 47DAC387A0EC6926 CRC64;

Query Match 67.8%; Score 40; DB 1; Length 399;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
DB 38 FRCRGDD 44

RESULT 13
PNCB_ECOLI
ID PNCB_ECOLI STANDARD; PRT; 399 AA.
AC P18133;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Nicotinate phosphoribosyltransferase (EC 2.4.2.11) (NAPRTase).
GN Name=pncB; OrderedLocusNames=b0931;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
RC STRAIN=CEC70;
RX MEDLINE=91009224; PubMed=2211655;
RA Wubbolds M.G., Terpstra P., van Beilen J.B., Kingma J.,
RA Meesters H.A.R., Witholt B.;
RT "Variation of cofactor levels in Escherichia coli. Sequence analysis
RT and expression of the pncB gene encoding nicotinic acid
RT phosphoribosyltransferase.";
RL J. Biol. Chem. 265:17665-17672 (1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Colliado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";

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RL Science 277.1453-1474 (1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshino T., Aiba H., Baba T., Fujita K., Hayaishi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RN DNA Res. 3:137-155(1996).
RC
CC -1- CATALYTIC ACTIVITY: Nicotinate D-ribonucleotide + diphosphate =
CC nicotinate + 5-phospho-alpha-D-ribose 1-diphosphate.
CC -1- PATHWAY: NAD biosynthesis; nicotinamide to NAMN; second step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- MISCELLANEOUS: Requires ATP as well as phosphoribosyl
CC pyrophosphate for activity.
CC -1- SIMILARITY: Belongs to the NAPRTase family.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J05568; AAA24400.1; -.
CC EMBL; U00096; AAC74017.1; -.
CC EMBL; D90731; BAA35683.1; -.
CC F1R; JQ0756; JQ0756.
CC EcoBASE; EB0735; -.
CC EcoGene; EG10742; pncB.
CC HAMAP; MF_00570; -.
CC InterPro; IPR007229; NAPRTase.
CC InterPro; IPR006406; Nic Prtrans.
CC InterPro; IPR008967; P53_like_DNA_bnd.
CC Pfam; PF04095; NAPRTase; 1.
CC PIRSF; PIRSF000484; Nicot_phos_ribo; 1.
CC TIGRFAMs; TIGR01514; NAPRTase; 1.
CC Complete proteome; direct protein sequencing; Glycosyltransferase;
KW Pyridine nucleotide biosynthesis; Transferase.
FT INIT MET 0
FT SEQUENCE 399 AA; 45766 MW; 37F0C0D2C3BA5C45 CRC64;
SQ
Query Match 67.8%; Score 40; DB 1; Length 399;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 YRCRGDD 8
DB :|||||
38 FRCRGDD 44
RESULT 14
PNCB_SALTI STANDARD; PRT; 399 AA.
AC Q827Y9;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Nicotinate phosphoribosyltransferase (EC 2.4.2.11) (NAPRTase).
GN Name=pncB; OrderedLocusNames=ST1010, t1930;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OC NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;

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RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RN Nature 413:848-852(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RX DOI=10.1128/JB.185.7.2330-2337.2003;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RN J. Bacteriol. 185:2330-2337(2003).
CC -1- CATALYTIC ACTIVITY: Nicotinate D-ribonucleotide + diphosphate =
CC nicotinate + 5-phospho-alpha-D-ribose 1-diphosphate.
CC -1- PATHWAY: NAD biosynthesis; nicotinamide to NAMN; second step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the NAPRTase family.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AL627268; CAD05404.1; -.
CC EMBL; AE016840; AAO69546.1; -.
CC HAMAP; MF_00570; -.
CC InterPro; IPR007229; NAPRTase.
CC InterPro; IPR006406; Nic Prtrans.
CC InterPro; IPR008967; P53_like_DNA_bnd.
CC Pfam; PF04095; NAPRTase; 1.
CC PIRSF; PIRSF000484; Nicot_phos_ribo; 1.
CC TIGRFAMs; TIGR01514; NAPRTase; 1.
CC Complete proteome; Glycosyltransferase;
KW Pyridine nucleotide biosynthesis; Transferase.
FT INIT MET 0
FT SEQUENCE 399 AA; 45562 MW; ADF38EAE4618214 CRC64;
SQ
Query Match 67.8%; Score 40; DB 1; Length 399;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 YRCRGDD 8
DB :|||||
38 FRCRGDD 44
RESULT 15
PNCB_SALTY STANDARD; PRT; 399 AA.
AC P22253;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Nicotinate phosphoribosyltransferase (EC 2.4.2.11) (NAPRTase).
GN Name=pncB; OrderedLocusNames=ST1004;
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OC NCBI_TaxID=602;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=91100340; PubMed=1987148;
RA Vinitesky A., Teng H., Grubmeyer C.T.;
RT "Cloning and nucleic acid sequence of the Salmonella typhimurium pncB
RL gene and structure of nicotinate phosphoribosyltransferase.";
RN J. Bacteriol. 173:536-540(1991).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11877609; DOI=10.1038/35101614;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RT Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RL LT2.";
CC -!- CATALYTIC ACTIVITY: Nicotinate D-ribonucleotide + diphosphate =
CC -!- nicotinate + 5-phospho-alpha-D-ribose 1-diphosphate.
CC -!- PATHWAY: NAD biosynthesis; nicotinamide to NADN, second step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the NAPRTase family.
CC
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CC
CC -----
DR EMBL; M55986; AA27190.1; -.
DR EMBL; AE008743; AL11938.1; -.
DR FIR; A39130; A39130.
DR StyGene; SGI0305; pncB.
DR HAMAP; MF_00570; -.
DR InterPro; IPR007229; NAPRTase.
DR InterPro; IPR006406; Nic_Ptrtrans.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR Pfam; PF04095; NAPRTase; 1.
DR TIGRFAMs; TIGR01514; NAPRTase; 1.
DR TIGRFAMs; TIGR01514; NAPRTase; 1.
KW Complete proteome; Glycosyltransferase;
KW Pyridine nucleotide biosynthesis; Transferase.
PT INIT MET 0
SQ SEQUENCE 399 AA; 45530 MW; 90D9C3EDD8C092A6 CRC64;

Query Match 67.8%; Score 40; DB 1; Length 399;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
DB 38 FRCRGDD 44

RESULT 16
Q7UD27 PRELIMINARY; PRT; 400 AA.
ID Q7UD27
AC Q7UD27;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nicotinate phosphoribosyltransferase.
GN Name=pncB; OrderedLocustNames=S0992;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE 399 AA; 45530 MW; 90D9C3EDD8C092A6 CRC64;

Query Match 67.8%; Score 40; DB 1; Length 399;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
DB 38 FRCRGDD 44

RESULT 17
Q83LN3 PRELIMINARY; PRT; 416 AA.
ID Q83LN3
AC Q83LN3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nicotinate phosphoribosyltransferase.
GN Name=pncB; OrderedLocustNames=Sf0928;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
DR EMBL; AE015122; BAN42557.1; -.
DR GO; GO:0004516; F:nicotinate phosphoribosyltransferase activity; IEA.
DR GO; GO:0016757; P:transferase activity, transferring glycosyl. . ; IEA.
DR GO; GO:0019357; P:nicotinate nucleotide biosynthesis; IEA.
DR GO; GO:0019363; P:pyridine nucleotide biosynthesis; IEA.
DR InterPro; IPR007229; NAPRTase.
DR InterPro; IPR006406; Nic_Ptrtrans.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR Pfam; PF04095; NAPRTase; 1.
DR PIRSF; PIRSF000484; Nicot_phos_ribo; 1.
DR TIGRFAMs; TIGR01514; NAPRTase; 1.
KW Complete proteome; Glycosyltransferase; Transferase.
SQ SEQUENCE 416 AA; 47700 MW; E43D723542AF2DD5 CRC64;

Query Match 67.8%; Score 40; DB 2; Length 416;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
DB 39 FRCRGDD 45

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RX MEDLINE=22590274; PubMed=12704152;
RX DOI=10.1128/IAI.71.5.2775-2786.2003;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).
DR EMBL; AE016981; AAP16443.1; -.
DR GO; GO:0004516; F:nicotinate phosphoribosyltransferase activity; IEA.
DR GO; GO:0016757; P:transferase activity, transferring glycosyl. . ; IEA.
DR GO; GO:0019357; P:nicotinate nucleotide biosynthesis; IEA.
DR GO; GO:0019363; P:pyridine nucleotide biosynthesis; IEA.
DR InterPro; IPR007229; NAPRTase.
DR InterPro; IPR006406; Nic_Ptrtrans.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR Pfam; PF04095; NAPRTase; 1.
DR PIRSF; PIRSF000484; Nicot_phos_ribo; 1.
DR TIGRFAMs; TIGR01514; NAPRTase; 1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 400 AA; 45911 MW; 53858CB1A8703095 CRC64;

Query Match 67.8%; Score 40; DB 2; Length 400;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
DB 39 FRCRGDD 45

RESULT 17
Q83LN3 PRELIMINARY; PRT; 416 AA.
ID Q83LN3
AC Q83LN3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nicotinate phosphoribosyltransferase.
GN Name=pncB; OrderedLocustNames=Sf0928;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
DR EMBL; AE015122; BAN42557.1; -.
DR GO; GO:0004516; F:nicotinate phosphoribosyltransferase activity; IEA.
DR GO; GO:0016757; P:transferase activity, transferring glycosyl. . ; IEA.
DR GO; GO:0019357; P:nicotinate nucleotide biosynthesis; IEA.
DR GO; GO:0019363; P:pyridine nucleotide biosynthesis; IEA.
DR InterPro; IPR007229; NAPRTase.
DR InterPro; IPR006406; Nic_Ptrtrans.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR Pfam; PF04095; NAPRTase; 1.
DR PIRSF; PIRSF000484; Nicot_phos_ribo; 1.
DR TIGRFAMs; TIGR01514; NAPRTase; 1.
KW Complete proteome; Glycosyltransferase; Transferase.
SQ SEQUENCE 416 AA; 47700 MW; E43D723542AF2DD5 CRC64;

Query Match 67.8%; Score 40; DB 2; Length 416;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
DB 39 FRCRGDD 45

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Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
Db 55 FRCRGDD 61

RESULT 18
Q8FU98 PRELIMINARY; PRT; 416 AA.
AC Q8FU98;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nicotinate phosphoribosyltransferase (EC 2.4.2.11).
GN Name=pncB; OrderedLocusNames=c1073;
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O6:H1 / CFT073 / ATCC 700928 / UPEC;
RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
DR EMBL; A2016758; AN79541.1; -.
DR GO; GO:0004516; P:nicotinate phosphoribosyltransferase activity; IEA.
DR GO; GO:0019357; P:nicotinate nucleotide biosynthesis; IEA.
DR GO; GO:0019363; P:pyridine nucleotide biosynthesis; IEA.
DR InterPro; IPR007229; NAPTase.
DR InterPro; IPR006406; Nic_Prtase.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR Pfam; PF04095; NAPTase; 1.
DR TIGSF; TIGSF00484; Nicot_phos_ribo; 1.
DR TIGRFAMs; TIGR01514; NAPTase; 1.
KW Complete proteome.
SQ SEQUENCE 416 AA; 47722 MW; F00AFC07B04B1E23 CRC64;

Query Match 67.8%; Score 40; DB 2; Length 416;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
Db 55 FRCRGDD 61

RESULT 19
Q50468 PRELIMINARY; PRT; 705 AA.
AC Q50468;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Pk8002a.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith D.R.;
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP ROBLSON K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.

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CC -!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
CC family.
CC EMBL; U00024; AAA50930.1; -.
DR HSP; P08659; ILCI.
DR GO; GO:0003824; P:catalytic activity; IEA.
DR GO; GO:0048037; P:cofactor binding; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR009081; ACP_like.
DR InterPro; IPR000873; AMP_bind.
DR InterPro; IPR006163; Sheppanteth_bind.
DR Pfam; PF00501; PP-binding; 1.
DR Pfam; PF00550; PP-binding; 1.
DR PRINTS; PR00154; AMPEBINDING.
DR PROSITE; PS50075; ACP_DOMAIN; 1.
SQ SEQUENCE 705 AA; 75169 MW; 9F9D4F500690BF5D CRC64;

Query Match 67.8%; Score 40; DB 2; Length 705;
Best Local Similarity 66.7%; Pred. No. 73;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YRCRGDDSK 10
Db 383 YRCRADDT 391

RESULT 20
P96283 PRELIMINARY; PRT; 705 AA.
ID P96283 QYD6D9;
AC P96283; QYD6D9;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE PROBABLE FATTY-ACID-CoA LIGASE FADD22 (FATTY-ACID-CoA SYNTHETASE)
DE (FATTY-ACID-CoA SYNTHASE) (EC 6.2.1.1-) (Substrate--CoA ligase).
GN Name=fadD22; OrderedLocusNames=MT3021, RV2948c;
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
RA Harris D.E., Gordon S.V., Eigmeier K., Gas S., Barry C.E. III,
RA Tekala F., Badcock K., Basham D., Brown D., Chillingworth T.,
RA Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
RA Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
RA Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RX DOI=10.1128/JB.184.19.5479-5490.2002;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J.D., Deboy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,
RA Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,
RA Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.,
RA Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
RA Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL J. Bacteriol. 184:5479-5490 (2002).
CC -!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
CC family.
CC EMBL; BX842581; CAB06101.1; -.
CC EMBL; AE000516; AAK47347.1; -.
DR PIR; A70669; A70669.

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DR HSSP; P08659; 1LCI.
DR TIGR; MT3021; -.
DR Tuberculin; Bv2948c; -.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:004803; F: cofactor binding; IEA.
DR GO; GO:0016874; F: ligase activity; IEA.
DR GO; GO:0008152; P: metabolism; IEA.
DR InterPro; IPR009081; ACP like.
DR InterPro; IPR000873; AMP-bind.
DR InterPro; IPR006163; Phosphanteth_bind.
DR Pfam; PF00501; AMP-binding; 1.
DR Pfam; PF00550; PP-binding; 1.
DR PRINTS; PR00154; AMPBINDING.
DR PROSITE; PS50075; ACP_DOMAIN; 1.
KW Ligase.
SQ SEQUENCE 705 AA; 75197 MW; 600F2D0EABFDF1DC CRC64;

Query Match 67.8%; Score 40; DB 2; Length 705;
Best Local Similarity 66.7%; Pred. No. 73;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YRCRGDGS 10
DB 383 YRCRADDT 391

RESULT 21
Q7TXK7
ID Q7TXK7 PRELIMINARY; PRT; 705 AA.
AC Q7TXK7
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PROBABLE FATTY-ACID-CoA LIGASE FAD22 (FATTY-ACID-CoA SYNTHETASE)
DE (FATTY-ACID-CoA SYNTHASE) (EC 6.2.1.-)
DE Name=fad22; OrderedLocusNames=MB2972c;
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21222/97; PubMed=12788972; DOI=10.1073/pnas.1130426100;
RA Garnier T., Biglmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrall B.G., Cole S.T., Gordon S.V., Hewison R.G.;
RT "The complete genome sequence of Mycobacterium bovis.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
DR EMBL; BX248344; CAD96659.1; -.
DR GO; GO:0048037; F: cofactor binding; IEA.
DR GO; GO:0016874; F: ligase activity; IEA.
DR GO; GO:0008152; P: metabolism; IEA.
DR InterPro; IPR009081; ACP like.
DR InterPro; IPR000873; AMP-bind.
DR InterPro; IPR006163; Phosphanteth_bind.
DR Pfam; PF00501; AMP-binding; 1.
DR Pfam; PF00550; PP-binding; 1.
DR PROSITE; PS50075; ACP_DOMAIN; 1.
KW Complete proteome; Ligase.
SQ SEQUENCE 705 AA; 75197 MW; 600F2D0EABFDF1DC CRC64;

Query Match 67.8%; Score 40; DB 2; Length 705;
Best Local Similarity 66.7%; Pred. No. 73;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YRCRGDGS 10
DB 383 YRCRADDT 391

RESULT 22
Q7TXK7
ID Q7TXK7 PRELIMINARY; PRT; 705 AA.
AC Q7TXK7
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PROBABLE FATTY-ACID-CoA LIGASE FAD22 (FATTY-ACID-CoA SYNTHETASE)
DE (FATTY-ACID-CoA SYNTHASE) (EC 6.2.1.-)
DE Name=fad22; OrderedLocusNames=MB2972c;
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=AF2122/97;
RX MEDLINE=21222/97; PubMed=12788972; DOI=10.1073/pnas.1130426100;
RA Garnier T., Biglmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrall B.G., Cole S.T., Gordon S.V., Hewison R.G.;
RT "The complete genome sequence of Mycobacterium bovis.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
DR EMBL; BX248344; CAD96659.1; -.
DR GO; GO:0048037; F: cofactor binding; IEA.
DR GO; GO:0016874; F: ligase activity; IEA.
DR GO; GO:0008152; P: metabolism; IEA.
DR InterPro; IPR009081; ACP like.
DR InterPro; IPR000873; AMP-bind.
DR InterPro; IPR006163; Phosphanteth_bind.
DR Pfam; PF00501; AMP-binding; 1.
DR Pfam; PF00550; PP-binding; 1.
DR PROSITE; PS50075; ACP_DOMAIN; 1.
KW Complete proteome; Ligase.
SQ SEQUENCE 705 AA; 75197 MW; 600F2D0EABFDF1DC CRC64;

Query Match 67.8%; Score 40; DB 2; Length 705;
Best Local Similarity 66.7%; Pred. No. 73;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YRCRGDGS 10
DB 383 YRCRADDT 391
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Q8WQJ3
ID Q8WQJ3 PRELIMINARY; PRT; 845 AA.
AC Q8WQJ3
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SRCR LGCL adhesive-like protein (Fragment).
GN Name=slap;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21982590; PubMed=11985859; DOI=10.1016/S0166-6851(02)00016-6;
RA Delrieu I., Waller C.C., Mota M.M., Grainger M., Langhorne J.,
RA Holder A.A.;
RT "PSLAP, a protein with multiple adhesive motifs, is expressed in
RT Plasmodium falciparum gametocytes.";
RL Mol. Biochem. Parasitol. 121:11-20(2002).
DR EMBL; AY072023; AAL58521.1; -.
DR GO; GO:0016020; C: membrane; IEA.
DR GO; GO:0005044; F: scavenger receptor activity; IEA.
DR Pfam; PF03815; LCCL; 3.
DR Pfam; PF00530; SRCR; 2.
DR SMART; SM00202; SR; 2.
DR PROSITE; PS50820; LCCL; 2.
DR PROSITE; PS50287; SRCR_2; 2.
FT NON_TER 1
FT NON_TER 845
SQ SEQUENCE 845 AA; 95032 MW; 06A389E4CC294477 CRC64;

Query Match 67.8%; Score 40; DB 2; Length 845;
Best Local Similarity 55.6%; Pred. No. 88;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYRCRGDGS 9
DB 340 NFRCKGDEA 348

RESULT 23
Q8WT63
ID Q8WT63 PRELIMINARY; PRT; 1304 AA.
AC Q8WT63
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Multidomain scavenger receptor protein pBSR precursor.
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22242506; PubMed=12354219;
RA Claudianos C., Dessens J.T., Trueman H.E., Arai M., Mendoza J.,
RA Butcher G.A., Crompton T., Sinden R.B.;
RT "A malaria scavenger receptor-like protein essential for parasite
RT development.";
RL Mol. Microbiol. 45:1473-1484(2002).
CC -!- SIMILARITY: Contains 1 PLAT domain.
DR EMBL; AY034780; AAK64185.1; -.
DR HSSP; O43405; 1UJBI.
DR GO; GO:0016020; C: membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0005044; F: scavenger receptor activity; IEA.
DR Pfam; PF03815; LCCL; 4.
DR Pfam; PF01477; PLAT; 1.
DR Pfam; PF00530; SRCR; 2.
DR SMART; SM00202; SR; 2.
DR PROSITE; PS50820; LCCL; 3.
DR PROSITE; PS50095; PLAT; 1.
DR PROSITE; PS50287; SRCR_2; 2.
KW Receptor; Signal.
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FT SIGNAL 1 22 Potential.
SQ SEQUENCE 1304 AA; 148247 MW; F936CC94E7B19F1C CRC64;

Query Match 67.8%; Score 40; DB 2; Length 1304;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYRCRGDGS 9
Db 614 NFRCKGDEA 622

RESULT 24
Q8P0M2 PRELIMINARY; PRT; 37 AA.
ID Q8P0M2 AC Q8P0M2
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical phase protein.
DE OrderedLocuNames=spym18_1296;
GN Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=186103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS8232;
RX MEDLINE=2197593; PubMed=11917108; DOI=10.1073/pnas.062526099;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
DR EMBL; AE010051; ALU97902.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 37 AA; 4398 MW; E7884FEAA642342 CRC64;

Query Match 66.1%; Score 39; DB 2; Length 37;
Best Local Similarity 70.0%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NYRCRGDGS 10
Db 14 NYHTNGDGS 23

RESULT 25
Q848W4 PRELIMINARY; PRT; 46 AA.
ID Q848W4 AC Q848W4
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
DE Bacillus megaterium.
OS Plasmid pBM400.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=QM B1551;
RX MEDLINE=22964369; PubMed=14602653;
RX DOI=10.1128/AEM.69.11.6888-6898.2003;
RA Scholle M.D., White C.A., Kummalaityaan M., Vary P.S.;
RT "Sequencing and characterization of pBM400 from Bacillus megaterium QM
RT B1551.";
RL Appl. Environ. Microbiol. 69:6888-6898(2003).
DR EMBL; AF142677; AA052802.1; -.
KW Hypothetical protein; Plasmid.

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SQ SEQUENCE 46 AA; 5449 MW; F4E4C4A3A050E138 CRC64;

Query Match 66.1%; Score 39; DB 2; Length 46;
Best Local Similarity 60.0%; Pred. No. 6.8;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NYRCRGDGS 10
Db 35 NYRCRGEVDK 44

RESULT 26
O8BUS2 PRELIMINARY; PRT; 154 AA.
ID O8BUS2 AC Q8BUS2
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus ES cells cDNA, RIKEN full-length enriched library,
DE clone:C330016E03 product:SRCRB-S4D PROTEIN homolog (Fragment).
GN Name=Srcrbad;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=9979253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsumi T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;

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RA Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Teijima Y., Toya T., Yamamura T., Yamanaka I., Yasunishi A.,
RA Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.,
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK082786; BAC38619.1; -.
DR HSSP; Q08380; 1BY2.
DR MGD; MGI:1924709; Sscr4d4.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005044; F:scavenger receptor activity; IEA.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF00530; SRCR; 1.
DR PRINTS; PR00258; SPERACTRCPTR.
DR SMART; SM00202; SR; 1.
DR PROSITE; PS00420; SRCR_1; 1.
DR PROSITE; PS50287; SRCR_2; 1.
FT NON_TER 1
SQ SEQUENCE 154 AA; 17028 MW; 8932AA223E2F14F5 CRC64;
Query Match 66.1%; Score 39; DB 2; Length 154;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 NVRCRGDS 9
DB 118 NVKRGDES 126
RESULT 27
Q20683
ID Q20683 PRELIMINARY; PRT; 179 AA.
AC Q20683;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein F52H3.5.
GN ORFNames=F52H3.5;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Gardner A.E.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z66512; CAA91325.1; -.
DR PIR; T22521; T22521.
DR WormBase; WBGene0009947; F52H3.5.
DR WormPep; F52H3.5; CE03401.
DR InterPro; IPR001440; TPR.
DR InterPro; IPR008941; TPR-like.
DR Pfam; PF00515; TPR_1; 1.
DR SMART; SM00028; TPR; 3.
DR PROSITE; PS50005; TPR; 1.
DR PROSITE; PS50293; TPR_REGION; 1.
KW Hypothetical protein_Repeat; TPR repeat.
SQ SEQUENCE 179 AA; 19648 MW; 6FF899837C65A18F CRC64;

Query Match 66.1%; Score 39; DB 2; Length 179;
Best Local Similarity 77.8%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 YRCRGDDSK 10
DB 125 YRLRGDDDK 133
RESULT 28
O70681
ID O70681 PRELIMINARY; PRT; 588 AA.
AC O70681;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Coat protein (Fragment).
OS Sugarcane streak mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=53954;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99162284; PubMed=10051385; DOI=10.1006/mpev.1998.0535;
RA Hall J.S., Adams B., Parsons T.J., French R., Lane L.C., Jensen S.G.;
RT "Molecular cloning, sequencing, and phylogenetic relationships of a
RT new potyvirus: sugarcane streak mosaic virus, and a reevaluation of
RT the classification of the potyviridae."
RL Mol. Phylogenet. Evol. 10:323-332(1998).
CC -!- SIMILARITY: Belongs to the potyviruses polyprotein family.
DR EMBL; U75456; AAC16271.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0006350; F:transcription; IEA.
DR GO; GO:0019079; F:viral genome replication; IEA.
DR InterPro; IPR001592; Poty_coat.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR001205; RNA_pol_P3D.
DR InterPro; IPR007094; RNA_pol_Psvir.
DR Pfam; PF00767; Poty_coat; 1.
DR Pfam; PF00680; RNA_dep_RNA_pol; 1.
KW Coat protein.
FT NON_TER 1
SQ SEQUENCE 588 AA; 66335 MW; 3876EEF59189EA32 CRC64;
Query Match 66.1%; Score 39; DB 2; Length 588;
Best Local Similarity 75.0%; Pred. No. 93;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 NVRCRGDD 8
DB 141 NYTCNGDD 148
RESULT 29
Q3YNE1
ID Q3YNE1 PRELIMINARY; PRT; 1420 AA.
AC Q3YNE1;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polyprotein (Fragment).
OS Sugarcane streak mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=53954;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99243201; PubMed=10226614;
RA Hema M., Joseph J., Gopinath K., Sreenivasulu P., Savithri H.S.;

RT "Molecular characterization and intervirial relationships of a flexuous
RT filamentous virus causing mosaic disease of sugarcane (Saccharum
RT officinarum L.) in India."
RL Arch. Virol. 144:479-490(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Hema M.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Belongs to the potyviruses polyprotein family.
DR EMBL; Y17738; CAA76842.3; -;
DR GO: 0019028; C:Viral capsid; IEA.
DR GO: 0008234; F:cysteine-type peptidase activity; IEA.
DR GO: 0003723; F:RNA binding; IEA.
DR GO: 0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO: 0005198; F:structural molecule activity; IEA.
DR GO: 0006508; P:proteolysis and peptidolysis; IEA.
DR GO: 0006350; P:transcription; IEA.
DR GO: 0019079; P:viral genome replication; IEA.
DR InterPro; IPR001730; Peptidase_C4.
DR InterPro; IPR001592; Poty_coat.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR001205; RNA_pol_P3D.
DR InterPro; IPR007094; RNA_pol_P5vir.
DR Pfam; PF00767; Poty_coat_1.
DR Pfam; PF00680; RNA_dep_RNA_pol; 1.
DR PRINTS; PR00966; NIAPOTYPTASE.
DR Coar protein; Polyprotein.
FT NON TER 1 1
FT CHAIN 1138 1420 coat protein.
SQ SEQUENCE 1420 AA; 160420 MW; 48B8456258D87275 CRC64;

Query Match 66.1%; Score 39; DB 2; Length 1420;
Best Local Similarity 75.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
DB 974 NYTCNGDD 981

RESULT 30
Q7RQM4 PRELIMINARY; PRT; 1615 AA.
AC Q7RQM4; (TREMREL. 26, Created)
DT 01-MAR-2004 (TREMREL. 26, Last sequence update)
DT 01-MAR-2004 (TREMREL. 26, Last annotation update)
DE Multidomain scavenger receptor protein Pbsr precursor.
GN Names:PY01071;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Anguilo S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shalom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegh M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -I- SIMILARITY: Contains 1 PLAT domain.
CC -I- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.

DR EMBL; ABL01000281; EAA20072.1; -;
DR HSSP; O57811; IG8A.
DR GO: 0016020; C:membrane; IEA.
DR GO: 0005634; C:nucleus; IEA.
DR GO: 0004872; F:receptor activity; IEA.
DR GO: 0003723; F:RNA binding; IEA.
DR GO: 0005044; F:scavenger receptor activity; IEA.
DR GO: 0006364; P:RNA processing; IEA.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR000692; Fibrillarin.
DR InterPro; IPR004043; LCCL.
DR InterPro; IPR001024; Lipoxigenase_LH2.
DR InterPro; IPR008976; PLAT_LH2.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF01269; Fibrillarin; 1.
DR Pfam; PF03815; LCCL; 4.
DR Pfam; PF01477; PLAT; 1.
DR Pfam; PF00530; SRCR; 2.
DR PRINTS; PR00052; FIBRILLARIN.
DR ProDom; PD004637; Fibrillarin; 1.
DR PROSITE; PS00566; FIBRILLARIN; 1.
DR PROSITE; PS00820; LCCL; 4.
DR PROSITE; PS00095; PLAT; 1.
DR PROSITE; PS00287; SRCR_2; 2.
KW Receptor.
SQ SEQUENCE 1615 AA; 180943 MW; 94053C4C9AC93505 CRC64;

Query Match 66.1%; Score 39; DB 2; Length 1615;
Best Local Similarity 62.5%; Pred. No. 2.6e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
DB 614 NFRCKGDE 621

RESULT 31
Q8VI63 PRELIMINARY; PRT; 121 AA.
AC Q8VI63;
DT 01-MAR-2002 (TREMREL. 20, Created)
DT 01-MAR-2002 (TREMREL. 20, Last sequence update)
DT 01-JUN-2003 (TREMREL. 24, Last annotation update)
DE Lambda 3 protein (fragment).
OS Reovirus sp.
OC Viruses; dsRNA viruses; Reoviridae; unclassified Reoviridae.
OX NCBI_TaxID=10891;
RN [1]_TaxID=10891;
RP SEQUENCE FROM N.A.
RX MEDLINE=21920879; PubMed=11923358;
RA Leary T.P., Erker J.C., Chalmers M.L., Cruz A.T., Wetzel J.D.,
RA Desai S.M., Mushahwar I.K., Dermody T.S.;
RT "Detection of mammalian reovirus RNA by using reverse transcription-
RT PCR: sequence diversity within the lambda3-encoding L1 gene."
RL J. Clin. Microbiol. 40:1368-1375(2002).
DR EMBL; AY007423; AAG28882.1; -;
DR HSSP; P17378; IN35.
DR GO: 0003723; F:RNA binding; IEA.
DR GO: 0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO: 00019079; P:viral genome replication; IEA.
FT NON TER 1 121
FT NON TER 121 121
SQ SEQUENCE 121 AA; 13363 MW; EA44987394A246CA CRC64;

Query Match 64.4%; Score 38; DB 2; Length 121;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
DB 96 NYVCQGDD 103

RESULT 32

Q8V164
ID Q8V164 PRELIMINARY; PRT; 121 AA.
AC Q8V164;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lambda 3 protein (Fragment).
OS Reovirus sp.
OC Viruses; dsRNA viruses; Reoviridae; unclassified Reoviridae.
OX NCBI_TaxID=10891;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21920879; PubMed=11923358;
RA Leary T.P., Erker J.C., Chalmers M.L., Cruz A.T., Wetzel J.D.,
Desai S.M., Mushahwar I.K., Dermody T.S.;
RT "Detection of mammalian reovirus RNA by using reverse transcription-
PCR: sequence diversity within the lambda3-encoding L1 gene.";
RL J. Clin. Microbiol. 40:1368-1375(2002).
DR EMBL; AY007422; AAG28881.1; -.
DR HSSP; P17378; 1N35.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0019079; P:Viral genome replication; IEA.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13349 MW; 2B8DA9F9BC00CCFB CRC64;

Query Match 64.4%; Score 38; DB 2; Length 121;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
|||:||||
Db 96 NYVCQGGD 103

RESULT 33

Q8V165
ID Q8V165 PRELIMINARY; PRT; 121 AA.
AC Q8V165;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lambda 3 protein (Fragment).
OS Reovirus sp.
OC Viruses; dsRNA viruses; Reoviridae; unclassified Reoviridae.
OX NCBI_TaxID=10891;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21920879; PubMed=11923358;
RA Leary T.P., Erker J.C., Chalmers M.L., Cruz A.T., Wetzel J.D.,
Desai S.M., Mushahwar I.K., Dermody T.S.;
RT "Detection of mammalian reovirus RNA by using reverse transcription-
PCR: sequence diversity within the lambda3-encoding L1 gene.";
RL J. Clin. Microbiol. 40:1368-1375(2002).
DR EMBL; AY007421; AAG28880.1; -.
DR HSSP; P17378; 1N35.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0019079; P:Viral genome replication; IEA.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13363 MW; EA44987394A246CA CRC64;

Query Match 64.4%; Score 38; DB 2; Length 121;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
|||:||||
Db 96 NYVCQGGD 103

RESULT 34

Q8V166
ID Q8V166 PRELIMINARY; PRT; 121 AA.
AC Q8V166;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lambda 3 protein (Fragment).
OS Reovirus sp.
OC Viruses; dsRNA viruses; Reoviridae; unclassified Reoviridae.
OX NCBI_TaxID=10891;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21920879; PubMed=11923358;
RA Leary T.P., Erker J.C., Chalmers M.L., Cruz A.T., Wetzel J.D.,
Desai S.M., Mushahwar I.K., Dermody T.S.;
RT "Detection of mammalian reovirus RNA by using reverse transcription-
PCR: sequence diversity within the lambda3-encoding L1 gene.";
RL J. Clin. Microbiol. 40:1368-1375(2002).
DR EMBL; AY007420; AAG28879.1; -.
DR HSSP; P17378; 1N35.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0019079; P:Viral genome replication; IEA.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13363 MW; EA44987394A246CA CRC64;

Query Match 64.4%; Score 38; DB 2; Length 121;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
|||:||||
Db 96 NYVCQGGD 103

RESULT 35

Q8V167
ID Q8V167 PRELIMINARY; PRT; 121 AA.
AC Q8V167;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lambda 3 protein (Fragment).
OS Reovirus sp.
OC Viruses; dsRNA viruses; Reoviridae; unclassified Reoviridae.
OX NCBI_TaxID=10891;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21920879; PubMed=11923358;
RA Leary T.P., Erker J.C., Chalmers M.L., Cruz A.T., Wetzel J.D.,
Desai S.M., Mushahwar I.K., Dermody T.S.;
RT "Detection of mammalian reovirus RNA by using reverse transcription-
PCR: sequence diversity within the lambda3-encoding L1 gene.";
RL J. Clin. Microbiol. 40:1368-1375(2002).
DR EMBL; AY007419; AAG28878.1; -.
DR HSSP; P17378; 1N35.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0019079; P:Viral genome replication; IEA.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13363 MW; EA44987394A246CA CRC64;

Query Match 64.4%; Score 38; DB 2; Length 121;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
|||:||||
Db 96 NYVCQGGD 103

```
Db          96 NYVCGDD 103

RESULT 36
Q8V168      PRELIMINARY;      PRT;      121 AA.
AC Q8V168;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lambda 3 protein (Fragment).
OS Reovirus sp.
OC Viruses; dsRNA viruses; Reoviridae; unclassified Reoviridae.
OX NCBI_TaxID=10891;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21920879; PubMed=11923358;
RA Leary T.P., Erker J.C., Chalmers M.L., Cruz A.T., Wetzel J.D.,
RA Desai S.M., Mushahwar I.K., Dermody T.S.;
RT "Detection of mammalian reovirus RNA by using reverse transcription-
RT PCR: sequence diversity within the lambda3-encoding L1 gene.";
RL J. Clin. Microbiol. 40:1368-1375(2002).
DR EMBL; AY007418; AAG28877.1; -.
DR HSSP; P17378; IN35.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0019079; P:Viral genome replication; IEA.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13363 MW; EA44987394A246CA CRC64;

Query Match      64.4%; Score 38; DB 2; Length 121;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
||| |||
Db 96 NYVCGDD 103

RESULT 37
Q8V169      PRELIMINARY;      PRT;      121 AA.
AC Q8V169;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lambda 3 protein (Fragment).
OS Reovirus sp.
OC Viruses; dsRNA viruses; Reoviridae; unclassified Reoviridae.
OX NCBI_TaxID=10891;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21920879; PubMed=11923358;
RA Leary T.P., Erker J.C., Chalmers M.L., Cruz A.T., Wetzel J.D.,
RA Desai S.M., Mushahwar I.K., Dermody T.S.;
RT "Detection of mammalian reovirus RNA by using reverse transcription-
RT PCR: sequence diversity within the lambda3-encoding L1 gene.";
RL J. Clin. Microbiol. 40:1368-1375(2002).
DR EMBL; AY007417; AAG28876.1; -.
DR HSSP; P17378; IN35.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0019079; P:Viral genome replication; IEA.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13363 MW; EA44987394A246CA CRC64;

Query Match      64.4%; Score 38; DB 2; Length 121;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
||| |||
Db 96 NYVCGDD 103

RESULT 38
Q8V170      PRELIMINARY;      PRT;      121 AA.
AC Q8V170;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lambda 3 protein (Fragment).
OS Reovirus sp.
OC Viruses; dsRNA viruses; Reoviridae; unclassified Reoviridae.
OX NCBI_TaxID=10891;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21920879; PubMed=11923358;
RA Leary T.P., Erker J.C., Chalmers M.L., Cruz A.T., Wetzel J.D.,
RA Desai S.M., Mushahwar I.K., Dermody T.S.;
RT "Detection of mammalian reovirus RNA by using reverse transcription-
RT PCR: sequence diversity within the lambda3-encoding L1 gene.";
RL J. Clin. Microbiol. 40:1368-1375(2002).
DR EMBL; AY007416; AAG28875.1; -.
DR HSSP; P17378; IN35.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0019079; P:Viral genome replication; IEA.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13363 MW; EA44987394A246CA CRC64;

Query Match      64.4%; Score 38; DB 2; Length 121;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
||| |||
Db 96 NYVCGDD 103

RESULT 39
Q8V171      PRELIMINARY;      PRT;      121 AA.
AC Q8V171;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lambda 3 protein (Fragment).
OS Reovirus sp.
OC Viruses; dsRNA viruses; Reoviridae; unclassified Reoviridae.
OX NCBI_TaxID=10891;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21920879; PubMed=11923358;
RA Leary T.P., Erker J.C., Chalmers M.L., Cruz A.T., Wetzel J.D.,
RA Desai S.M., Mushahwar I.K., Dermody T.S.;
RT "Detection of mammalian reovirus RNA by using reverse transcription-
RT PCR: sequence diversity within the lambda3-encoding L1 gene.";
RL J. Clin. Microbiol. 40:1368-1375(2002).
DR EMBL; AY007415; AAG28874.1; -.
DR HSSP; P17378; IN35.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0019079; P:Viral genome replication; IEA.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13363 MW; EA44987394A246CA CRC64;

Query Match      64.4%; Score 38; DB 2; Length 121;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
||| |||
Db 96 NYVCGDD 103
```

QY 1 NYRCRGDD 8

Db 96 NYVCGDD 103
|| |:|||

RESULT 40

Q8V172 PRELIMINARY; PRT; 121 AA.
AC Q8V172;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lambda 3 protein (fragment).
OS Reovirus sp.
OC Viruses; dsRNA viruses; Reoviridae; unclassified Reoviridae.
OX NCBI_TaxID=10891;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21920879; PubMed=11923358;
RA Leary T.P., Erker J.C., Chalmers M.L., Cruz A.T., Wetzel J.D.,
RA Desai S.M., Mushahwar I.K., Dermody T.S.;
RT "Detection of mammalian reovirus RNA by using reverse transcription-PCR: sequence diversity within the lambda3-encoding L1 gene.";
RT J. Clin. Microbiol. 40:1368-1375(2002).
RL EMBL; AY007414; AAG28873.1; -.
DR HSSP; P17378; 1N35.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0019079; P:Viral genome replication; IEA.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13391 MW; 4A53987DB0292B7C CRC64;

Query Match 64.4%; Score 38; DB 2; Length 121;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
|| |:|||
Db 96 NYVCGDD 103

RESULT 41

Q8V173 PRELIMINARY; PRT; 121 AA.
AC Q8V173;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lambda 3 protein (fragment).
OS Reovirus sp.
OC Viruses; dsRNA viruses; Reoviridae; unclassified Reoviridae.
OX NCBI_TaxID=10891;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21920879; PubMed=11923358;
RA Leary T.P., Erker J.C., Chalmers M.L., Cruz A.T., Wetzel J.D.,
RA Desai S.M., Mushahwar I.K., Dermody T.S.;
RT "Detection of mammalian reovirus RNA by using reverse transcription-PCR: sequence diversity within the lambda3-encoding L1 gene.";
RT J. Clin. Microbiol. 40:1368-1375(2002).
RL EMBL; AY007413; AAG28872.1; -.
DR HSSP; P17378; 1N35.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0019079; P:Viral genome replication; IEA.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13391 MW; 4A53987DB0292B7C CRC64;

Query Match 64.4%; Score 38; DB 2; Length 121;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
|| |:|||
Db 96 NYVCGDD 103

RESULT 42

Q8V174 PRELIMINARY; PRT; 121 AA.
AC Q8V174;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lambda 3 protein (fragment).
OS Reovirus sp.
OC Viruses; dsRNA viruses; Reoviridae; unclassified Reoviridae.
OX NCBI_TaxID=10891;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21920879; PubMed=11923358;
RA Leary T.P., Erker J.C., Chalmers M.L., Cruz A.T., Wetzel J.D.,
RA Desai S.M., Mushahwar I.K., Dermody T.S.;
RT "Detection of mammalian reovirus RNA by using reverse transcription-PCR: sequence diversity within the lambda3-encoding L1 gene.";
RT J. Clin. Microbiol. 40:1368-1375(2002).
RL EMBL; AY007412; AAG28871.1; -.
DR HSSP; P17378; 1N35.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0019079; P:Viral genome replication; IEA.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13391 MW; 4A53987DB0292B7C CRC64;

Query Match 64.4%; Score 38; DB 2; Length 121;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
|| |:|||
Db 96 NYVCGDD 103

RESULT 43

Q8V175 PRELIMINARY; PRT; 121 AA.
AC Q8V175;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lambda 3 protein (fragment).
OS Reovirus sp.
OC Viruses; dsRNA viruses; Reoviridae; unclassified Reoviridae.
OX NCBI_TaxID=10891;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21920879; PubMed=11923358;
RA Leary T.P., Erker J.C., Chalmers M.L., Cruz A.T., Wetzel J.D.,
RA Desai S.M., Mushahwar I.K., Dermody T.S.;
RT "Detection of mammalian reovirus RNA by using reverse transcription-PCR: sequence diversity within the lambda3-encoding L1 gene.";
RT J. Clin. Microbiol. 40:1368-1375(2002).
RL EMBL; AY007411; AAG28870.1; -.
DR HSSP; P17378; 1N35.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0019079; P:Viral genome replication; IEA.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13402 MW; 4A5D98791A892B7C CRC64;

Query Match 64.4%; Score 38; DB 2; Length 121;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 NYRCRGDD 8
Db 96 NYVCQGDD 103

RESULT 44
Q8V176 PRELIMINARY; PRT; 121 AA.
ID Q8V176;
AC Q8V176;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lambda 3 protein (Fragment).
OS Reovirus sp.
OC Viruses; dsRNA viruses; Reoviridae; unclassified Reoviridae.
OX NCBI_TaxID=10891;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21920879; PubMed=11923358;
RA Leary T.P., Erker J.C., Chalmers M.L., Cruz A.T., Wetzel J.D.,
RA Desai S.M., Mushahwar I.K., Dermody T.S.;
RT "Detection of mammalian reovirus RNA by using reverse transcription-
RT PCR: sequence diversity within the lambda3-encoding L1 gene.";
RL J. Clin. Microbiol. 40:1368-1375(2002).
DR EMBL; AY007410; AAG28869.1; -.
DR HSSP; P17378; IN35.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0019079; P:Viral genome replication; IEA.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13363 MW; EA44987394A246CA CRC64;

Query Match 64.4%; Score 38; DB 2; Length 121;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
Db 96 NYVCQGDD 103

RESULT 45
Q8V177 PRELIMINARY; PRT; 121 AA.
ID Q8V177;
AC Q8V177;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lambda 3 protein (Fragment).
OS Reovirus sp.
OC Viruses; dsRNA viruses; Reoviridae; unclassified Reoviridae.
OX NCBI_TaxID=10891;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21920879; PubMed=11923358;
RA Leary T.P., Erker J.C., Chalmers M.L., Cruz A.T., Wetzel J.D.,
RA Desai S.M., Mushahwar I.K., Dermody T.S.;
RT "Detection of mammalian reovirus RNA by using reverse transcription-
RT PCR: sequence diversity within the lambda3-encoding L1 gene.";
RL J. Clin. Microbiol. 40:1368-1375(2002).
DR EMBL; AY007409; AAG28868.1; -.
DR HSSP; P17378; IN35.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0019079; P:Viral genome replication; IEA.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13353 MW; B947AB7396CDBB58 CRC64;

Query Match 64.4%; Score 38; DB 2; Length 121;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
Db 96 NYVCQGDD 103

RESULT 46
Q8V178 PRELIMINARY; PRT; 121 AA.
ID Q8V178;
AC Q8V178;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lambda 3 protein (Fragment).
OS Reovirus sp.
OC Viruses; dsRNA viruses; Reoviridae; unclassified Reoviridae.
OX NCBI_TaxID=10891;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21920879; PubMed=11923358;
RA Leary T.P., Erker J.C., Chalmers M.L., Cruz A.T., Wetzel J.D.,
RA Desai S.M., Mushahwar I.K., Dermody T.S.;
RT "Detection of mammalian reovirus RNA by using reverse transcription-
RT PCR: sequence diversity within the lambda3-encoding L1 gene.";
RL J. Clin. Microbiol. 40:1368-1375(2002).
DR EMBL; AY007408; AAG28867.1; -.
DR HSSP; P17378; IN35.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0019079; P:Viral genome replication; IEA.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13353 MW; B947AB7396CDBB58 CRC64;

Query Match 64.4%; Score 38; DB 2; Length 121;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
Db 96 NYVCQGDD 103

RESULT 47
Q8V179 PRELIMINARY; PRT; 121 AA.
ID Q8V179;
AC Q8V179;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lambda 3 protein (Fragment).
OS Reovirus sp.
OC Viruses; dsRNA viruses; Reoviridae; unclassified Reoviridae.
OX NCBI_TaxID=10891;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21920879; PubMed=11923358;
RA Leary T.P., Erker J.C., Chalmers M.L., Cruz A.T., Wetzel J.D.,
RA Desai S.M., Mushahwar I.K., Dermody T.S.;
RT "Detection of mammalian reovirus RNA by using reverse transcription-
RT PCR: sequence diversity within the lambda3-encoding L1 gene.";
RL J. Clin. Microbiol. 40:1368-1375(2002).
DR EMBL; AY007407; AAG28866.1; -.
DR HSSP; P17378; IN35.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0019079; P:Viral genome replication; IEA.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13377 MW; EA44987393D246CA CRC64;

Query Match 64.4%; Score 38; DB 2; Length 121;
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Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 NYRCRGDD 8
DB 96 NYVCQGGD 103

RESULT 48

Q8V180 PRELIMINARY; PRT; 121 AA.
AC Q8V180;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lambda 3 protein (Fragment).
OS Reovirus sp.
OC Viruses; deRNA viruses; Reoviridae; unclassified Reoviridae.
OX NCBI_TaxID=10891;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21920879; PubMed=11923358;
RA Leary T.P., Erker J.C., Chalmers M.L., Cruz A.T., Wetzel J.D.,
RA Desai S.M., Mushahwar I.K., Dermody T.S.;
RT "Detection of mammalian reovirus RNA by using reverse transcription-
PCR: sequence diversity within the lambda3-encoding L1 gene.";
RL J. Clin. Microbiol. 40:1368-1375(2002).
RL EMBL; AY007406; BAG28865.1; -.
DR HSSP; P17378; IN35.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13377 MW; EA44987393D246CA CRC64;

Query Match 64.4%; Score 38; DB 2; Length 121;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
DB 96 NYVCQGGD 103

RESULT 49

Q8V181 PRELIMINARY; PRT; 121 AA.
AC Q8V181;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lambda 3 protein (Fragment).
OS Reovirus sp.
OC Viruses; deRNA viruses; Reoviridae; unclassified Reoviridae.
OX NCBI_TaxID=10891;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21920879; PubMed=11923358;
RA Leary T.P., Erker J.C., Chalmers M.L., Cruz A.T., Wetzel J.D.,
RA Desai S.M., Mushahwar I.K., Dermody T.S.;
RT "Detection of mammalian reovirus RNA by using reverse transcription-
PCR: sequence diversity within the lambda3-encoding L1 gene.";
RL J. Clin. Microbiol. 40:1368-1375(2002).
RL EMBL; AY007405; BAG28864.1; -.
DR HSSP; P17378; IN35.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13377 MW; EA44987393D246CA CRC64;

Query Match 64.4%; Score 38; DB 2; Length 121;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 NYRCRGDD 8
DB 96 NYVCQGGD 103

RESULT 50

Q8V182 PRELIMINARY; PRT; 121 AA.
AC Q8V182;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lambda 3 protein (Fragment).
OS Reovirus sp.
OC Viruses; deRNA viruses; Reoviridae; unclassified Reoviridae.
OX NCBI_TaxID=10891;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21920879; PubMed=11923358;
RA Leary T.P., Erker J.C., Chalmers M.L., Cruz A.T., Wetzel J.D.,
RA Desai S.M., Mushahwar I.K., Dermody T.S.;
RT "Detection of mammalian reovirus RNA by using reverse transcription-
PCR: sequence diversity within the lambda3-encoding L1 gene.";
RL J. Clin. Microbiol. 40:1368-1375(2002).
RL EMBL; AY007404; BAG28863.1; -.
DR HSSP; P17378; IN35.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13377 MW; EA44987393D246CA CRC64;

Query Match 64.4%; Score 38; DB 2; Length 121;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
DB 96 NYVCQGGD 103

Search completed: September 7, 2005, 19:57:27
Job time : 50.1163 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 7, 2005, 19:44:24 ; Search time 12.5581 Seconds
(without alignments)
59.443 Million cell updates/sec

Title: US-10-812-238B-20

Perfect score: 59

Sequence: 1 NYRCRDDSK 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	233	4	US-09-360-376-55
2	40	67.8	424	4	US-09-489-039A-12030
3	40	67.8	705	4	US-08-311-731A-4
4	39	66.1	501	4	US-09-270-767-41177
5	39	66.1	501	4	US-09-270-767-56393
6	37	62.7	275	4	US-09-489-039A-11789
7	37	62.7	488	4	US-09-489-039A-13164
8	36	61.0	416	4	US-09-949-016-8237
9	26	61.0	498	4	US-09-786-240-1
10	35	59.3	94	4	US-09-198-452A-1290
11	35	59.3	269	4	US-10-000-489-78
12	35	59.3	269	4	US-09-949-016-6121
13	35	59.3	276	4	US-09-949-016-7261
14	35	59.3	439	3	US-08-985-950-12
15	35	59.3	439	3	US-09-310-463-8
16	35	59.3	439	4	US-08-842-248A-8
17	35	59.3	439	4	US-09-546-049-12
18	35	59.3	503	4	US-09-248-796A-17110
19	35	59.3	621	2	US-08-419-652-4
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22	35	59.3	662	1	US-08-248-532-2
23	35	59.3	662	2	US-08-419-652-2
24	35	59.3	662	2	US-08-685-118-4
25	35	59.3	662	2	US-08-915-495-4
26	35	59.3	662	2	US-08-914-520-4
27	35	59.3	662	3	US-08-789-350-2
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28	59.3	662	4	US-09-949-016-6624	Sequence 5624, Ap
29	59.3	683	4	US-09-949-016-10092	Sequence 10092, A
30	59.3	700	4	US-09-252-991A-23746	Sequence 23746, A
31	57.6	163	4	US-09-252-991A-18617	Sequence 18617, A
32	57.6	272	4	US-09-489-039A-13748	Sequence 13748, A
33	57.6	280	4	US-09-601-478-5	Sequence 5, Appl
34	57.6	280	4	US-09-601-478-8	Sequence 8, Appl
35	57.6	280	4	US-09-442-013-13	Sequence 13, Appl
36	57.6	280	4	US-09-513-365A-1	Sequence 1, Appl
37	57.6	280	4	US-09-513-365A-6	Sequence 6, Appl
38	57.6	289	4	US-09-902-540-15729	Sequence 15729, A
39	57.6	316	4	US-09-583-110-4948	Sequence 4948, Ap
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41	57.6	328	4	US-09-252-991A-30671	Sequence 30671, A
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43	57.6	447	3	US-09-627-376-10	Sequence 10, Appl
44	57.6	447	4	US-10-047-676B-10	Sequence 10, Appl
45	57.6	971	3	US-09-107-149-19	Sequence 19, Appl
46	57.6	1036	3	US-08-968-752B-4	Sequence 4, Appl
47	57.6	1036	3	US-09-536-224-4	Sequence 4, Appl
48	57.6	1074	2	US-08-768-147B-2	Sequence 2, Appl
49	57.6	1074	3	US-08-968-752B-2	Sequence 2, Appl
50	57.6	1074	3	US-09-107-149-3	Sequence 3, Appl
51	57.6	1074	3	US-09-536-224-2	Sequence 2, Appl
52	57.6	1086	4	US-09-949-016-11159	Sequence 11159, A
53	55.9	103	4	US-09-107-532A-7072	Sequence 7072, Ap
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55	55.9	174	4	US-09-107-532A-4715	Sequence 4715, Ap
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57	55.9	201	3	US-09-515-311-12	Sequence 12, Appl
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59	55.9	236	4	US-09-515-311-7	Sequence 7, Appl
60	55.9	253	3	US-09-252-991A-32459	Sequence 32459, A
61	55.9	255	3	US-09-015-734-2	Sequence 2, Appl
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68	55.9	686	4	US-09-253-991A-18115	Sequence 18115, A
69	55.9	730	1	US-08-121-713D-58	Sequence 58, Appl
70	55.9	730	1	US-08-835-268-58	Sequence 58, Appl
71	55.9	730	2	US-09-060-692-58	Sequence 58, Appl
72	55.9	730	3	US-08-833-391-58	Sequence 58, Appl
73	55.9	730	3	US-09-060-610-58	Sequence 58, Appl
74	55.9	730	5	PCT-US94-10151A-58	Sequence 58, Appl
75	55.9	800	4	US-09-489-039A-7191	Sequence 7191, Ap
76	55.9	819	4	US-09-949-016-11044	Sequence 11044, A
77	55.9	825	4	US-09-489-039A-8469	Sequence 8469, Ap
78	55.9	837	4	US-09-949-016-6515	Sequence 6515, Ap
79	54.2	7	1	US-08-421-702A-17	Sequence 17, Appl
80	54.2	7	1	US-08-303-052A-17	Sequence 17, Appl
81	54.2	7	1	US-08-421-696A-17	Sequence 17, Appl
82	54.2	7	1	US-08-421-697A-17	Sequence 17, Appl
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86	54.2	9	1	US-08-421-702A-26	Sequence 26, Appl
87	54.2	9	1	US-08-421-696A-26	Sequence 26, Appl
88	54.2	9	1	US-08-421-697A-26	Sequence 26, Appl
89	54.2	9	1	US-08-421-698A-26	Sequence 26, Appl
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93	54.2	35	3	US-08-857-076-30	Sequence 30, Appl
94	54.2	43	3	US-08-857-076-28	Sequence 28, Appl
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96	54.2	90	4	US-09-270-767-31781	Sequence 31781, A
97	54.2	90	4	US-09-270-767-38050	Sequence 38050,

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102	32	54.2	118	4	US-08-794-028B-21	Sequence 21, Appl	175	32	54.2	214	3	US-08-846-790A-1	Sequence 1, Appli
103	32	54.2	118	4	US-08-794-028B-22	Sequence 22, Appl	176	32	54.2	214	3	US-08-935-333-1	Sequence 1, Appli
104	32	54.2	119	3	US-08-753-642-2	Sequence 2, Appli	177	32	54.2	229	4	US-09-252-991A-22195	Sequence 22195, A
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106	32	54.2	120	1	US-08-440-049-1	Sequence 1, Appli	179	32	54.2	241	1	US-08-451-947-5	Sequence 5, Appli
107	32	54.2	120	1	US-08-440-049-3	Sequence 3, Appli	180	32	54.2	241	2	US-08-424-826A-5	Sequence 5, Appli
108	32	54.2	120	2	US-08-441-513A-1	Sequence 1, Appli	181	32	54.2	241	2	US-08-595-043A-75	Sequence 75, Appl
109	32	54.2	120	2	US-08-441-513A-3	Sequence 3, Appli	182	32	54.2	241	3	US-08-970-865-1	Sequence 1, Appli
110	32	54.2	120	3	US-08-970-865-2	Sequence 2, Appli	183	32	54.2	241	3	US-08-928-694-5	Sequence 5, Appli
111	32	54.2	120	3	US-08-970-865-3	Sequence 3, Appli	184	32	54.2	241	3	US-09-363-573-1	Sequence 1, Appli
112	32	54.2	120	3	US-08-581-662-31	Sequence 31, Appl	185	32	54.2	241	3	US-09-447-356-3	Sequence 3, Appli
113	32	54.2	120	3	US-09-363-573-2	Sequence 2, Appli	186	32	54.2	241	4	US-08-450-842-5	Sequence 5, Appli
114	32	54.2	120	3	US-09-363-573-3	Sequence 3, Appli	187	32	54.2	241	4	US-08-451-390-5	Sequence 5, Appli
115	32	54.2	120	3	US-08-845-541B-1	Sequence 1, Appli	188	32	54.2	241	4	US-09-620-174-2	Sequence 2, Appli
116	32	54.2	120	3	US-08-845-541B-3	Sequence 3, Appli	189	32	54.2	241	5	PCT-US91-06950-5	Sequence 5, Appli
117	32	54.2	120	3	US-08-845-541B-4	Sequence 4, Appli	190	32	54.2	241	5	PCT-US95-05423-4	Sequence 4, Appli
118	32	54.2	120	3	US-08-845-541B-5	Sequence 5, Appli	191	32	54.2	242	4	US-09-675-503-1	Sequence 1, Appli
119	32	54.2	120	3	US-08-845-541B-6	Sequence 6, Appli	192	32	54.2	242	4	US-10-072-681-1	Sequence 1, Appli
120	32	54.2	120	3	US-08-845-541B-7	Sequence 7, Appli	193	32	54.2	247	4	US-09-368-819A-2	Sequence 2, Appli
121	32	54.2	120	3	US-08-845-541B-8	Sequence 8, Appli	194	32	54.2	264	4	US-09-368-819A-4	Sequence 4, Appli
122	32	54.2	120	3	US-08-845-541B-9	Sequence 9, Appli	195	32	54.2	280	4	US-09-252-991A-18217	Sequence 18217, A
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126	32	54.2	120	3	US-08-845-541B-13	Sequence 13, Appl	199	32	54.2	350	4	US-10-200-344-12	Sequence 12, Appl
127	32	54.2	120	3	US-08-845-541B-17	Sequence 17, Appl	200	32	54.2	369	4	US-09-252-991A-25394	Sequence 25394, A
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129	32	54.2	120	3	US-08-845-541B-19	Sequence 19, Appl	202	32	54.2	390	3	US-08-993-380-4	Sequence 4, Appli
130	32	54.2	120	3	US-08-845-541B-20	Sequence 20, Appl	203	32	54.2	410	4	US-09-252-991A-31174	Sequence 31174, A
131	32	54.2	120	3	US-08-845-541B-21	Sequence 21, Appl	204	32	54.2	437	4	US-09-675-305-10	Sequence 10, Appl
132	32	54.2	120	3	US-09-066-065A-1	Sequence 1, Appli	205	32	54.2	437	4	US-10-200-344-10	Sequence 10, Appl
133	32	54.2	120	3	US-09-066-065A-3	Sequence 3, Appli	206	32	54.2	508	4	US-09-858-664A-18	Sequence 18, Appl
134	32	54.2	120	3	US-09-066-065A-4	Sequence 4, Appli	207	32	54.2	508	4	US-10-274-978-19	Sequence 19, Appl
135	32	54.2	120	3	US-09-066-065A-5	Sequence 5, Appli	208	32	54.2	508	4	US-10-697-263-19	Sequence 19, Appl
136	32	54.2	120	3	US-09-066-065A-6	Sequence 6, Appli	209	32	54.2	539	2	US-08-978-182-3	Sequence 3, Appli
137	32	54.2	120	3	US-09-066-065A-7	Sequence 7, Appli	210	32	54.2	539	2	US-09-205-681-3	Sequence 3, Appli
138	32	54.2	120	3	US-09-066-065A-8	Sequence 8, Appli	211	32	54.2	556	4	US-09-252-991A-26282	Sequence 26282, A
139	32	54.2	120	3	US-09-066-065A-9	Sequence 9, Appli	212	32	54.2	714	4	US-09-328-352-5347	Sequence 5347, Ap
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141	32	54.2	120	3	US-09-066-065A-11	Sequence 11, Appl	214	32	54.2	1429	2	US-08-365-486A-13	Sequence 13, Appl
142	32	54.2	120	3	US-09-066-065A-12	Sequence 12, Appl	215	32	54.2	1429	2	US-08-319-866-11	Sequence 11, Appl
143	32	54.2	120	3	US-09-066-065A-13	Sequence 13, Appl	216	32	54.2	1429	3	US-08-880-342-13	Sequence 13, Appl
144	32	54.2	120	3	US-09-066-065A-17	Sequence 17, Appl	217	32	54.2	1429	3	US-09-661-258-2	Sequence 2, Appli
145	32	54.2	120	3	US-09-066-065A-18	Sequence 18, Appl	218	32	54.2	1429	4	US-08-809-917-11	Sequence 11, Appl
146	32	54.2	120	3	US-09-066-065A-19	Sequence 19, Appl	219	32	54.2	1430	2	US-08-705-625-4	Sequence 4, Appli
147	32	54.2	120	3	US-09-066-065A-20	Sequence 20, Appl	220	32	54.2	1430	3	US-09-010-998-5	Sequence 5, Appli
148	32	54.2	120	3	US-09-066-065A-21	Sequence 21, Appl	221	32	54.2	1430	3	US-09-220-574-4	Sequence 4, Appli
149	32	54.2	120	3	US-09-447-356-1	Sequence 1, Appli	222	32	54.2	1433	2	US-08-365-486A-21	Sequence 21, Appl
150	32	54.2	120	4	US-09-664-295-31	Sequence 31, Appl	223	32	54.2	1433	3	US-09-123-708-4	Sequence 4, Appli
151	32	54.2	120	4	US-08-794-028B-1	Sequence 1, Appli	224	32	54.2	1433	3	US-09-123-624-4	Sequence 4, Appli
152	32	54.2	120	4	US-08-794-028B-3	Sequence 3, Appli	225	32	54.2	1433	3	US-08-880-342-21	Sequence 21, Appl
153	32	54.2	120	5	PCT-US93-11282-1	Sequence 1, Appli	226	32	54.2	1434	2	US-08-365-486A-19	Sequence 19, Appl
154	32	54.2	120	5	PCT-US95-06918-1	Sequence 1, Appli	227	32	54.2	1434	3	US-08-880-342-19	Sequence 19, Appl
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156	32	54.2	121	4	US-09-675-503-2	Sequence 2, Appli	229	32	54.2	1434	4	US-09-538-092-1034	Sequence 1034, Ap
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158	32	54.2	121	4	US-10-072-681-2	Sequence 2, Appli	231	32	54.2	1554	3	US-08-705-625-3	Sequence 3, Appli
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160	32	54.2	125	4	US-09-489-039A-11259	Sequence 11259, A	233	32	54.2	1554	3	US-09-220-574-3	Sequence 3, Appli
161	32	54.2	153	4	US-09-675-922-2	Sequence 2, Appli	234	32	54.2	9	1	US-08-482-106-12	Sequence 12, Appl
162	32	54.2	155	4	US-09-270-767-36322	Sequence 36322, A	235	31	52.5	45	6	5240706-3	Patent No. 5240706
163	32	54.2	155	4	US-09-270-767-51539	Sequence 51539, A	236	31	52.5	45	6	5240706-3	Patent No. 5240706
164	32	54.2	157	4	US-09-675-922-4	Sequence 4, Appli	237	31	52.5	98	4	US-09-198-452A-1291	Sequence 1291, Ap
165	32	54.2	163	4	US-09-675-922-6	Sequence 6, Appli	238	31	52.5	100	4	US-09-621-976-6277	Sequence 6277, Ap
166	32	54.2	164	4	US-09-949-016-10989	Sequence 10989, A	239	31	52.5	107	4	US-09-484-577A-86	Sequence 86, Appl
167	32	54.2	167	4	US-09-675-922-8	Sequence 8, Appli	240	31	52.5	115	4	US-09-270-767-40288	Sequence 40288, A
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172	32	54.2	171	4	US-09-949-016-10669	Sequence 10669, A	245	31	52.5	182	2	US-08-284-391B-25	Sequence 25, Appl
173	32	54.2	171	5	PCT-US92-01785-24	Sequence 24, Appl	246	31	52.5	182	3	US-09-218-950-25	Sequence 25, Appl

247	31	52.5	182	4	US-08-394-388A-25	Sequence 25, Appl	320	30	50.8	160	2	US-08-448-438-6	Sequence 6, Appli
248	31	52.5	182	5	PCT-US92-01785-25	Sequence 25, Appl	321	30	50.8	160	2	US-08-448-438-7	Sequence 7, Appli
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255	31	52.5	265	4	US-09-252-991A-32218	Sequence 32218, A	328	30	50.8	210	2	US-09-258-371-2	Sequence 2, Appli
256	31	52.5	301	4	US-09-252-991A-17405	Sequence 17405, A	329	30	50.8	210	3	US-08-569-721A-2	Sequence 2, Appli
257	31	52.5	302	4	US-08-311-731A-206	Sequence 206, App	330	30	50.8	210	3	US-08-751-230-2	Sequence 2, Appli
258	31	52.5	338	4	US-09-248-796A-17967	Sequence 17967, A	331	30	50.8	210	3	US-09-499-082-2	Sequence 2, Appli
259	31	52.5	340	4	US-09-489-039A-11464	Sequence 11464, A	332	30	50.8	210	3	US-09-258-372-2	Sequence 2, Appli
260	31	52.5	341	4	US-09-252-991A-16890	Sequence 16890, A	333	30	50.8	210	3	US-09-006-783A-7	Sequence 7, Appli
261	31	52.5	347	3	US-09-259-369-2	Sequence 2, Appli	334	30	50.8	210	3	US-09-159-871-13	Sequence 13, Appl
262	31	52.5	364	4	US-09-328-352-4659	Sequence 4659, Ap	335	30	50.8	210	4	US-09-532-868-2	Sequence 2, Appli
263	31	52.5	374	4	US-09-252-991A-17863	Sequence 17863, A	336	30	50.8	210	4	US-09-451-739H-6	Sequence 6, Appli
264	31	52.5	374	4	US-09-252-991A-23565	Sequence 23565, A	337	30	50.8	217	4	US-09-369-247-113	Sequence 113, App
265	31	52.5	385	4	US-09-489-039A-10159	Sequence 10159, A	338	30	50.8	225	4	US-09-673-395A-354	Sequence 354, App
266	31	52.5	401	3	US-09-005-298-17	Sequence 17, Appl	339	30	50.8	230	4	US-09-252-991A-22765	Sequence 22765, A
267	31	52.5	401	4	US-08-768-619-17	Sequence 17, Appl	340	30	50.8	235	4	US-09-451-739H-7	Sequence 7, Appli
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271	31	52.5	407	5	PCT-US96-09848-15	Sequence 15, Appl	344	30	50.8	269	4	US-09-159-871-11	Sequence 11, Appl
272	31	52.5	450	4	US-09-252-991A-18376	Sequence 18376, A	345	30	50.8	270	3	US-09-085-305-16	Sequence 16, Appl
273	31	52.5	450	4	US-09-252-991A-25835	Sequence 25835, A	346	30	50.8	270	3	US-09-085-305-19	Sequence 19, Appl
274	31	52.5	475	4	US-09-302-540-15337	Sequence 15337, A	347	30	50.8	278	4	US-09-248-796A-16036	Sequence 16036, A
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276	31	52.5	495	3	US-09-249-200-2	Sequence 2, Appli	349	30	50.8	279	4	US-09-442-013-11	Sequence 11, Appl
277	31	52.5	520	2	US-08-794-795-6	Sequence 6, Appli	350	30	50.8	279	4	US-09-451-739H-5	Sequence 5, Appli
278	31	52.5	520	3	US-09-249-200-6	Sequence 6, Appli	351	30	50.8	279	4	US-09-513-365A-8	Sequence 8, Appli
279	31	52.5	521	3	US-09-252-991A-18266	Sequence 18266, A	352	30	50.8	282	4	US-09-360-376-54	Sequence 54, Appl
280	31	52.5	562	3	US-09-012-515A-14	Sequence 14, Appl	353	30	50.8	282	4	US-09-270-767-41831	Sequence 41831, A
281	31	52.5	562	3	US-08-360-144A-14	Sequence 14, Appl	354	30	50.8	283	4	US-09-258-371-10	Sequence 10, Appl
282	31	52.5	562	4	US-09-012-504A-14	Sequence 14, Appl	355	30	50.8	294	2	US-08-751-230-10	Sequence 10, Appl
283	31	52.5	562	4	US-09-012-399A-14	Sequence 14, Appl	356	30	50.8	294	3	US-09-499-082-10	Sequence 10, Appl
284	31	52.5	562	5	PCT-US95-06722-14	Sequence 14, Appl	357	30	50.8	294	3	US-09-258-372-10	Sequence 10, Appl
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286	31	52.5	625	4	US-09-252-991A-19871	Sequence 19871, A	359	30	50.8	294	3	US-09-159-871-2	Sequence 2, Appli
287	31	52.5	718	4	US-09-252-991A-25696	Sequence 25696, A	360	30	50.8	294	4	US-09-442-013-12	Sequence 12, Appl
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289	30	50.8	24	2	US-09-369-247-118	Sequence 118, App	362	30	50.8	294	4	US-09-451-739H-19	Sequence 19, Appl
290	30	50.8	29	2	US-08-620-151-71	Sequence 71, Appl	363	30	50.8	294	4	US-09-902-540-14353	Sequence 14353, A
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292	30	50.8	29	1	US-07-602-847C-16	Sequence 16, Appl	365	30	50.8	301	4	US-09-252-991A-27921	Sequence 27921, A
293	30	50.8	39	3	US-08-817-787-32	Sequence 32, Appl	366	30	50.8	308	4	US-08-485-511A-4	Sequence 4, Appli
294	30	50.8	39	4	US-09-583-808-32	Sequence 32, Appl	367	30	50.8	321	3	US-09-949-016-8302	Sequence 8302, Ap
295	30	50.8	41	3	US-08-817-787-36	Sequence 36, Appl	368	30	50.8	357	4	US-09-949-016-8624	Sequence 8624, Ap
296	30	50.8	41	4	US-09-583-808-36	Sequence 36, Appl	369	30	50.8	360	2	US-08-506-864A-1	Sequence 1, Appli
297	30	50.8	42	3	US-08-817-787-34	Sequence 34, Appl	370	30	50.8	375	2	US-09-252-991A-29934	Sequence 29934, A
298	30	50.8	42	4	US-08-358-160-126	Sequence 126, App	371	30	50.8	377	4	US-08-851-968-1	Sequence 1, Appli
299	30	50.8	57	1	US-08-358-160-126	Sequence 126, App	372	30	50.8	377	4	US-09-949-016-8302	Sequence 8302, Ap
300	30	50.8	60	4	US-08-469-260A-450	Sequence 450, App	373	30	50.8	379	4	US-09-345-828-2	Sequence 2, Appli
301	30	50.8	60	4	US-08-488-446-450	Sequence 450, App	374	30	50.8	389	4	US-09-949-016-9951	Sequence 9951, Ap
302	30	50.8	60	4	US-08-467-344A-450	Sequence 450, App	375	30	50.8	395	4	US-09-949-016-9496	Sequence 9496, Ap
303	30	50.8	60	4	US-08-424-550B-450	Sequence 450, App	376	30	50.8	406	4	US-09-543-681A-7962	Sequence 7962, Ap
304	30	50.8	92	4	US-09-302-540-14307	Sequence 14307, A	377	30	50.8	412	4	US-09-252-991A-30352	Sequence 30352, A
305	30	50.8	97	4	US-09-370-767-57075	Sequence 57075, A	378	30	50.8	416	4	US-09-949-016-6648	Sequence 6648, Ap
306	30	50.8	99	4	US-09-621-976-4220	Sequence 4220, Ap	379	30	50.8	417	3	US-08-705-771-18	Sequence 18, Appl
307	30	50.8	132	4	US-09-252-991A-30452	Sequence 30452, A	380	30	50.8	417	4	US-09-417-540-18	Sequence 18, Appl
308	30	50.8	137	3	US-09-188-930-174	Sequence 174, App	381	30	50.8	428	1	US-07-973-324A-4	Sequence 4, Appli
309	30	50.8	137	4	US-09-312-283C-174	Sequence 174, App	382	30	50.8	428	1	US-08-343-380-4	Sequence 4, Appli
310	30	50.8	141	1	US-07-695-564-5	Sequence 5, Appli	383	30	50.8	428	3	US-09-072-435-4	Sequence 4, Appli
311	30	50.8	141	1	US-08-241-387-5	Sequence 5, Appli	384	30	50.8	428	3	US-09-072-917A-4	Sequence 4, Appli
312	30	50.8	142	2	US-08-448-438-1	Sequence 1, Appli	385	30	50.8	433	3	US-09-697-367-22	Sequence 22, Appl
313	30	50.8	142	2	US-08-448-438-2	Sequence 2, Appli	386	30	50.8	433	3	US-09-918-909A-22	Sequence 22, Appl
314	30	50.8	142	2	US-08-448-438-3	Sequence 3, Appli	387	30	50.8	434	1	US-07-923-692C-6	Sequence 6, Appli
315	30	50.8	149	1	US-07-695-564-7	Sequence 7, Appli	388	30	50.8	434	1	US-08-184-237-6	Sequence 6, Appli
316	30	50.8	149	1	US-08-241-387-7	Sequence 7, Appli	389	30	50.8	434	2	US-08-483-920-6	Sequence 6, Appli
317	30	50.8	156	1	US-07-766-682A-3	Sequence 3, Appli	390	30	50.8	434	3	US-08-484-341-6	Sequence 6, Appli
318	30	50.8	156	4	US-09-398-412B-6	Sequence 6, Appli	391	30	50.8	434	3	US-08-483-502-6	Sequence 6, Appli
319	30	50.8	160	2	US-08-448-438-5	Sequence 5, Appli	392	30	50.8	434	4	US-09-726-651A-6	Sequence 6, Appli

393	30	50.8	437	4	US-09-918-909A-28	Sequence 28, Appl	466	29	49.2	80	4	US-09-134-000C-5829	Sequence 5829, Ap
394	30	50.8	440	4	US-09-902-540-9852	Sequence 9852, Ap	467	29	49.2	82	4	US-09-134-000C-6553	Sequence 6553, Ap
395	30	50.8	441	4	US-09-949-016-9778	Sequence 9778, Ap	468	29	49.2	83	4	US-09-107-433-4178	Sequence 4178, Ap
396	30	50.8	461	4	US-09-252-991A-28623	Sequence 28623, A	469	29	49.2	99	4	US-09-489-039A-7470	Sequence 7470, Ap
397	30	50.8	469	4	US-09-452-991A-26584	Sequence 26584, A	470	29	49.2	101	1	US-08-335-583C-54	Sequence 54, Appl
398	30	50.8	471	4	US-09-902-540-11973	Sequence 11973, A	471	29	49.2	101	3	US-08-931-858E-155	Sequence 155, App
399	30	50.8	483	4	US-09-905-999-20	Sequence 20, Appl	472	29	49.2	101	3	US-08-981-739-155	Sequence 155, App
400	30	50.8	502	2	US-08-459-818-19	Sequence 19, Appl	473	29	49.2	101	4	US-09-128-026-155	Sequence 155, App
401	30	50.8	502	2	US-08-889-666-19	Sequence 19, Appl	474	29	49.2	101	4	US-09-220-616-155	Sequence 155, App
402	30	50.8	502	2	US-08-465-078-19	Sequence 19, Appl	475	29	49.2	101	4	US-09-220-527-155	Sequence 155, App
403	30	50.8	502	2	US-08-725-776-19	Sequence 19, Appl	476	29	49.2	101	4	US-09-220-407-155	Sequence 155, App
404	30	50.8	502	2	US-08-488-062-19	Sequence 19, Appl	477	29	49.2	105	4	US-09-489-039A-13562	Sequence 13562, A
405	30	50.8	517	4	US-09-252-991A-22249	Sequence 22249, A	478	29	49.2	118	3	US-08-624-635-21	Sequence 21, Appl
406	30	50.8	596	4	US-09-902-540-13547	Sequence 13547, A	479	29	49.2	120	4	US-09-513-999C-6407	Sequence 6407, Ap
407	30	50.8	597	4	US-09-949-016-7800	Sequence 7800, Ap	480	29	49.2	122	4	US-09-775-932-10	Sequence 10, Appl
408	30	50.8	615	4	US-09-540-236-2639	Sequence 2639, Ap	481	29	49.2	124	4	US-09-252-991A-29290	Sequence 29290, A
409	30	50.8	673	4	US-09-538-092-1270	Sequence 1270, Ap	482	29	49.2	124	4	US-09-621-976-4699	Sequence 4699, Ap
410	30	50.8	717	6	5262177-5	Patent No. 5262177	483	29	49.2	126	2	US-08-482-728A-15	Sequence 15, Appl
411	30	50.8	717	6	5262177-5	Patent No. 5262177	484	29	49.2	126	4	US-08-849-303-27	Sequence 27, Appl
412	30	50.8	719	4	US-08-520-933-3	Sequence 3, Appl	485	29	49.2	131	4	US-09-621-976-5011	Sequence 5011, Ap
413	30	50.8	719	4	US-09-285-040-3	Sequence 3, Appl	486	29	49.2	136	4	US-09-690-454-131	Sequence 131, App
414	30	50.8	738	6	5262177-2	Patent No. 5262177	487	29	49.2	137	4	US-09-270-767-53045	Sequence 53045, A
415	30	50.8	738	6	5262177-2	Patent No. 5262177	488	29	49.2	138	4	US-09-540-236-2621	Sequence 2621, Ap
416	30	50.8	776	4	US-09-949-016-10829	Sequence 10829, A	489	29	49.2	138	4	US-09-270-767-34849	Sequence 34849, A
417	30	50.8	777	4	US-09-270-767-44409	Sequence 44409, A	490	29	49.2	138	4	US-09-270-767-50066	Sequence 50066, A
418	30	50.8	911	4	US-09-252-991A-25237	Sequence 25237, A	491	29	49.2	139	4	US-09-270-767-34282	Sequence 34282, A
419	30	50.8	943	4	US-09-623-624-4	Sequence 4, Appl	492	29	49.2	139	4	US-09-270-767-49499	Sequence 49499, A
420	30	50.8	943	4	US-10-270-595-4	Sequence 4, Appl	493	29	49.2	142	3	US-08-744-138-4	Sequence 4, Appl
421	30	50.8	964	4	US-09-556-877-177	Sequence 177, App	494	29	49.2	142	3	US-09-431-480-7	Sequence 7, Appl
422	30	50.8	964	4	US-09-620-413C-177	Sequence 177, App	495	29	49.2	142	3	US-09-617-302-7	Sequence 7, Appl
423	30	50.8	964	4	US-09-598-419-177	Sequence 177, App	496	29	49.2	142	3	US-09-241-376-4	Sequence 4, Appl
424	30	50.8	977	4	US-09-556-877-191	Sequence 191, App	497	29	49.2	142	4	US-09-940-497-4	Sequence 4, Appl
425	30	50.8	977	4	US-09-620-413C-191	Sequence 191, App	498	29	49.2	142	4	US-09-976-594-358	Sequence 358, App
426	30	50.8	977	4	US-09-598-419-191	Sequence 191, App	499	29	49.2	142	4	US-08-849-303-20	Sequence 20, Appl
427	30	50.8	1073	1	US-07-695-564-1	Sequence 1, Appl	500	29	49.2	145	2	US-08-788-584-5	Sequence 5, Appl
428	30	50.8	1073	1	US-08-241-387-1	Sequence 1, Appl							
429	30	50.8	1091	1	US-07-695-564-3	Sequence 3, Appl							
430	30	50.8	1091	1	US-08-241-387-3	Sequence 3, Appl							
431	30	50.8	1205	4	US-09-491-522-11	Sequence 11, Appl							
432	30	50.8	1248	4	US-09-949-016-10595	Sequence 10595, A							
433	30	50.8	1248	4	US-09-949-016-10596	Sequence 10596, A							
434	30	50.8	1338	4	US-09-949-016-6029	Sequence 6029, Ap							
435	30	50.8	3924	4	US-09-538-092-1246	Sequence 1246, Ap							
436	30	50.8	4544	1	US-08-469-486-52	Sequence 52, Appl							
437	30	50.8	4544	2	US-08-469-658-52	Sequence 52, Appl							
438	29	49.2	7	1	US-08-421-702A-8	Sequence 8, Appl							
439	29	49.2	7	1	US-08-421-696A-8	Sequence 8, Appl							
440	29	49.2	7	1	US-08-421-697A-8	Sequence 8, Appl							
441	29	49.2	7	1	US-08-421-698A-8	Sequence 8, Appl							
442	29	49.2	7	1	US-08-421-695A-8	Sequence 8, Appl							
443	29	49.2	7	5	PCT-US95-04741-8	Sequence 8, Appl							
444	29	49.2	34	4	US-09-270-767-34502	Sequence 34502, A							
445	29	49.2	34	4	US-09-270-767-49719	Sequence 49719, A							
446	29	49.2	46	3	US-09-257-218-16	Sequence 16, Appl							
447	29	49.2	46	3	US-09-311-760-16	Sequence 16, Appl							
448	29	49.2	46	4	US-08-865-579-16	Sequence 16, Appl							
449	29	49.2	46	4	US-10-059-749-16	Sequence 16, Appl							
450	29	49.2	56	3	US-08-711-417C-186	Sequence 186, App							
451	29	49.2	56	3	US-08-711-417C-187	Sequence 187, App							
452	29	49.2	56	3	US-08-711-417C-188	Sequence 188, App							
453	29	49.2	56	3	US-08-711-417C-189	Sequence 189, App							
454	29	49.2	56	3	US-09-187-789-58	Sequence 58, Appl							
455	29	49.2	56	4	US-09-139-600-53	Sequence 53, Appl							
456	29	49.2	56	4	US-09-723-909-186	Sequence 186, App							
457	29	49.2	56	4	US-09-723-909-187	Sequence 187, App							
458	29	49.2	56	4	US-09-723-909-188	Sequence 188, App							
459	29	49.2	56	4	US-09-723-909-189	Sequence 189, App							
460	29	49.2	56	4	US-09-989-903-58	Sequence 58, Appl							
461	29	49.2	64	4	US-09-328-352-5321	Sequence 5321, Ap							
462	29	49.2	66	4	US-09-270-767-58777	Sequence 58777, A							
463	29	49.2	68	4	US-09-248-796A-21682	Sequence 21682, A							
464	29	49.2	72	4	US-09-248-796A-23186	Sequence 23186, A							
465	29	49.2	73	4	US-09-248-796A-17432	Sequence 17432, A							

ALIGNMENTS

RESULT 1

US-09-360-376-55

; Sequence 55, Application US/09360376

; Patent No. 6495739

; GENERAL INFORMATION:

; APPLICANT: Lasner, Michael

; APPLICANT: Ruesinsky, Diane

; TITLE OF INVENTION: PLANT PHOSPHATIDIC ACID PHOSPHATASES

; FILE REFERENCE: 17026/01/US

; CURRENT APPLICATION NUMBER: US/09/360,376

; CURRENT FILING DATE: 1999-07-23

; PRIOR APPLICATION NUMBER: US 09/122,315

; PRIOR FILING DATE: 1998-07-24

; NUMBER OF SEQ ID NOS: 55

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 55

; LENGTH: 233

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-360-376-55

Query Match 100.0%; Score 59; DB 4; Length 233;

Best Local Similarity 100.0%; Pred. No. 0.023;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYRCRGDSK 10

Db 178 NYRCRGDSK 187

RESULT 2

US-09-489-039A-12030

; Sequence 12030, Application US/09489039A

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; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12030
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12030

Query Match 67.8%; Score 40; DB 4; Length 424;
Best Local Similarity 85.7%; Pred. No. 54;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
DB 63 FRCRGDD 69

RESULT 3
US-08-311-731A-4
; Sequence 4, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P. C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: MYCOBACTERIUM TUBERCULOSIS
US-08-311-731A-4

Query Match 67.8%; Score 40; DB 4; Length 705;
Best Local Similarity 66.7%; Pred. No. 88;

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Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YRCRGDDSK 10
DB 383 YRCRADDTTE 391

RESULT 4
US-09-270-767-41177
; Sequence 41177, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41177
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41177

Query Match 66.1%; Score 39; DB 4; Length 501;
Best Local Similarity 75.0%; Pred. No. 92;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YRCRGDDSS 9
DB 485 YRCRGDDSS 492

RESULT 5
US-09-270-767-56393
; Sequence 56393, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56393
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-56393

Query Match 66.1%; Score 39; DB 4; Length 501;
Best Local Similarity 75.0%; Pred. No. 92;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YRCRGDDSS 9
DB 485 YRCRGDDSS 492

RESULT 6
US-09-489-039A-11789
; Sequence 11789, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

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FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11789
LENGTH: 275
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11789

Query Match 62.7%; Score 37; DB 4; Length 275;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCGDDDS 9
Db 32 NWRCGGDS 40

RESULT 7
US-09-489-039A-13164
Sequence 13164, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13164
LENGTH: 488
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13164

Query Match 62.7%; Score 37; DB 4; Length 488;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RCRGDD 8
Db 102 RCRGDD 107

RESULT 8
US-09-949-016-8237
Sequence 8237, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8237
LENGTH: 416
TYPE: PRT
ORGANISM: Human

US-09-949-016-8237

Query Match 61.0%; Score 36; DB 4; Length 416;
Best Local Similarity 60.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
Db 400 NWRCPGTDSE 409

RESULT 9
US-09-786-240-1
Sequence 1, Application US/09786240
Patent No. 6558935
GENERAL INFORMATION:
APPLICANT: INCYTE PHARMACEUTICALS, INC.
APPLICANT: TANG, Y. Tom
APPLICANT: CORLEY, Neil C.
APPLICANT: GUEGLER, Karl J.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: LAL, Preeti
APPLICANT: YUE, Henry
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: AZIMZAI, Yalda
TITLE OF INVENTION: HUMAN TRANSFERASE PROTEINS
FILE REFERENCE: PF-0592 PCT
CURRENT APPLICATION NUMBER: US/09/786,240
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 09/150,657; unassigned; 09/186,779; unassigned; 60/133,642
PRIOR FILING DATE: 1998-09-10; 1998-09-10; 1998-11-04; 1998-11-04; 1999-05-11
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PERL Program
SEQ ID NO 1
LENGTH: 498
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6558935 1632930CD1
US-09-786-240-1

Query Match 61.0%; Score 36; DB 4; Length 498;
Best Local Similarity 60.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
Db 482 NWRCPGTDSE 491

RESULT 10
US-09-198-452A-1290
Sequence 1290, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffois, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1290
LENGTH: 94
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1290

Query Match 59.3%; Score 35; DB 4; Length 94;
Best Local Similarity 85.7%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1  NVRCRGD 7
      |||||
Db     13  NRRCRGD 19

RESULT 11
US-10-000-489-78
; Sequence 78, Application US/10000489
; Patent No. 6794363
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US6.DIV
; CURRENT APPLICATION NUMBER: US/10/000,489
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 78
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..21
US-10-000-489-78

Query Match      59.3%; Score 35; DB 4; Length 269;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2  YRCRGDDSK 10
      |||||
Db     183 YRCNGTSSK 191

RESULT 12
US-09-949-016-6121
; Sequence 6121, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6121
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6121

Query Match      59.3%; Score 35; DB 4; Length 269;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2  YRCRGDDSK 10
      |||||
Db     183 YRCNGTSSK 191

RESULT 13
US-09-949-016-7261
; Sequence 7261, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7261
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7261

Query Match      59.3%; Score 35; DB 4; Length 276;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2  YRCRGDDSK 10
      |||||
Db     190 YRCNGTSSK 198

RESULT 14
US-08-985-950-12
; Sequence 12, Application US/08985950
; Patent No. 6140076
; GENERAL INFORMATION:
; APPLICANT: Adema, Gosse Jan
; TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,950
; FILING DATE: 05-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,279
; FILING DATE: 21-MARCH-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,181
```

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/
/ FILING DATE: 16-DEC-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/032,252
/ FILING DATE: 06-DEC-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ching, Edwin P.
/ REGISTRATION NUMBER: 34,090
/ REFERENCE/DOCKET NUMBER: DX0670K
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650)852-9196
/ TELEFAX: (650)496-1204
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 439 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-985-950-12

Query Match 59.3%; Score 35; DB 3; Length 439;
Best Local Similarity 60.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
Db :||| |||
194 SYRCYGYSR 203

RESULT 15
US-09-310-463-8
/ Sequence 8, Application US/09310463A
/ Patent No. 6384203
/ GENERAL INFORMATION:
/ APPLICANT: Cosman, David J.
/ APPLICANT: Anderson, Dirk M.
/ APPLICANT: Borges, Luis
/ TITLE OF INVENTION: Family of Immunoregulators Designated Leukocyte Immunoglobulin-
/ TITLE OF INVENTION: Like Receptors (LIR)
/ FILE REFERENCE: 2624-A
/ CURRENT APPLICATION NUMBER: US/09/310,463A
/ CURRENT FILING DATE: 1999-05-12
/ EARLIER APPLICATION NUMBER: 08/842,248
/ EARLIER FILING DATE: 1997-04-24
/ NUMBER OF SEQ ID NOS: 39
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO: 8
/ LENGTH: 439
/ TYPE: PRT
/ ORGANISM: human
/ US-09-310-463-8

Query Match 59.3%; Score 35; DB 3; Length 439;
Best Local Similarity 60.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
Db :||| |||
194 SYRCYGYSR 203

RESULT 16
US-08-842-248A-8
/ Sequence 8, Application US/08842248A
/ Patent No. 6448035
/ GENERAL INFORMATION:
/ APPLICANT: Cosman, David J.
/ TITLE OF INVENTION: Family of Immunoregulators Designated
/ TITLE OF INVENTION: Leukocyte Immunoglobulin-Like Receptors (LIR)
/ NUMBER OF SEQUENCES: 29
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Janis C. Henry, Immunex Corporation
/ STREET: 51 University Street
/ CITY: Seattle
```

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/
/ STATE: WA
/ COUNTRY: US
/ ZIP: 98101
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM/PC Compatible
/ OPERATING SYSTEM: Microsoft Word 7.0
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/842,248A
/ FILING DATE: April 24, 1997
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Henry, Janis C.
/ REGISTRATION NUMBER: 34,347
/ REFERENCE/DOCKET NUMBER: 2624
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 587-0430
/ TELEFAX: (206) 233-0644
/ TELEX: 756822
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 439 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-842-248A-8

Query Match 59.3%; Score 35; DB 4; Length 439;
Best Local Similarity 60.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
Db :||| |||
194 SYRCYGYSR 203

RESULT 17
US-09-546-049-12
/ Sequence 12, Application US/09546049
/ Patent No. 6479638
/ GENERAL INFORMATION:
/ APPLICANT: Adema, Gosse Jan
/ APPLICANT: Meygaard, Linde
/ APPLICANT: Gorman, Daniel M.
/ APPLICANT: McClanahan, Terrill K.
/ APPLICANT: Zurawski, Sandra M.
/ APPLICANT: Zurawski, Gerard
/ APPLICANT: Lanier, Lewis L.
/ APPLICANT: Phillips Jr., Joseph H.
/ TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
/ RELATED REAGENTS
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: DNAX Research Institute
/ STREET: 901 California Avenue
/ CITY: Palo Alto
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94304-1104
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/546,049
/ FILING DATE: 10-Apr-2000
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/985,950
/ FILING DATE: 05-DEC-1997
/ APPLICATION NUMBER: US 60/041,279
/ FILING DATE: 21-MARCH-1997
```


APPLICATION NUMBER: US 60/033,181
FILING DATE: 16-DEC-1996
APPLICATION NUMBER: US 60/032,252
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0670K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1204
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 439 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-546-049-12

Query Match 59.3%; Score 35; DB 4; Length 439;
Best Local Similarity 60.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NYRCRGDDSK 10
Db 194 SYRCYGDSR 203

RESULT 18
US-09-248-796A-17110
Sequence 17110, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstein et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
PRIOR FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 17110
LENGTH: 503
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-17110

Query Match 59.3%; Score 35; DB 4; Length 503;
Best Local Similarity 66.7%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 YRCRGDDSK 10
Db 288 YRCFSDDDK 296

RESULT 19
US-08-419-652-4
Sequence 4, Application US/08419652
Patent No. 5831007
GENERAL INFORMATION:
APPLICANT: Chua, Anne O
APPLICANT: Gubler, Ulrich A
TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley

STATE: New Jersey
COUNTRY: United States of America
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,652
FILING DATE: 11-APR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,532
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/094,713
FILING DATE: 19-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: CD 9174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4205
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 621 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Region
LOCATION: 1..621
OTHER INFORMATION: /note: "Represents residues 42 to
US-08-419-652-4

Query Match 59.3%; Score 35; DB 2; Length 621;
Best Local Similarity 75.0%; Pred. No. 5.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RCRGDDSK 10
Db 443 RCRDEDSK 450

RESULT 20
US-08-248-532-3
Sequence 3, Application US/08248532
Patent No. 5536657
GENERAL INFORMATION:
APPLICANT: Chua, Anne O
APPLICANT: Gubler, Ulrich A
TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/248,532
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 08/094,713
; FILING DATE: 19-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kass, Alan P
; REGISTRATION NUMBER: 32142
; REFERENCE/DOCKET NUMBER: CD 8973
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-4205
; TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 660 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-248-532-3

Query Match 59.3%; Score 35; DB 1; Length 660;
Best Local Similarity 75.0%; Pred. No. 5.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 RCRGDSK 10
DB 484 RCRDEDSK 491

RESULT 21
US-08-419-652-3
; Sequence 3, Application US/08419652
; Patent No. 5831007
; GENERAL INFORMATION:
; APPLICANT: Chua, Anne O
; APPLICANT: Gubler, Ulrich A
; TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,652
; FILING DATE: 11-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,532
; FILING DATE: 31-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/094,713
; FILING DATE: 19-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kass, Alan P
; REGISTRATION NUMBER: 32142
; REFERENCE/DOCKET NUMBER: CD 9174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-4205
; TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 660 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-419-652-3

Query Match 59.3%; Score 35; DB 2; Length 660;

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Best Local Similarity 75.0%; Pred. No. 5.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 RCRGDSK 10
DB 484 RCRDEDSK 491

RESULT 22
US-08-248-532-2
; Sequence 2, Application US/08248532
; Patent No. 5536657
; GENERAL INFORMATION:
; APPLICANT: Chua, Anne O
; APPLICANT: Gubler, Ulrich A
; TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248,532
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/094,713
; FILING DATE: 19-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kass, Alan P
; REGISTRATION NUMBER: 32142
; REFERENCE/DOCKET NUMBER: CD 8973
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-4205
; TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 662 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..23
; OTHER INFORMATION: /note= "N-terminal signal peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 541..570
; OTHER INFORMATION: /note= "transmembrane region"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 571..662
; OTHER INFORMATION: /note= "cytoplasmic tail region"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 577..584
; OTHER INFORMATION: /note= "conserved area of cytoplasmic
; OTHER INFORMATION: tail region"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 618..629
; OTHER INFORMATION: /note= "conserved area of cytoplasmic
; OTHER INFORMATION: tail region"
; FEATURE:

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; NAME/KEY: Region
; LOCATION: 52..64
; OTHER INFORMATION: /note= "sequence motif of cytokine
; OTHER INFORMATION: receptor superfamily Cys52..Cys62SW"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 222..226
; OTHER INFORMATION: /note= "cytokine receptor
; OTHER INFORMATION: superfamily motif (W222SKWS)"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 121..123
; OTHER INFORMATION: /note= "N-linked glycosylation
; OTHER INFORMATION: site"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 329..331
; OTHER INFORMATION: /note= "N-linked glycosylation
; OTHER INFORMATION: site"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 346..348
; OTHER INFORMATION: /note= "N-linked glycosylation
; OTHER INFORMATION: site"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 352..354
; OTHER INFORMATION: /note= "N-linked glycosylation
; OTHER INFORMATION: site"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 442..444
; OTHER INFORMATION: /note= "N-linked glycosylation
; OTHER INFORMATION: site"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 456..458
; OTHER INFORMATION: /note= "N-linked glycosylation
; OTHER INFORMATION: site"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 24..540
; OTHER INFORMATION: /note= "Extracellular region"
;
; US-08-248-532-2
;
Query Match 59.3%; Score 35; DB 1; Length 662;
Best Local Similarity 75.0%; Pred. No. 5.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 RCRGDSK 10
Db 484 RCRDEDSK 491

RESULT 23
US-08-419-652-2
; Sequence 2, Application US/08419652
; Patent No. 5831007
; GENERAL INFORMATION:
; APPLICANT: Chua, Anne O
; APPLICANT: Gubler, Ulrich A
; TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: PC compatible
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; OPERATING SYSTEM: MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,652
; FILING DATE: 11-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,532
; FILING DATE: 31-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/094,713
; FILING DATE: 19-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kass, Alan P
; REGISTRATION NUMBER: 32142
; REFERENCE/DOCKET NUMBER: CD 9174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-4205
; TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 662 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..23
; OTHER INFORMATION: /note= "N-terminal signal peptide
; OTHER INFORMATION: (1..20 or 23 or 24)"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 541..570
; OTHER INFORMATION: /note= "transmembrane region"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 571..662
; OTHER INFORMATION: /note= "cytoplasmic tail region"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 577..584
; OTHER INFORMATION: /note= "conserved area of cytoplasmic
; OTHER INFORMATION: tail region"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 618..629
; OTHER INFORMATION: /note= "conserved area of cytoplasmic
; OTHER INFORMATION: tail region"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 52..64
; OTHER INFORMATION: /note= "sequence motif of cytokine
; OTHER INFORMATION: receptor superfamily Cys52..Cys62SW"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 222..226
; OTHER INFORMATION: /note= "cytokine receptor
; OTHER INFORMATION: superfamily motif (W222SKWS)"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 121..123
; OTHER INFORMATION: /note= "N-linked glycosylation
; OTHER INFORMATION: site"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 329..331
; OTHER INFORMATION: /note= "N-linked glycosylation
; OTHER INFORMATION: site"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 346..348
; OTHER INFORMATION: /note= "N-linked glycosylation
; OTHER INFORMATION: site"
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; FEATURE:
; NAME/KEY: Region
; LOCATION: 352..354
; OTHER INFORMATION: /note= "N-linked glycosylation
; OTHER INFORMATION: site"
;
; FEATURE:
; NAME/KEY: Region
; LOCATION: 442..444
; OTHER INFORMATION: /note= "N-linked glycosylation
; OTHER INFORMATION: site"
;
; FEATURE:
; NAME/KEY: Region
; LOCATION: 456..458
; OTHER INFORMATION: /note= "N-linked glycosylation
; OTHER INFORMATION: site"
;
; NAME/KEY: Region
; LOCATION: 24..540
; OTHER INFORMATION: /note= "Extracellular region"
;
US-08-419-652-2

Query Match 59.3%; Score 35; DB 2; Length 662;
Best Local Similarity 75.0%; Pred. No. 5.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 RCRGDDSK 10
   ||| :|||
Db 484 RCRDEDSK 491

RESULT 24
US-08-685-118-4
; Sequence 4, Application US/08685118
; Patent No. 5840530
; GENERAL INFORMATION:
; APPLICANT: Gubler, Ulrich A
; APPLICANT: Presky, David H
; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: USA
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,118
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silverman, Robert A.
; REGISTRATION NUMBER: 35,682
; REFERENCE/DOCKET NUMBER: CD 9195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-2863
; TELEFAX: (201) 235-2363
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 662 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..20
; OTHER INFORMATION: /note= "N-terminal signal peptide
; OTHER INFORMATION: (1..20 or 23 or 24)"

```

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;
; FEATURE:
; NAME/KEY: Region
; LOCATION: 541..570
; OTHER INFORMATION: /note= "transmembrane region"
;
; FEATURE:
; NAME/KEY: Region
; LOCATION: 571..662
; OTHER INFORMATION: /note= "cytoplasmic tail region"
;
; FEATURE:
; NAME/KEY: Region
; LOCATION: 52..64
; OTHER INFORMATION: /note= "sequence motif of cytokine
; OTHER INFORMATION: receptor superfamily Cys52..Cys62SW"
;
; NAME/KEY: Region
; LOCATION: 222..226
; OTHER INFORMATION: /note= "cytokine receptor
; OTHER INFORMATION: superfamily motif (W222SKWS)"
;
; FEATURE:
; NAME/KEY: Region
; LOCATION: 121..123
; OTHER INFORMATION: /note= "N-linked glycosylation
; OTHER INFORMATION: site"
;
; FEATURE:
; NAME/KEY: Region
; LOCATION: 329..331
; OTHER INFORMATION: /note= "N-linked glycosylation
; OTHER INFORMATION: site"
;
; FEATURE:
; NAME/KEY: Region
; LOCATION: 346..348
; OTHER INFORMATION: /note= "N-linked glycosylation
; OTHER INFORMATION: site"
;
; FEATURE:
; NAME/KEY: Region
; LOCATION: 352..354
; OTHER INFORMATION: /note= "N-linked glycosylation
; OTHER INFORMATION: site"
;
; FEATURE:
; NAME/KEY: Region
; LOCATION: 442..444
; OTHER INFORMATION: /note= "N-linked glycosylation
; OTHER INFORMATION: site"
;
; FEATURE:
; NAME/KEY: Region
; LOCATION: 456..458
; OTHER INFORMATION: /note= "N-linked glycosylation
; OTHER INFORMATION: site"
;
; NAME/KEY: Region
; LOCATION: 24..540
; OTHER INFORMATION: /note= "Extracellular region"
;
US-08-685-118-4

Query Match 59.3%; Score 35; DB 2; Length 662;
Best Local Similarity 75.0%; Pred. No. 5.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 RCRGDDSK 10
   ||| :|||
Db 484 RCRDEDSK 491

RESULT 25
US-08-915-495-4
; Sequence 4, Application US/08915495
; Patent No. 5852176
; GENERAL INFORMATION:
; APPLICANT: Gubler, Ulrich A
; APPLICANT: Presky, David H
; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

```

;; ADDRESSEE: Hoffmann-La Roche Inc.
;; STREET: 340 Kingsland Street
;; CITY: Nutley
;; STATE: NJ
;; COUNTRY: USA
;; ZIP: 07110
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/915,495
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/685,118
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Silverman, Robert A.
;; REGISTRATION NUMBER: 35,682
;; REFERENCE/DOCKET NUMBER: CD 9195
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (201) 235-2863
;; TELEFAX: (201) 235-2363
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 662 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FEATURE:
;; NAME/KEY: Region
;; LOCATION: 1..20
;; OTHER INFORMATION: /note= "N-terminal signal peptide
;; OTHER INFORMATION: (1..20 or 23 or 24)"
;; FEATURE:
;; NAME/KEY: Region
;; LOCATION: 541..570
;; OTHER INFORMATION: /note= "transmembrane region"
;; FEATURE:
;; NAME/KEY: Region
;; LOCATION: 571..662
;; OTHER INFORMATION: /note= "cytoplasmic tail region"
;; FEATURE:
;; NAME/KEY: Region
;; LOCATION: 52..64
;; OTHER INFORMATION: /note= "sequence motif of cytokine
;; OTHER INFORMATION: receptor superfamily Cys52..Cys62SW"
;; FEATURE:
;; NAME/KEY: Region
;; LOCATION: 222..226
;; OTHER INFORMATION: /note= "cytokine receptor
;; OTHER INFORMATION: superfamily motif (W222SKWS)"
;; FEATURE:
;; NAME/KEY: Region
;; LOCATION: 121..123
;; OTHER INFORMATION: /note= "N-linked glycosylation
;; OTHER INFORMATION: site"
;; FEATURE:
;; NAME/KEY: Region
;; LOCATION: 329..331
;; OTHER INFORMATION: /note= "N-linked glycosylation
;; OTHER INFORMATION: site"
;; FEATURE:
;; NAME/KEY: Region
;; LOCATION: 346..348
;; OTHER INFORMATION: /note= "N-linked glycosylation
;; OTHER INFORMATION: site"
;; FEATURE:
;; NAME/KEY: Region
;; LOCATION: 352..354
;; OTHER INFORMATION: /note= "N-linked glycosylation

;; OTHER INFORMATION: site"
;; FEATURE:
;; NAME/KEY: Region
;; LOCATION: 442..444
;; OTHER INFORMATION: /note= "N-linked glycosylation
;; OTHER INFORMATION: site"
;; FEATURE:
;; NAME/KEY: Region
;; LOCATION: 456..458
;; OTHER INFORMATION: /note= "N-linked glycosylation
;; OTHER INFORMATION: site"
;; FEATURE:
;; NAME/KEY: Region
;; LOCATION: 24..540
;; OTHER INFORMATION: /note= "Extracellular region"
;; US-08-915-495-4
;; Query Match 59.3%; Score 35; DB 2; Length 662;
;; Best Local Similarity 75.0%; Pred. No. 5.5e+02;
;; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 3 RCRGDDSK 10
Db 484 RCRDEDSK 491
RESULT 26
US-08-914-520-4
; Sequence 4, Application US/08914520
; Patent No. 5919903
; GENERAL INFORMATION:
; APPLICANT: Gubler, Ulrich A
; APPLICANT: Presky, David H
; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: USA
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/914,520
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/685,118
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Silverman, Robert A.
; REGISTRATION NUMBER: 35,682
; REFERENCE/DOCKET NUMBER: CD 9195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-2863
; TELEFAX: (201) 235-2363
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 662 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..20
; OTHER INFORMATION: /note= "N-terminal signal peptide
; OTHER INFORMATION: (1..20 or 23 or 24)"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..20
; OTHER INFORMATION: /note= "N-terminal signal peptide
; OTHER INFORMATION: (1..20 or 23 or 24)"
; FEATURE:

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/ NAME/KEY: Region
/ LOCATION: 541..570
/ OTHER INFORMATION: /note= "transmembrane region"
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 571..662
/ OTHER INFORMATION: /note= "cytoplasmic tail region"
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 52..64
/ OTHER INFORMATION: /note= "sequence motif of cytokine
/ OTHER INFORMATION: receptor superfamily Cys52..Cys62SW"
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 222..226
/ OTHER INFORMATION: /note= "cytokine receptor
/ OTHER INFORMATION: superfamily motif (W222SKWS)"
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 121..123
/ OTHER INFORMATION: /note= "N-linked glycosylation
/ OTHER INFORMATION: site"
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 329..331
/ OTHER INFORMATION: /note= "N-linked glycosylation
/ OTHER INFORMATION: site"
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 346..348
/ OTHER INFORMATION: /note= "N-linked glycosylation
/ OTHER INFORMATION: site"
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 352..354
/ OTHER INFORMATION: /note= "N-linked glycosylation
/ OTHER INFORMATION: site"
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 442..444
/ OTHER INFORMATION: /note= "N-linked glycosylation
/ OTHER INFORMATION: site"
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 456..458
/ OTHER INFORMATION: /note= "N-linked glycosylation
/ OTHER INFORMATION: site"
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 24..540
/ OTHER INFORMATION: /note= "Extracellular region"
US-08-914-520-4
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Query Match 59.3%; Score 35; DB 2; Length 662;
Best Local Similarity 75.0%; Pred. NO. 5.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Qy 3 RCRGDDSK 10
|||:||||
Db 484 RCRDEDSK 491
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RESULT 27
US-08-789-350-2
; Sequence 2, Application US/08789350
; Patent No. 6046012
; GENERAL INFORMATION:
; APPLICANT: Chizzonite, Richard A
; TITLE OF INVENTION: Antibody to IL-12 Receptor
; FILE REFERENCE: Antibody to IL-12
; CURRENT APPLICATION NUMBER: US/08/789,350
; CURRENT FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 08/248,531
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/ EARLIER FILING DATE: 1994-05-31
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 2
/ LENGTH: 662
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (1)..(23)
/ OTHER INFORMATION: N-terminal signal peptide (1...20 or 23 or 24)
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (541)..(570)
/ OTHER INFORMATION: transmembrane region
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (571)..(662)
/ OTHER INFORMATION: cytoplasmic tail region
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (52)..(64)
/ OTHER INFORMATION: sequence motif of cytokine receptor superfamily
/ OTHER INFORMATION: Cys52...Cys62SW
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (222)..(226)
/ OTHER INFORMATION: cytokine receptor superfamily motif (W222SKWS)
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (121)..(123)
/ OTHER INFORMATION: N-linked glycosylation site
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (329)..(331)
/ OTHER INFORMATION: N-linked glycosylation site
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (346)..(348)
/ OTHER INFORMATION: N-linked glycosylation site
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (352)..(354)
/ OTHER INFORMATION: N-linked glycosylation site
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (442)..(444)
/ OTHER INFORMATION: N-linked glycosylation site
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (456)..(458)
/ OTHER INFORMATION: N-linked glycosylation site
/ LOCATION: (24)..(540)
/ OTHER INFORMATION: Extracellular region
US-08-789-350-2
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Query Match 59.3%; Score 35; DB 3; Length 662;
Best Local Similarity 75.0%; Pred. NO. 5.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Qy 3 RCRGDDSK 10
|||:||||
Db 484 RCRDEDSK 491
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RESULT 28
US-09-949-016-6624
; Sequence 6624, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
```

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; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6624
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6624

Query Match          59.3%; Score 35; DB 4; Length 662;
Best Local Similarity 75.0%; Pred. No. 5.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 RCRGDDSK 10
DB      484 RCRDEDSK 491

RESULT 29
US-09-949-016-10092
; Sequence 10092, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10092
; LENGTH: 683
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10092

Query Match          59.3%; Score 35; DB 4; Length 683;
Best Local Similarity 75.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 RCRGDDSK 10
DB      505 RCRDEDSK 512

RESULT 30
US-09-252-991A-23746
; Sequence 23746, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
```

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; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23746
; LENGTH: 700
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23746

Query Match          59.3%; Score 35; DB 4; Length 700;
Best Local Similarity 75.0%; Pred. No. 5.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 YRCRGDGS 9
DB      530 YRCRGDLA 537

RESULT 31
US-09-252-991A-18617
; Sequence 18617, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18617
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18617

Query Match          57.6%; Score 34; DB 4; Length 163;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 RCRGDDDS 9
DB      82 RCRGPDS 88

RESULT 32
US-09-489-039A-13748
; Sequence 13748, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13748
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13748

Query Match          57.6%; Score 34; DB 4; Length 272;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
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Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10

Db 210 NVRFKGDGDAK 219

RESULT 33
US-09-601-478-5
; Sequence 5, Application US/09601478
; Patent No. 6403785
; GENERAL INFORMATION:
; APPLICANT: Oetuka Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: Human TSC403 gene and human INGIL gene
; FILE REFERENCE: Q60193
; CURRENT APPLICATION NUMBER: US/09/601,478
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP H10-134679
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: JP H10-73234
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: JP H10-38133
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human embryonic brain cDNA library
US-09-601-478-5

Query Match 57.6%; Score 34; DB 4; Length 280;
Best Local Similarity 62.5%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 RCRGDDSK 10

Db 257 KCRGDNEK 264

RESULT 34
US-09-601-478-8
; Sequence 8, Application US/09601478
; Patent No. 6403785
; GENERAL INFORMATION:
; APPLICANT: Oetuka Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: Human TSC403 gene and human INGIL gene
; FILE REFERENCE: Q60193
; CURRENT APPLICATION NUMBER: US/09/601,478
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP H10-134679
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: JP H10-73234
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: JP H10-38133
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: human embryonic brain cDNA library
US-09-601-478-8

Query Match 57.6%; Score 34; DB 4; Length 280;
Best Local Similarity 62.5%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 RCRGDDSK 10

:|||||:

Db 257 KCRGDNEK 264

RESULT 35
US-09-442-013-13
; Sequence 13, Application US/09442013
; Patent No. 6737232
; GENERAL INFORMATION:
; APPLICANT: Lou, Ying
; APPLICANT: Xu, Xiang
; APPLICANT: Leo, Cindy
; APPLICANT: Huang, Betty
; APPLICANT: Shen, Mary
; TITLE OF INVENTION: NOVEL IAPS ASSOCIATED CELL CYCLE PROTEINS, COMPOSITIONS
; FILE REFERENCE: A-68289/DJB/RMS/DAV
; CURRENT APPLICATION NUMBER: US/09/442,013
; CURRENT FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-442-013-13

Query Match 57.6%; Score 34; DB 4; Length 280;
Best Local Similarity 62.5%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 RCRGDDSK 10

:|||||:

Db 257 KCRGDNEK 264

RESULT 36
US-09-513-365A-1
; Sequence 1, Application US/09513365A
; Patent No. 6790948
; GENERAL INFORMATION:
; APPLICANT: Harris, Curtis C
; APPLICANT: Nagashima, Makoto
; APPLICANT: Government of United States as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: New Tumor Suppressor Gene P33ING2
; FILE REFERENCE: 015280-376100US
; CURRENT APPLICATION NUMBER: US/09/513,365A
; CURRENT FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: US 60/121,891
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: p33ING2
; OTHER INFORMATION: polypeptide sequence
US-09-513-365A-1

Query Match 57.6%; Score 34; DB 4; Length 280;
Best Local Similarity 62.5%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 RCRGDDSK 10

:|||||:

Db 257 KCRGDNEK 264

RESULT 37
US-09-513-365A-6
; Sequence 6, Application US/09513365A


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; Patent No. 6790948
; GENERAL INFORMATION:
; APPLICANT: Harris, Curtis C
; APPLICANT: Nagashima, Makoto
; APPLICANT: Government of United States as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: New Tumor Suppressor Gene P33ING2
; FILE REFERENCE: 015280-376100US
; CURRENT APPLICATION NUMBER: US/09/513,365A
; CURRENT FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: US 60/121,891
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: missense
; OTHER INFORMATION: p33ING2 sequence - Arg 153 to Ser
US-09-513-365A-6

Query Match          57.6%; Score 34; DB 4; Length 280;
Best Local Similarity 62.5%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      3 RCRGDDSK 10
DB      257 KCRGDNEK 264
          :||||:
          :||||:

RESULT 38
US-09-902-540-15729
; Sequence 15729, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15729
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-15729

Query Match          57.6%; Score 34; DB 4; Length 289;
Best Local Similarity 85.7%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 RCRGDDDS 9
DB      85 RCPGDDDS 91
          |||
          |||

RESULT 39
US-09-583-110-4948
; Sequence 4948, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
```

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; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4948
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4948

Query Match          57.6%; Score 34; DB 4; Length 316;
Best Local Similarity 30.8%; Pred. No. 3.9e+02;
Matches 8; Conservative 2; Mismatches 0; Indels 16; Gaps 1;

QY      1 MYRCR-----GDDSK 10
DB      229 NFRCSRSTFWETIHNKILMGDDSR 254
          |:|
          |:|

RESULT 40
US-09-107-433-5053
; Sequence 5053, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; TITLE OF INVENTION: SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; TITLE OF INVENTION: THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5053:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...321
; SEQUENCE DESCRIPTION: SEQ ID NO: 5053:
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US-09-107-433-5053

Query Match 57.6%; Score 34; DB 4; Length 321;
Best Local Similarity 30.8%; Pred. No. 4e+02;
Matches 8; Conservative 2; Mismatches 0; Indels 16; Gaps 1;

QY 1 NYRCR-----GDGSK 10
:|||||
Db 234 NFRCRSNSTFWETIHNKILMGDDSR 259

RESULT 41

US-09-252-991A-30671
; Sequence 30671, Application US/09252991A
; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30671
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-30671

Query Match 57.6%; Score 34; DB 4; Length 328;
Best Local Similarity 62.5%; Pred. No. 4.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 RCRGDSK 10
|||||
Db 93 RCRGSDAR 100

RESULT 42

US-09-248-796A-21669
; Sequence 21669, Application US/09248796A
; Patent No. 6747137

GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 21669
LENGTH: 357
TYPE: PRT

ORGANISM: Candida albicans

US-09-248-796A-21669

Query Match 57.6%; Score 34; DB 4; Length 357;
Best Local Similarity 62.5%; Pred. No. 4.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
:|:|:|
Db 241 SYVCKGDD 248

RESULT 43

US-09-627-376-10
; Sequence 10, Application US/09627376
; Patent No. 6342385

GENERAL INFORMATION:

; APPLICANT: Qi, Fengxia
; TITLE OF INVENTION: MUTACIN I BIOSYNTHESIS GENES AND PROTEINS
; FILE REFERENCE: UAB-17402/22
; CURRENT APPLICATION NUMBER: US/09/627,376
; CURRENT FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Streptococcus mutans

US-09-627-376-10

Query Match 57.6%; Score 34; DB 3; Length 447;
Best Local Similarity 60.0%; Pred. No. 5.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
|||:|:|
Db 410 NYHLQDSSK 419

RESULT 44

US-10-047-676B-10
; Sequence 10, Application US/10047676B
; Patent No. 6699970

GENERAL INFORMATION:

; APPLICANT: Qi, Fengxia
; APPLICANT: Caufield, Page W.
; TITLE OF INVENTION: MUTACIN I BIOSYNTHESIS GENES AND PROTEINS
; FILE REFERENCE: UAB-17403/22
; CURRENT APPLICATION NUMBER: US/10/047,676B
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 09/627,376
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Streptococcus mutans

US-10-047-676B-10

Query Match 57.6%; Score 34; DB 4; Length 447;
Best Local Similarity 60.0%; Pred. No. 5.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
|||:|:|
Db 410 NYHLQDSSK 419

RESULT 45

US-09-107-149-19
; Sequence 19, Application US/09107149
; Patent No. 6274363

GENERAL INFORMATION:

; APPLICANT: Leung, David W.
; APPLICANT: Tompkins, Christopher K.
; TITLE OF INVENTION: PHOSPHATIDYLCHOLINE PHOSPHOLIPASE D
; FILE REFERENCE: 077319/0144
; CURRENT APPLICATION NUMBER: US/09/107,149
; CURRENT FILING DATE: 1998-06-30
; EARLIER APPLICATION NUMBER: 08/768,147
; EARLIER FILING DATE: 1996-12-17
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 19
; LENGTH: 971
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-107-149-19

Query Match          57.6%; Score 34; DB 3; Length 971;
Best Local Similarity 63.8%; Pred. No. 1.2e+03;
Matches 7; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY      1 NVR--CRGDDS 9
      ||| |||::|
Db      846 NYRTMCRGENS 856

RESULT 46
US-08-968-752B-4
; Sequence 4, Application US/08968752B
; Patent No. 6043073
; GENERAL INFORMATION:
; APPLICANT: Frohman, Michael A.
; APPLICANT: Morris, Andrew
; TITLE OF INVENTION: No. 6043073el Phospholipase D Polypeptide and
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ONYX Pharmaceuticals, Inc.
; STREET: 3031 Research Drive
; CITY: Richmond
; STATE: California
; COUNTRY: USA
; ZIP: 94806
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,752B
; FILING DATE: 05-SEP-1996
; PRIORITY INFORMATION:
; NAME: Giotta, Gregory J.
; REGISTRATION NUMBER: 32,028
; REFERENCE/DOCKET NUMBER: ONYX2004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-222-9758
; TELEFAX: 510-222-9758
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1036 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-968-752B-4

Query Match          57.6%; Score 34; DB 3; Length 1036;
Best Local Similarity 63.8%; Pred. No. 1.2e+03;
Matches 7; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY      1 NVR--CRGDDS 9
      ||| |||::|
Db      808 NYRTMCRGENS 818

RESULT 47
US-09-536-224-4
; Sequence 4, Application US/09536224
; Patent No. 6379665
; GENERAL INFORMATION:
```

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; APPLICANT: Frohman, Michael A.
; APPLICANT: Morris, Andrew
; TITLE OF INVENTION: No. 6379665el Phospholipase D Polypeptide and
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ONYX Pharmaceuticals, Inc.
; STREET: 3031 Research Drive
; CITY: Richmond
; STATE: California
; COUNTRY: USA
; ZIP: 94806
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,224
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/968,752
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Giotta, Gregory J.
; REGISTRATION NUMBER: 32,028
; REFERENCE/DOCKET NUMBER: ONYX2004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-222-9700
; TELEFAX: 510-222-9758
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1036 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-536-224-4

Query Match          57.6%; Score 34; DB 3; Length 1036;
Best Local Similarity 63.6%; Pred. No. 1.2e+03;
Matches 7; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY      1 NVR--CRGDDS 9
      ||| |||::|
Db      808 NYRTMCRGENS 818

RESULT 48
US-08-768-147B-2
; Sequence 2, Application US/08768147B
; Patent No. 5859222
; GENERAL INFORMATION:
; APPLICANT: Leung, David W.
; APPLICANT: Tompkins, Christopher
; TITLE OF INVENTION: PHOSPHATIDYLCHOLINE PHOSPHOLIPASE D
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cell Therapeutics, Inc.
; STREET: 200 Elliott Avenue West, Suite 400
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98119
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" disk, 1.44Mb, double side, high density
; COMPUTER: Hewlett Packard-IBM Compatible
; OPERATING SYSTEM: MS-DOS Version 6
; SOFTWARE: WORD for WINDOWS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/768,147B
; FILING DATE: 16-Dec-1996
; CLASSIFICATION:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: Provisional US60008768
; FILING DATE: 15-Dec-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Faciszewski, Stephen
; REGISTRATION NUMBER: 36,131,
; REFERENCE/DOCKET NUMBER: 1802A
; TELEPHONE: (206)282-7100
; TELEFAX: (206)284-6206
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1074
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE: NAME/KEY: hPLD1
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 2:
US-08-768-147B-2

```

Query Match 57.6%; Score 34; DB 2; Length 1074;
 Best Local Similarity 63.6%; Pred. No. 1.3e+03;
 Matches 7; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 1 NYR--CRGDDS 9
 ||| |||:|
 Db 846 NYRTWCRGENS 856

```

RESULT 49
US-08-968-752B-2
; Sequence 2, Application US/08968752B
; Patent No. 6043073
; GENERAL INFORMATION:
; APPLICANT: Frohman, Michael A.
; APPLICANT: Morris, Andrew
; TITLE OF INVENTION: No. 6043073el Phospholipase D Polypeptide and

```

```

; TITLE OF INVENTION: DNA Sequences
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ONYX Pharmaceuticals, Inc.
; STREET: 3031 Research Drive
; CITY: Richmond
; STATE: California
; COUNTRY: USA
; ZIP: 94806
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,752B
; FILING DATE: 13-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/025,469
; FILING DATE: 05-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Giotta, Gregory J.
; REGISTRATION NUMBER: 32,028
; REFERENCE/DOCKET NUMBER: ONYX2004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-222-9700
; TELEFAX: 510-222-9758
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1074 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-968-752B-2

```

Query Match 57.6%; Score 34; DB 3; Length 1074;
 Best Local Similarity 63.6%; Pred. No. 1.3e+03;
 Matches 7; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 1 NYR--CRGDDS 9
 ||| |||:|
 Db 846 NYRTWCRGENS 856

```

RESULT 50
US-09-107-149-3
; Sequence 3, Application US/09107149
; Patent No. 6274363
; GENERAL INFORMATION:
; APPLICANT: Leung, David W.
; APPLICANT: Tompkins, Christopher K.
; TITLE OF INVENTION: PHOSPHATIDYLCHOLINE PHOSPHOLIPASE D
; FILE REFERENCE: 077319/0144
; CURRENT APPLICATION NUMBER: US/09/107,149
; CURRENT FILING DATE: 1998-06-30
; EARLIER APPLICATION NUMBER: 08/768,147
; EARLIER FILING DATE: 1996-12-17
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1074
; TYPE: PPT
; ORGANISM: Homo sapiens
US-09-107-149-3

```

Query Match 57.6%; Score 34; DB 3; Length 1074;
 Best Local Similarity 63.6%; Pred. No. 1.3e+03;
 Matches 7; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 1 NYR--CRGDDS 9
 ||| |||:|
 Db 846 NYRTWCRGENS 856

Search completed: September 7, 2005, 19:58:08
Job time : 18.5581 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 7, 2005, 19:37:54 ; Search time 72.093 Seconds
 (without alignments)
 53.647 Million cell updates/sec

Title: US-10-812-238B-20
 Perfect score: 59
 Sequence: 1 NYRCRGDDSK 10

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseq19808:*

2: Geneseq19908:*

3: Geneseq20008:*

4: Geneseq20018:*

5: Geneseq20028:*

6: Geneseq20038:*

7: Geneseq20038b:*

8: Geneseq20048:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	311	2 AAW79286	Human pro
2	59	100.0	311	7 ADE60703	Human pro
3	59	100.0	311	8 ADM72103	Human tau
4	59	100.0	311	8 ADN04415	Antipsori
5	59	100.0	311	8 ADP24274	PRO polyp
6	55	93.2	312	5 ABB99112	Rat Phosp
7	55	93.2	312	7 ADE60701	Rat Prote
8	41	69.5	152	4 ABG23434	Novel hum
9	41	69.5	237	8 AAU28253	Novel hum
10	41	69.5	237	8 ADS12199	Human the
11	41	69.5	421	8 ADJ50947	Human nov
12	41	69.5	424	8 ADJ50945	Human nov
13	41	69.5	428	6 ADA83857	Human POM
14	41	69.5	481	8 ADR09234	Human pro
15	41	69.5	481	8 ADS10966	Human the
16	41	69.5	489	6 ADM04303	Human pro
17	40	67.8	400	6 ABU31582	Protein e
18	40	67.8	400	6 ABU45262	Protein e
19	40	67.8	400	6 ABU48051	Protein e
20	40	67.8	400	6 ABU15369	Protein e
21	40	67.8	424	7 ABO65513	Klebsiell
22	40	67.8	705	7 ADB74255	Mycobacte
23	40	67.8	1304	6 ABP72189	Plasmodiu
24	39	66.1	451	4 ABB67864	Drosophil
25	39	66.1	1299	6 ABP72191	Plasmodiu

26	38	64.4	822	2	AAW99087	Aaw99087	Human ser
27	38	64.4	875	2	AAW83361	Aaw83361	Human neu
28	38	64.4	875	8	ADQ21226	Adq21226	Human sof
29	38	64.4	875	8	ADQ89082	Adq89082	Human uro
30	37	62.7	77	5	ABP42738	Abp42738	Human ova
31	37	62.7	92	4	AAU61299	Aau61299	Propionib
32	37	62.7	92	6	ABM57818	Abm57818	Propionib
33	37	62.7	113	4	AAW91935	Aaw91935	Human dig
34	37	62.7	113	4	AAW38569	Aaw38569	Human col
35	37	62.7	113	5	ABG97621	Abg97621	Human col
36	37	62.7	113	7	ADN92877	Adn92877	Human col
37	37	62.7	140	4	ABB11487	Abb11487	Human sec
38	37	62.7	275	7	ABO65272	AbO65272	Klebsiell
39	37	62.7	488	7	ABO66647	AbO66647	Klebsiell
40	37	62.7	1269	7	ADD46237	Add46237	Rat Prote
41	37	62.7	1272	7	ADD46239	Add46239	Human pro
42	36	61.0	59	4	AAU49621	Aau49621	Propionib
43	36	61.0	59	6	ABM46140	Abm46140	Propionib
44	36	61.0	405	6	ABM69291	Abm69291	Phototrab
45	36	61.0	466	8	ADN20343	Adn20343	Bacterial
46	36	61.0	470	8	ADN20289	Adn20289	Bacterial
47	36	61.0	485	7	ADM04173	Adm04173	Human pro
48	36	61.0	498	3	AAW79209	Aaw79209	Human tra
49	36	61.0	498	7	ADN95772	Adn95772	Human BEC
50	36	61.0	498	8	ADP23807	Adp23807	PRO polyp
51	36	61.0	1365	6	ABP72194	Abp72194	Plasmodiu
52	36	61.0	1812	6	ABP70268	Abp70268	Amino aci
53	35	59.3	20	5	ABP56183	Abp56183	Chimeric
54	35	59.3	69	4	AAU44985	Aau44985	Propionib
55	35	59.3	94	2	ABM41504	Abm41504	Propionib
56	35	59.3	94	2	AAW35872	Aaw35872	Chlamydia
57	35	59.3	181	4	ABB67977	Abb67977	Drosophil
58	35	59.3	269	2	AAR60558	Aar60558	Human bas
59	35	59.3	269	2	AAW39464	Aaw39464	CD147 pro
60	35	59.3	269	5	AAU79095	Aau79095	Human EMM
61	35	59.3	269	6	ABP97416	Abp97416	Human HAB
62	35	59.3	269	6	ABU05047	Abu05047	Human exp
63	35	59.3	269	6	ABU05036	Abu05036	Human exp
64	35	59.3	269	6	ABU05042	Abu05042	Human exp
65	35	59.3	269	6	ABU05041	Abu05041	Human exp
66	35	59.3	269	6	ABU05037	Abu05037	Human exp
67	35	59.3	269	6	ABU05038	Abu05038	Human exp
68	35	59.3	269	6	ABU05043	Abu05043	Human exp
69	35	59.3	269	6	ABU05045	Abu05045	Human exp
70	35	59.3	269	6	ABU05039	Abu05039	Human exp
71	35	59.3	269	6	ABU05040	Abu05040	Human exp
72	35	59.3	269	6	ABU05046	Abu05046	Human exp
73	35	59.3	269	6	ABR48491	AbR48491	Human bas
74	35	59.3	269	7	ADJ68581	Adj68581	Human hea
75	35	59.3	269	8	ADI82502	Adi82502	Human mod
76	35	59.3	269	8	ABM81976	Abm81976	Tumour-as
77	35	59.3	269	8	ADR68491	Adr68491	Apoptosis
78	35	59.3	276	3	AAW57003	Aaw57003	Human pro
79	35	59.3	276	4	ABU05044	Abu05044	Human exp
80	35	59.3	283	4	ABM68798	Abm68798	Drosophil
81	35	59.3	301	8	ADE26705	Ade26705	Bacterial
82	35	59.3	301	8	ADS27091	Ads27091	Bacterial
83	35	59.3	302	8	ADS26338	Ads26338	Bacterial
84	35	59.3	385	5	ABG314071	Abg314071	Human PRO
85	35	59.3	385	5	ADA011352	Ada011352	Human PRO
86	35	59.3	385	6	ADA43781	Ada43781	Human sec
87	35	59.3	385	6	ADA43549	Ada43549	Human sec
88	35	59.3	385	6	ADA011224	Ada011224	Human PRO
89	35	59.3	385	7	ADA011108	Ada011108	Human sec
90	35	59.3	385	7	ADA43665	Ada43665	Human sec
91	35	59.3	385	7	ADA06927	Ada06927	Human PRO
92	35	59.3	385	7	ADA08415	Ada08415	Novel hum
93	35	59.3	385	7	ADB99708	AdB99708	Human PRO
94	35	59.3	385	7	ADB86991	AdB86991	Human PRO
95	35	59.3	385	7	ADB66146	AdB66146	Human sec
96	35	59.3	385	7	ADB99824	AdB99824	Human PRO
97	35	59.3	385	7	ADB99479	AdB99479	Novel hum
98	35	59.3	385	7	ADB66030	AdB66030	Human sec

99	35	59.3	385	7	ADC23428	Adc23428	Human	tra	172	35	59.3	422	4	AAE09446	Aae09446	Human	sbg
100	35	59.3	385	7	ADC26121	Adc26121	Human	PRO	173	35	59.3	427	2	AAW69231	Aaw69231	Human	pro
101	35	59.3	385	7	ADC04948	Adc04948	Human	PRO	174	35	59.3	427	2	ADG46570	Adg46570	Human	fc
102	35	59.3	385	7	ADE11254	Adel1254	Human	PRO	175	35	59.3	427	8	ADR28644	Adr28644	Human	fc
103	35	59.3	385	7	ADD88185	AdD88185	Human	PRO	176	35	59.3	432	2	ADM04721	Adm04721	Human	pro
104	35	59.3	385	7	ADD95480	AdD95480	Human	sec	177	35	59.3	432	2	AAW82546	Aaw82546	Human	LIR
105	35	59.3	385	7	ADE06410	AdE06410	Human	PRO	178	35	59.3	439	2	AAW53464	Aaw53464	Human	gp4
106	35	59.3	385	7	ADE38185	AdE38185	Human	PRO	179	35	59.3	439	2	AAW62777	Aaw62777	Protein	e
107	35	59.3	385	7	ADD88301	AdD88301	Human	PRO	180	35	59.3	439	2	ABO41171	AbO41171	Leukocyte	
108	35	59.3	385	7	ADD90882	AdD90882	Human	sec	181	35	59.3	439	8	ADO24389	AdO24389	Human	PRO
109	35	59.3	385	7	ADP99437	AdP99437	Human	sec	182	35	59.3	439	8	ADP23998	AdP23998	PRO	polyP
110	35	59.3	385	7	ADG06530	AdG06530	Human	PRO	183	35	59.3	453	8	ADN23929	AdN23929	Bacterial	
111	35	59.3	385	7	ADG05481	AdG05481	Human	PRO	184	35	59.3	453	8	ADN23928	AdN23928	Bacterial	
112	35	59.3	385	7	ADG82482	AdG82482	Human	PRO	185	35	59.3	453	8	ADN23930	AdN23930	Bacterial	
113	35	59.3	385	8	ADE51735	AdE51735	Human	sec	186	35	59.3	473	4	ABG27154	AbG27154	Novel	hum
114	35	59.3	385	8	ADE51881	AdE51881	Human	sec	187	35	59.3	478	4	ABG27155	AbG27155	Novel	hum
115	35	59.3	385	8	ADE37709	AdE37709	Human	sec	188	35	59.3	552	4	AAE09447	Aae09447	Human	sbg
116	35	59.3	385	8	ADE37593	AdE37593	Human	sec	189	35	59.3	575	7	ADC13555	AdC13555	Human	NOV
117	35	59.3	385	8	ADD95364	AdD95364	Human	sec	190	35	59.3	614	8	ADR99920	AdR99920	Immune	Re
118	35	59.3	385	8	ADDE38064	AdE38064	Human	PRO	191	35	59.3	615	8	ADO39859	AdO39859	Human	myo
119	35	59.3	385	8	ADE76153	AdE76153	Human	PRO	192	35	59.3	616	8	ADR99921	AdR99921	Immune	Re
120	35	59.3	385	8	ADE39476	AdE39476	Human	PRO	193	35	59.3	656	5	ABB93180	AbB93180	Herbicide	
121	35	59.3	385	8	ADE04280	AdE04280	Human	PRO	194	35	59.3	660	2	AAE69633	Aae69633	Human	int
122	35	59.3	385	8	ADE39877	AdE39877	Human	PRO	195	35	59.3	662	2	AAE69632	Aae69632	Human	int
123	35	59.3	385	8	ADE19742	AdE19742	Human	PRO	196	35	59.3	662	2	AAW12772	Aaw12772	Human	int
124	35	59.3	385	8	ADE77320	AdE77320	Human	sec	197	35	59.3	662	3	AY83950	Ay83950	Human	int
125	35	59.3	385	8	ADE65428	AdE65428	Human	PRO	198	35	59.3	662	7	ABE39706	AbE39706	Human	int
126	35	59.3	385	8	ADE76037	AdE76037	Human	PRO	199	35	59.3	662	8	ADK90610	AdK90610	Human	il-
127	35	59.3	385	8	ADE37948	AdE37948	Human	PRO	200	35	59.3	662	8	ADQ33833	AdQ33833	Human	IL-
128	35	59.3	385	8	ADE64558	AdE64558	Human	PRO	201	35	59.3	662	8	ADQ39861	AdQ39861	Human	myo
129	35	59.3	385	8	ADE38893	AdE38893	Human	PRO	202	35	59.3	662	8	ADQ39860	AdQ39860	Human	myo
130	35	59.3	385	8	ADE51967	AdE51967	Human	sec	203	35	59.3	694	8	ADO26838	AdO26838	Human	rec
131	35	59.3	385	8	ADQ9098	AdQ9098	Human	sec	204	35	59.3	700	7	ABO75000	AbO75000	Pseudomon	
132	35	59.3	385	8	ADE38777	AdE38777	Human	PRO	205	35	59.3	702	8	ADO39863	AdO39863	Human	myo
133	35	59.3	385	8	ADE37477	AdE37477	Human	sec	206	35	59.3	754	8	ADO39862	AdO39862	Human	myo
134	35	59.3	385	8	ADE06294	AdE06294	Human	PRO	207	34	57.6	115	6	AAU48996	Aau48996	Propionib	
135	35	59.3	385	8	ADD90153	AdD90153	Human	sec	208	34	57.6	115	6	ABM45515	AbM45515	Propionib	
136	35	59.3	385	8	ADE38661	AdE38661	Human	PRO	209	34	57.6	121	4	AAW79769	Aaw79769	Human	pro
137	35	59.3	385	8	ADQ39592	AdQ39592	Human	PRO	210	34	57.6	121	4	ABG18440	AbG18440	Novel	hum
138	35	59.3	385	8	ADQ89197	AdQ89197	Human	PRO	211	34	57.6	127	4	AAW95510	Aaw95510	Human	rep
139	35	59.3	385	8	ADD88964	AdD88964	Human	PRO	212	34	57.6	127	4	ABE96193	AbE96193	Human	tes
140	35	59.3	385	8	ADE19858	AdE19858	Human	PRO	213	34	57.6	131	3	AAW75402	Aaw75402	Neisseria	
141	35	59.3	385	8	ADE77436	AdE77436	Human	sec	214	34	57.6	131	3	AAW75400	Aaw75400	Neisseria	
142	35	59.3	385	8	ADE65312	AdE65312	Human	PRO	215	34	57.6	135	3	ADL92508	AdL92508	Imab111	V
143	35	59.3	385	8	ADQ39360	AdQ39360	Human	PRO	216	34	57.6	135	8	ADK41823	AdK41823	Versatile	
144	35	59.3	385	8	ADQ38545	AdQ38545	Human	sec	217	34	57.6	137	7	ABE65039	AbE65039	Human	pro
145	35	59.3	385	8	ADG11098	AdG11098	Human	sec	218	34	57.6	147	4	AAO07776	Aao07776	Human	pol
146	35	59.3	385	8	ADG10982	AdG10982	Human	sec	219	34	57.6	156	7	ABO69871	AbO69871	Pseudomon	
147	35	59.3	385	8	ADH31510	AdH31510	Human	PRO	220	34	57.6	163	7	ABO69871	AbO69871	Pseudomon	
148	35	59.3	385	8	ADH38758	AdH38758	Human	sec	221	34	57.6	172	6	ABU26330	AbU26330	Protein	e
149	35	59.3	385	8	ADH29393	AdH29393	Human	sec	222	34	57.6	182	8	ADN46681	AdN46681	Thermococ	
150	35	59.3	385	8	ADH23696	AdH23696	Human	sec	223	34	57.6	235	8	ADR10154	AdR10154	Human	pro
151	35	59.3	385	8	ADH27026	AdH27026	Human	sec	224	34	57.6	240	3	AAW52199	Aaw52199	Human	tum
152	35	59.3	385	8	ADH38294	AdH38294	Novel	hum	225	34	57.6	272	7	ABO67231	AbO67231	Klebsiell	
153	35	59.3	385	8	ADH26910	AdH26910	Human	sec	226	34	57.6	273	5	ABB93016	AbB93016	Herbicide	
154	35	59.3	385	8	ADH38178	AdH38178	Novel	hum	227	34	57.6	280	2	AAW29606	Aaw29606	Human	ING
155	35	59.3	385	8	ADH38874	AdH38874	Human	sec	228	34	57.6	280	3	AAQ05772	Aaq05772	Arabidops	
156	35	59.3	385	8	ADH23812	AdH23812	Human	sec	229	34	57.6	280	4	AAE06675	Aae06675	Tumour	su
157	35	59.3	385	8	ADH40187	AdH40187	Human	PRO	230	34	57.6	280	8	ADH09685	AdH09685	Human	hos
158	35	59.3	385	8	ADH40072	AdH40072	Human	PRO	231	34	57.6	280	8	ADH09683	AdH09683	Human	hos
159	35	59.3	385	8	ADH31394	AdH31394	Human	PRO	232	34	57.6	280	8	ADH09686	AdH09686	Human	hos
160	35	59.3	385	8	ADH29272	AdH29272	Human	sec	233	34	57.6	280	8	ADH09684	AdH09684	Human	hos
161	35	59.3	385	8	ADH49487	AdH49487	Novel	hum	234	34	57.6	280	8	ADH09687	AdH09687	Human	hos
162	35	59.3	385	8	ADH51951	AdH51951	Novel	hum	235	34	57.6	280	8	ADR43904	AdR43904	Human	sup
163	35	59.3	385	8	ADH49806	AdH49806	Novel	hum	236	34	57.6	280	8	ADR43899	AdR43899	Human	sup
164	35	59.3	385	8	ADH52407	AdH52407	Novel	hum	237	34	57.6	287	3	AAQ49721	Aaq49721	Arabidops	
165	35	59.3	385	8	ADH52523	AdH52523	Novel	hum	238	34	57.6	288	3	AAQ49733	Aaq49733	Arabidops	
166	35	59.3	385	8	ADH58520	AdH58520	Novel	hum	239	34	57.6	289	3	AAQ21354	Aaq21354	Arabidops	
167	35	59.3	385	8	ADH51835	AdH51835	Novel	hum	240	34	57.6	299	3	AAQ05771	Aaq05771	Arabidops	
168	35	59.3	385	8	ADH58396	AdH58396	Novel	hum	241	34	57.6	300	5	AAE22290	Aae22290	Rodent	tu
169	35	59.3	385	8	ADH13593	AdH13593	Novel	hum	242	34	57.6	316	8	ADK48433	AdK48433	Streptoco	
170	35	59.3	385	8	ADK00849	AdK00849	Human	PRO	243	34	57.6	321	3	AAQ21353	Aaq21353	Arabidops	
171	35	59.3	385	8	ADL08590	AdL08590	Human	sec	244	34	57.6	321	8	ADR96418	AdR96418	Novel	S.

245	34	57.6	323	8	ADS24081	AdS24081 Bacterial	318	33	55.9	490	4	AAW40334	AAW40334 Human pol
246	34	57.6	328	7	ABO81925	ABO81925 Pseudomon	319	33	55.9	490	5	ABW84260	ABW84260 Human kat
247	34	57.6	362	8	ADQ15100	ADQ15100 Human can	320	33	55.9	490	5	AAU74352	AAU74352 Human cyt
248	34	57.6	396	4	ABG14749	ABG14749 Novel hum	321	33	55.9	490	7	ADM05650	ADM05650 Human pro
249	34	57.6	397	4	AAU61160	AAU61160 Propionib	322	33	55.9	542	4	ABG17714	ABG17714 Novel hum
250	34	57.6	397	5	ABM57679	ABM57679 Propionib	323	33	55.9	557	3	AAV87913	AAV87913 D. opposi
251	34	57.6	447	5	ABM09643	ABM09643 MutP prot	324	33	55.9	582	2	AAW92256	AAW92256 Neural ce
252	34	57.6	447	6	ABG72541	ABG72541 Streptoco	325	33	55.9	629	8	ADR31370	ADR31370 Stresse re
253	34	57.6	645	6	ABM68401	ABM68401 Phototrab	326	33	55.9	636	4	ABG21734	ABG21734 Novel hum
254	34	57.6	801	4	AAU34022	AAU34022 Staphyloc	327	33	55.9	654	8	ADS27333	ADS27333 Bacterial
255	34	57.6	801	6	AAU36926	AAU36926 Staphyloc	328	33	55.9	654	8	ADS26605	ADS26605 Bacterial
256	34	57.6	801	6	ABU16301	ABU16301 Protein e	329	33	55.9	654	8	ADS26980	ADS26980 Bacterial
257	34	57.6	801	6	ABM70889	ABM70889 Staphyloc	330	33	55.9	654	8	ADM26780	ADM26780 Bacterial
258	34	57.6	808	7	ADB64170	ADB64170 Human pro	331	33	55.9	654	8	ADM26504	ADM26504 Bacterial
259	34	57.6	867	7	ADE71288	ADE71288 Novel hum	332	33	55.9	675	8	ADM20157	ADM20157 Bacterial
260	34	57.6	971	3	AAU44717	AAU44717 Human pho	333	33	55.9	678	5	ABP41931	ABP41931 Human ova
261	34	57.6	971	4	AAW85981	AAW85981 Human pho	334	33	55.9	680	8	ADH28720	ADH28720 Bacterial
262	34	57.6	1036	2	AAW53280	AAW53280 Human pho	335	33	55.9	686	7	ABO69369	ABO69369 Pseudomon
263	34	57.6	1074	2	AAW53279	AAW53279 Human pho	336	33	55.9	729	8	ADR08965	ADR08965 Human pro
264	34	57.6	1074	4	AAW85976	AAW85976 Human pho	337	33	55.9	730	2	AAW71379	AAW71379 Grasshopp
265	34	57.6	1074	7	ADE63117	ADE63117 Human pro	338	33	55.9	761	2	AAW92255	AAW92255 Neural ce
266	34	57.6	1074	7	ADD46309	ADD46309 Human Pro	339	33	55.9	800	7	ABO60674	ABO60674 Klebsiell
267	34	57.6	1125	4	ABG18927	ABG18927 Novel hum	340	33	55.9	810	8	ADH72220	ADH72220 Human pro
268	34	57.6	4601	4	ABW59371	ABW59371 Drosophil	341	33	55.9	825	7	ABO61952	ABO61952 Klebsiell
269	33	55.9	14	2	AAW63598	AAW63598 Human com	342	33	55.9	837	8	ADI24547	ADI24547 Human mod
270	33	55.9	14	2	AAW63597	AAW63597 Human com	343	33	55.9	842	4	AAU36357	AAU36357 Pseudomon
271	33	55.9	21	2	AAW93161	AAW93161 Human blo	344	33	55.9	842	6	ABU38620	ABU38620 Protein e
272	33	55.9	21	2	AAW63606	AAW63606 Human com	345	33	55.9	897	8	ADI45373	ADI45373 Rice isop
273	33	55.9	21	2	AAW63607	AAW63607 Human com	346	33	55.9	1004	6	ABU54557	ABU54557 Human NOV
274	33	55.9	21	2	AAW63605	AAW63605 Human com	347	33	55.9	1004	8	ADH72222	ADH72222 Human pro
275	33	55.9	22	8	ADS33747	ADS33747 cMET-HGF	348	33	55.9	1004	8	ADH72214	ADH72214 Human pro
276	33	55.9	28	2	AAW63609	AAW63609 Human com	349	33	55.9	1004	8	ADH72224	ADH72224 Human pro
277	33	55.9	40	8	ADP21704	ADP21704 Human IGE	350	33	55.9	1048	2	AAW44506	AAW44506 BAMV coa
278	33	55.9	51	4	AAU51114	AAU51114 Propionib	351	33	55.9	1138	6	ABJ26107	ABJ26107 Aspergill
279	33	55.9	51	6	ABM47633	ABM47633 Propionib	352	33	55.9	1202	2	AAW44507	AAW44507 BAMV coa
280	33	55.9	57	4	AAU59258	AAU59258 Propionib	353	33	55.9	1231	6	ABU07436	ABU07436 Protein d
281	33	55.9	57	6	ABM55777	ABM55777 Propionib	354	33	55.9	1286	4	ABG10455	ABG10455 Novel hum
282	33	55.9	65	2	AAW63591	AAW63591 Human com	355	33	55.9	1907	6	ABU62071	ABU62071 Human ske
283	33	55.9	69	4	AAW92908	AAW92908 Human dig	356	33	55.9	2647	8	ADP25446	ADP25446 Plasmodiu
284	33	55.9	70	6	AAU45337	AAU45337 Propionib	357	33	55.9	2931	4	ABW68229	ABW68229 Drosophil
285	33	55.9	70	6	ABM41856	ABM41856 Propionib	358	33	55.9	3069	5	AAE20787	AAE20787 Human C3b
286	33	55.9	103	7	ADC97445	ADC97445 E. faeciu	359	33	55.9	3069	5	AAE20900	AAE20900 Human C3b
287	33	55.9	154	3	AAW40710	AAW40710 Human ORF	360	33	55.9	3100	5	AAE20789	AAE20789 Human C3b
288	33	55.9	155	6	ABM69477	ABM69477 Phototrab	361	33	55.9	3100	5	AAE20901	AAE20901 Human C3b
289	33	55.9	174	7	ADC95088	ADC95088 E. faeciu	362	33	55.9	3389	7	ADJ70480	ADJ70480 Human hea
290	33	55.9	180	4	AAU43388	AAU43388 Propionib	363	33	55.9	3567	8	ADH72216	ADH72216 Human pro
291	33	55.9	180	6	ABM39907	ABM39907 Propionib	364	33	55.9	4753	8	ADN22466	ADN22466 Bacterial
292	33	55.9	184	7	ADF13889	ADF13889 Human end	365	32.5	55.1	76	4	AAU42558	AAU42558 Propionib
293	33	55.9	185	6	ABU55961	ABU55961 Protein e	366	32.5	55.1	76	6	ABW39077	ABW39077 Propionib
294	33	55.9	190	5	AAE18631	AAE18631 Equine hi	367	32	54.2	7	2	AAW96393	AAW96393 RGD cycli
295	33	55.9	191	6	ABU54593	ABU54593 Human NOV	368	32	54.2	7	2	AAW66831	AAW66831 Peptide u
296	33	55.9	201	2	AAU27061	AAU27061 Recombina	369	32	54.2	7	2	AAW96984	AAW96984 Peptide u
297	33	55.9	230	4	AAU53393	AAU53393 Propionib	370	32	54.2	9	2	AAW96408	AAW96408 RGD cycli
298	33	55.9	230	6	ABM49912	ABM49912 Propionib	371	32	54.2	9	2	AAW66840	AAW66840 Cyclic pe
299	33	55.9	232	4	AAW42120	AAW42120 Human pol	372	32	54.2	9	2	AAW97003	AAW97003 Peptide u
300	33	55.9	236	2	AAU27060	AAU27060 Equine Pc	373	32	54.2	10	1	AAW90621	AAW90621 Peptide c
301	33	55.9	248	8	ADN18186	ADN18186 Bacterial	374	32	54.2	19	2	AAW13390	AAW13390 (59-78) hN
302	33	55.9	253	7	ABO83713	ABO83713 Pseudomon	375	32	54.2	20	2	ADF77514	ADF77514 DAF-7 pro
303	33	55.9	255	2	AAU27058	AAU27058 Equine Pc	376	32	54.2	20	3	AAW606057	AAW606057 Caenorhab
304	33	55.9	252	2	AAW92254	AAW92254 Neural ce	377	32	54.2	23	6	AAE30217	AAE30217 Human LP2
305	33	55.9	299	7	ABO73111	ABO73111 Pseudomon	378	32	54.2	23	6	AAE30316	AAE30316 Human LP2
306	33	55.9	299	8	ADH72218	ADH72218 Human pro	379	32	54.2	29	5	AAE18630	AAE18630 Human imm
307	33	55.9	349	4	AAW42035	AAW42035 Human pro	380	32	54.2	35	2	AAE29504	AAE29504 NGF, rat.
308	33	55.9	352	5	ABW1426	ABW1426 Herbicida	381	32	54.2	35	2	ADF77517	ADF77517 DAF-7 pro
309	33	55.9	411	4	ABW61304	ABW61304 Drosophil	382	32	54.2	35	3	AAW606060	AAW606060 Caenorhab
310	33	55.9	416	2	ADH11311	ADH11311 Vertebrat	383	32	54.2	35	8	ADP21822	ADP21822 Low densi
311	33	55.9	420	4	ABW66076	ABW66076 Novel hum	384	32	54.2	42	2	AAW29473	AAW29473 NGF, huma
312	33	55.9	460	4	AAW57313	AAW57313 Human bra	385	32	54.2	42	2	AAW29472	AAW29472 NGF, rat.
313	33	55.9	460	4	ABW51397	ABW51397 Human liv	386	32	54.2	43	2	ADF77515	ADF77515 DAF-7 pro
314	33	55.9	460	4	AAW05198	AAW05198 Peptide #	387	32	54.2	43	3	AAW606058	AAW606058 Caenorhab
315	33	55.9	461	7	ADG33762	ADG33762 Actinomyc	388	32	54.2	46	3	AAW25736	AAW25736 Human sec
316	33	55.9	474	6	ABU11478	ABU11478 Human MDD	389	32	54.2	60	3	AAW59598	AAW59598 Arabidops
317	33	55.9	488	6	ABU11731	ABU11731 Human MDD	390	32	54.2	60	3	AAW11176	AAW11176 Arabidops

PT regulate levels of lipid cellular mediators and in gene therapy of e.g.
 XX cancer.
 PS Claim 8; Fig 3A-B; 62pp; English.
 XX This is the amino acid sequence of human mature phosphatidic acid
 CC phosphatase-beta (PAP-beta), an enzyme that catalyses the conversion of
 CC phosphatidic acid into diacylglycerol. 3 Variants of human PAP, i.e. PAP-
 CC alpha 1 and 2 (see AAW79284-85), PAP-beta (see AAW79286) and PAP-gamma
 CC (see AAW79287) have been identified. The invention provides PAP
 CC polynucleotides (see AAV69086-89) and polypeptides, a method of preparing
 CC PAP in a transformed host cell, and a method of using PAP to
 CC dephosphorylate a substrate, especially lysophosphatidic acid, ceramide 1
 CC -phosphate or sphingosine 1-phosphate, particularly for production of
 CC diacylglycerol, but also monoacylglycerol, ceramide and sphingosine. PAP
 CC is able to control the balance of lipid mediators of cellular activation
 CC and signal transduction. Sequences that encode PAP are potentially
 CC useful, in gene therapy, for treatment of cancer (PAP may be tumour
 CC suppressors, PAP-alpha is expressed at lower levels in cancer cells than
 CC in normal cells of same tissue type), inflammatory disease and diabetes-
 XX associated obesity
 XX
 SQ Sequence 311 AA;
 Query Match 100.0%; Score 59; DB 2; Length 311;
 Best Local Similarity 100.0%; Pred. No. 0.095;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NYRCRGDDSK 10
 Db 178 NYRCRGDDSK 187
 |||||
 RESULT 2
 AD60703
 ID ADE60703 standard; protein; 311 AA.
 XX ADE60703;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein NP_003704, SEQ ID NO 6615.
 XX
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX
 OS Homo sapiens.
 XX
 PN WO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 XX (GEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 PA
 XX
 XX Woolf C, D'urso D, Befort K, Costigan M;
 XX
 XX WPI; 2003-268312/26.
 DR GENBANK; NP_003704.
 DR
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX
 XX The invention discloses a composition comprising two or more isolated rat

CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 311 AA;
 Query Match 100.0%; Score 59; DB 7; Length 311;
 Best Local Similarity 100.0%; Pred. No. 0.095;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NYRCRGDDSK 10
 Db 178 NYRCRGDDSK 187
 |||||
 RESULT 3
 ADM72103
 ID ADM72103 standard; protein; 311 AA.
 XX ADM72103;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Human tau-related polypeptide PPAP2B.
 XX
 KW Tau; PPAP2A; PPAP2B; IHPK1; IHPK3; IHPK2; FLJ20530; DJ434014.5; EZF1;
 KW LOC127424; LOC113179; KIAA0826; neuroprotective; neurotropic;
 KW antiparkinsonian; tau-protein kinase; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2004022708-A2.
 XX
 PD 18-MAR-2004.
 XX
 PF 04-SEP-2003; 2003WO-US027590.
 XX
 PR 09-SEP-2002; 2002US-0408877P.
 PR
 XX (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 PA
 XX Peany MB, Shulman JM;
 XX
 XX WPI; 2004-248456/23.
 DR
 XX New substantially pure Tau-related polypeptides and polynucleotides,
 PT useful for diagnosing and/or treating neurological conditions with
 PT aberrant expression of the Tau-related polypeptide, such as Alzheimer's
 PT disease.
 XX

PS Claim 1; SEQ ID NO 2; 62pp; English.

XX The invention relates to tau-related polypeptide consisting essentially

CC of an amino acid sequence selected from PPAP2A, PPAP2B, IHPK1, IHPK3,

CC IHPK2, FLJ20530, D434014.5, EF1, LOC127424, LOC113179 and KIAA0826

CC (ADW72102-ADM72112 respectively). The methods and compositions of the

CC present invention are useful for the diagnosis and/or treatment of

CC neurological diseases or conditions associated with aberrant expression

CC or activity of the Tau-related polypeptide, such as Alzheimer's disease

CC and Parkinson's disease. The present sequence represents a human tau-

CC related polypeptide homologue PPAP2B.

XX Sequence 311 AA;

QY Query Match 100.0%; Score 59; DB 8; Length 311;

XX Best Local Similarity 100.0%; Pred. No. 0.095; 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0;

QY 1 NYRCRGDDSK 10

DB 178 NYRCRGDDSK 187

RESULT 4

ADN04415

ID ADN04415 standard; protein; 311 AA.

XX AC ADN04415;

XX 01-JUL-2004 (first entry)

XX Antipsoriatic protein sequence #401.

XX antipsoriatic; gene therapy; psoriasis; diagnosis.

XX Homo sapiens.

XX WO2004028479-A2.

XX 08-APR-2004.

XX 25-SEP-2003; 2003WO-US030907.

XX 25-SEP-2002; 2002US-0414006P.

XX (GETH) GENENTECH INC.

XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;

PI Wu TD;

XX WPI: 2004-305105/28.

DR N-PSDB; ADN04414.

XX New PRO nucleic acid or polypeptide, useful for preparing a

PT pharmaceutical composition for diagnosing or treating psoriasis in a

PT mammal.

PS Claim 9; SEQ ID NO 809; 3069pp; English.

XX The invention relates to novel polynucleotide and polypeptides for

CC treating psoriasis or a sequence having at least 80% identity to the

CC above sequences. The nucleic acid is useful for preparing a composition

CC for diagnosing or treating psoriasis in a mammal. This sequence

CC corresponds to one of the polypeptides of the invention.

XX Sequence 311 AA;

QY Query Match 100.0%; Score 59; DB 8; Length 311;

XX Best Local Similarity 100.0%; Pred. No. 0.095;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10

DB 178 NYRCRGDDSK 187

DB 178 NYRCRGDDSK 187

RESULT 5

ADP24274

ID ADP24274 standard; protein; 311 AA.

XX ADP24274;

AC ADP24274;

XX 18-NOV-2004 (first entry)

DT PRO polypeptide SEQ ID NO:1452.

XX

XX PRO: antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;

KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;

KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.

XX Unidentified.

OS WO2004041170-A2.

PN 21-MAY-2004.

PD 30-OCT-2003; 2003WO-US034312.

PF 01-NOV-2002; 2002US-0423394P.

XX (GETH) GENENTECH INC.

XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;

PI Wu TD;

XX WPI: 2004-419628/39.

DR N-PSDB; ADP24273.

XX New PRO polypeptides and polynucleotides, useful for treating e.g.

PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated

PT renal disease, or demyelinating diseases of the central or peripheral

PT nervous system.

XX Claim 7; SEQ ID NO 1452; 2940pp; English.

PS The invention relates to a novel isolated nucleic acid and the PRO

CC polypeptide encoded by it. A protein of the invention has

CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,

CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,

CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide

CC of the invention may have a use in gene therapy. The PRO polypeptide, its

CC agonist, antagonist, or antibody that specifically binds to the

CC polypeptide is useful for treating an immune related disorder such as

CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,

CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an

CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic

CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune

CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal

CC disease, a demyelinating disease of the central or peripheral nervous

CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,

CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary

CC disease, infectious or autoimmune chronic active hepatitis, primary

CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,

CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's

CC disease, an autoimmune or immune-mediated skin disease, a bullous skin

CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic

CC disease, asthma, allergic rhinitis, atopic dermatitis, food

CC hypersensitivity, urticaria, an immunologic disease of the lung,

CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity

CC pneumonitis, a transplantation associated disease, graft rejection or

CC graft-versus-host disease. The present sequence represents a PRO protein

CC of the invention.

XX Sequence 311 AA;

SQ Query Match 100.0%; Score 59; DB 8; Length 311;

Best Local Similarity 100.0%; Pred. No. 0.095;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
Db 178 NYRCRGDDSK 187

RESULT 6
ABB99112
ID ABB99112 standard; protein; 312 AA.
XX
AC ABB99112;
XX
DT 29-OCT-2002 (first entry)
XX
DE Rat phosphatase #2.
XX
KW Phosphatase; prenilyphosphoric acid; prenily alcohol; rat.
XX
OS Rattus norvegicus.
XX
PN WO200253751-A1.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-JP011223.
XX
PR 28-DEC-2000; 2000JP-00401515.
PR 28-DEC-2000; 2000JP-00401806.
XX
PA (TOYW) TOYOTA CHUO KENKYUSHO KK.
PA (TOYT) TOYOTA JIDOSHA KK.
XX
PI Tokuhiko K, Muramoto N, Yamada Y, Asami O, Hirai M, Ohto C;
PI Obata S, Muramatsu M;
XX
DR WPI; 2002-643303/69.
DR N-PSDB; ABQ78948.
XX
PT Phosphatase polypeptides and encoded polynucleotides with substrate-
PT specificity for prenilyphosphoric acid, applicable in mass-production of
PT all-trans-prenily alcohols by culturing transformants.
XX
PS Claim 1; Page 67-68; 93pp; Japanese.
XX
CC The invention relates to a novel phosphatase polypeptide, exhibiting
CC substrate-specificity for not less than 15C prenilyphosphoric acid. The
CC polynucleotides and encoded polypeptides are applicable in mass-
CC production of all-trans-prenily alcohols. The sequence represents a rat
CC phosphatase polypeptide of the invention
XX
SQ Sequence 312 AA;

Query Match 93.2%; Score 55; DB 5; Length 312;
Best Local Similarity 90.0%; Pred. No. 0.45;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
Db 179 NYRCRGDDSK 188

RESULT 7
ADE60701
ID ADE60701 standard; protein; 312 AA.
XX
AC ADE60701;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein CAA69106, SEQ ID NO 6613.
XX

KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; CAA69106.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 312 AA;

Query Match 93.2%; Score 55; DB 7; Length 312;
Best Local Similarity 90.0%; Pred. No. 0.45;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
Db 179 NYRCRGDDSK 188

RESULT 8
ABG23434
ID ABG23434 standard; protein; 152 AA.
XX
AC ABG23434;
XX

DT 18-FEB-2002 (first entry)
XX Novel human diagnostic protein #23425.
DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
KW Homo sapiens.
OS WO200175067-A2.
PN 11-OCT-2001.
PD 30-MAR-2001; 2001WO-US008631.
XX 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
PI WPI; 2001-639362/73.
XX N-PSDB; AAS87621.
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX Claim 20; SEQ ID NO 53793; 103pp; English.
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 152 AA;
Query Match 69.5%; Score 41; DB 4; Length 152;
Best Local Similarity 70.0%; Pred. No. 50;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 NYRCRGDDSK 10
Db 68 NHRCRGDLTK 77
-:|||||:-|
RESULT 9
AAU28253
ID AAU28253 standard; protein; 237 AA.
XX AAU28253;
AC AAU28253;
XX 18-DEC-2001 (first entry)
DT

DE Novel human secretory protein, Seq ID No 610.
XX Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
KW gut protection; lung; liver fibrosis; immune deficiency; infection;
KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
KW fertility; analgesic; pain; antigen.
XX Homo sapiens.
XX WO200166689-A2.
XX 13-SEP-2001.
XX 05-MAR-2001; 2001WO-US004942.
XX 07-MAR-2000; 2000US-00519705.
PR 19-MAY-2000; 2000US-00574454.
PR 17-JUN-2000; 2000US-00596193.
PR 14-JUL-2000; 2000US-00616847.
PR 19-SEP-2000; 2000US-00665363.
PR 20-OCT-2000; 2000US-00693267.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
XX WPI; 2001-589934/66.
XX N-PSDB; AAS45153.
XX Novel polypeptides and nucleic acids obtained from cDNA libraries
PT prepared from various human tissues, for diagnosis and treatment of
PT cancer, neurological, inflammatory, and autoimmune disorders.
XX Example 2; SEQ ID NO 610; 107pp; English.
XX The invention relates to novel isolated human secreted polypeptides (I)
CC and polynucleotides (II). (I) and (II) are useful for treating
CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
CC involved in increasing haematopoiesis, stem cell survival, bone growth
CC and remodeling. (I), (II) and modulators of (II) are useful for
CC prophylaxis or treatment of one or more cancers. (II) is also useful for
CC creating transgenic animals useful for studying the in vivo activities of
CC the polypeptide as well as for studying modulators of the polypeptides.
CC (I) induces the proliferation of neural cells and regeneration of nerve
CC and brain tissue and is useful for the treatment of central and
CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
CC activity, regulation of haematopoiesis and is useful for treating myeloid
CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
CC and for regeneration of bone, cartilage tendon, ligament and/or nerve
CC tissue growth, and in tissue repair, healing of burns, incisions, ulcers,
CC for treating osteoporosis, osteoarthritis, bone degenerative disorders,
CC or periodontal disease. Furthermore, (I) is also useful for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues, various immune deficiencies and
CC disorders including severe combined immunodeficiency (SCID), bacterial or
CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
CC reactions and conditions, such as asthma or other respiratory problems.
CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
CC fertility, metabolism, catabolism, anabolism, storage or elimination of
CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
CC analgesic effects or other pain reducing effects, immunoglobulin like
CC activity and can act as an antigen in a vaccine composition to raise an
CC immune response. AAU28020-AAU28395 represent novel human secreted protein

CC amino acid sequences of the invention
SQ Sequence 237 AA;

Query Match 69.5%; Score 41; DB 4; Length 237;
Best Local Similarity 70.0%; Pred. No. 78;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
|:|||||:
Db 5 NHRCRGDLTK 14

RESULT 10

ADSL2199
ID ADSL2199 standard; protein; 237 AA.

XX AC ADSL2199;

DT 16-DEC-2004 (first entry)

XX DE Human therapeutic contig protein - SEQ ID 2436.

XX KW antiinflammatory; neuroprotective; antianaemic; cytostatic; vulneryary;
XX KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
XX KW aplastic anaemia; cancer; wound healing; gene therapy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 1..237 /label= Unknown, OTHER

FT FT /note= "OTHER = In-frame STOP codon"

XX PN WO2004080148-A2.

XX PD 23-SEP-2004.

XX PF 30-SEP-2003; 2003WO-US030720.

XX PR 02-OCT-2002; 2002US-0416186P.

XX PA (NUVE-) NUVELO INC.

XX PI Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
XX PI Wang D, Chen E, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;

XX DR WPI: 2004-668857/65.

XX DR N-PSDB; ADSL1601.

XX PT New polynucleotide, useful in preparing a composition for diagnosing or
XX PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
XX PT aplastic anemia or cancer for promoting wound healing.

XX PS Example 2; SEQ ID NO 2436; 718pp; English.

XX CC The invention relates to a novel isolated polynucleotide and the encoded
XX CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
XX CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
XX CC be useful in preparing a composition for diagnosing or treating
XX CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
XX CC disorders, such as aplastic anaemia or cancer, as well as for promoting
XX CC wound healing. The molecules may also be utilised during gene therapy
XX CC procedures. The current sequence is that of a human therapeutic contig
XX CC protein of the invention.

XX SQ Sequence 237 AA;

Query Match 69.5%; Score 41; DB 8; Length 237;
Best Local Similarity 70.0%; Pred. No. 78;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10

Db |:|||||:
5 NHRCRGDLTK 14

RESULT 11

ADJ50947

ID ADJ50947 standard; protein; 421 AA.

XX AC ADJ50947;

XX DT 06-MAY-2004 (first entry)

XX DE Human novel protein NOV4b.

XX KW Human; NOVX; autoimmune disease; Alzheimer's disease; stroke; allergy;
XX KW Parkinson's disease; Huntington's disease; multiple sclerosis; anxiety;
XX KW pain; diabetes; graft versus host disease; pancreatitis; obesity; ulcer;
XX KW anaemia; cancer; viral infection; bacterial infection;
XX KW parasitic infection.

XX OS Homo sapiens.

XX PN US2004030096-A1.

XX PD 12-FEB-2004.

XX PF 01-AUG-2002; 2002US-00210281.

XX PR 02-AUG-2001; 2001US-0309501P.

XX PR 03-AUG-2001; 2001US-0310291P.

XX PR 08-AUG-2001; 2001US-0310951P.

XX PR 09-AUG-2001; 2001US-0311292P.

XX PR 13-AUG-2001; 2001US-0311979P.

XX PR 14-AUG-2001; 2001US-0312203P.

XX PR 17-AUG-2001; 2001US-0313201P.

XX PR 20-AUG-2001; 2001US-0313643P.

XX PR 20-AUG-2001; 2001US-0313702P.

XX PR 21-AUG-2001; 2001US-0314031P.

XX PR 23-AUG-2001; 2001US-0314466P.

XX PR 28-AUG-2001; 2001US-0315403P.

XX PR 29-AUG-2001; 2001US-0315853P.

XX PR 05-MAR-2002; 2002US-0361775P.

XX PR 05-MAR-2002; 2002US-0361832P.

XX (GORM/) GORMAN L.

XX (ZERR/) ZERHUSEN B D.

XX (EDIN/) EDINGER S R.

XX (PADI/) PADIGARU M.

XX (GUOX/) GUO X.

XX (KEKU/) KEKUDA R.

XX (ZHON/) ZHONG M.

XX (PATT/) PATTURAJAN M.

XX (MILL/) MILLER C E.

XX (JIWU/) JI W.

XX (PERA/) PERA C E A.

XX (BURG/) BURGESS C E.

XX (SCIO/) SCIORE P.

XX (STON/) STONE D J.

XX (TAUP/) TAUPIER R J.

XX (CASH/) CASHMAN S J.

XX (ROTH/) ROTHENBERG M E.

XX (MAL/) MALYANKAR U M.

XX (BOLD/) BOLDOG F L.

XX Gorman L, Zerhusen BD, Edinger SR, Padigaru M, Guo X, Kekuda R;

XX Zhong M, Patturajan M, Miller CE, Ji W, Pena, CEA, Burgess CE;

XX Sciore P, Stone DJ, Taupier RJ, Casman SJ, Rothenberg MS;

XX Malyankar UM, Boldog FL;

XX WPI: 2004-168942/16.

XX DR N-PSDB; ADJ50946.

XX XT New NOVX polypeptides and polynucleotides, useful in diagnosing, treating

PT or preventing diseases or conditions, e.g. autoimmune disease,
 PT Alzheimer's disease, diabetes, graft versus host disease, cancer or viral
 PT or bacterial infections.

XX Claim 2; SEQ ID NO 12; 342pp; English.

XX The invention relates to an isolated NOVX polypeptide (of 44 disclosed)
 CC comprising its mature form, a sequence having at least 95% sequence
 CC identity to NOVX or a sequence comprising one or more conservative
 CC substitutions in the amino acid sequence of NOVX. Also included are a
 CC composition comprising NOVX and a carrier, a kit comprising, in one or
 CC more containers, the composition, a method of identifying an agent that
 CC binds to NOVX, a method for identifying a potential therapeutic agent for
 CC use in treatment of a pathology related to aberrant expression or
 CC aberrant physiological interactions of NOVX, a method for screening for a
 CC modulator of activity of or of latency or predisposition to a pathology
 CC associated with NOVX, a method for modulating the activity of NOVX, a
 CC method of treating or preventing a pathology associated with NOVX or a
 CC pathological state in a mammal, an isolated nucleic acid molecule
 CC encoding a NOVX protein, a vector comprising the nucleic acid molecule,
 CC a cell comprising the vector, an antibody that immunospecifically binds
 CC to NOVX, a method for determining the presence or amount of NOVX or the
 CC nucleic acid molecule in a sample, a method for determining the presence
 CC of or predisposition to a disease associated with altered levels of
 CC expression of NOVX or the nucleic acid molecule in a first mammalian
 CC subject and a method of producing NOVX (comprising culturing the cell
 CC under conditions that lead to expression of the polypeptide). NOVX is
 CC useful in the manufacture of a medicament for treating a syndrome
 CC associated with a human disease associated with NOVX. The polypeptides
 CC and nucleic acid molecules are useful in diagnosing, treating or
 CC preventing diseases or conditions, e.g. autoimmune disease, Alzheimer's
 CC disease, stroke, allergies, Parkinson's disease, Huntington's disease,
 CC multiple sclerosis, anxiety, pain, diabetes, graft versus host disease,
 CC pancreatitis, obesity, ulcers, anæmia, cancer, viral or bacterial and
 CC parasitic infections (many more diseases and disorders are listed in the
 CC specification). The present sequence represents a NOVX protein.

XX Sequence 421 AA;

Query Match 69.5%; Score 41; DB 8; Length 421;

Best Local Similarity 70.0%; Pred. NO. 1.4e+02;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NVRCRGDSDK 10

Db 197 NHRCRGDLTK 206

RESULT 12

ADJ50945

ID ADJ50945 standard; protein; 424 AA.

AC ADJ50945;

DT 06-MAY-2004 (first entry)

DE Human novel protein NOV4a.

XX Human; NOVX; autoimmune disease; Alzheimer's disease; stroke; allergy;
 KW Parkinson's disease; Huntington's disease; multiple sclerosis; anxiety;
 KW pain; diabetes; graft versus host disease; pancreatitis; obesity; ulcer;
 KW anaemia; cancer; viral infection; bacterial infection;
 KW parasitic infection.

XX Homo sapiens.

XX US2004030096-A1.

XX 12-FEB-2004.

XX 01-AUG-2002; 2002US-00210281.

XX 02-AUG-2001; 2001US-0309501P.

PR 03-AUG-2001; 2001US-0310291P.
 PR 08-AUG-2001; 2001US-0310951P.
 PR 09-AUG-2001; 2001US-0311292P.
 PR 13-AUG-2001; 2001US-0311979P.
 PR 14-AUG-2001; 2001US-0312203P.
 PR 17-AUG-2001; 2001US-0313201P.
 PR 20-AUG-2001; 2001US-0313643P.
 PR 20-AUG-2001; 2001US-0313702P.
 PR 21-AUG-2001; 2001US-0314031P.
 PR 23-AUG-2001; 2001US-0314466P.
 PR 28-AUG-2001; 2001US-0315403P.
 PR 29-AUG-2001; 2001US-0315853P.
 PR 05-MAR-2002; 2002US-0361775P.
 PR 05-MAR-2002; 2002US-0361832P.

XX (GORM/) GORMAN L.
 PA (ZERRH/) ZERRHUSEN B D.
 PA (EDIN/) EDINGER S R.
 PA (PADI/) PADIGARU M.
 PA (GUOX/) GUO X.
 PA (KEKU/) KEKUDA R.
 PA (ZHON/) ZHONG M.
 PA (PATI/) PATTURAJAN M.
 PA (MILL/) MILLER C E.
 PA (JIWW/) JI W.
 PA (PENA/) PENA C E A.
 PA (BURG/) BURGESS C E.
 PA (SCIO/) SCIORE P.
 PA (STON/) STONE D J.
 PA (TAUP/) TAUPIER R J.
 PA (CASM/) CASMAN S J.
 PA (ROTH/) ROTHENBERG M E.
 PA (MALY/) MALYANKAR U M.
 PA (BOLD/) BOLDG F L.

XX Gorman L, Zerrhusen BD, Edinger SR, Padigaru M, Guo X, Kekuda R;
 PI Zhong M, Patturajan M, Miller CE, Ji W, Pena CEA, Burgess CE;
 PI Sciore P, Stone DJ, Taupier RJ, Casman SJ, Rothenberg ME;
 PI Malyankar UM, Boldog FL;
 XX WPI; 2004-168942/16.
 DR N-PSDB; ADJ50944.

XX New NOVX polypeptides and polynucleotides, useful in diagnosing, treating
 PT or preventing diseases or conditions, e.g. autoimmune disease,
 PT Alzheimer's disease, diabetes, graft versus host disease, cancer or viral
 PT or bacterial infections.

PS Claim 2; SEQ ID NO 10; 342pp; English.

XX The invention relates to an isolated NOVX polypeptide (of 44 disclosed)
 CC comprising its mature form, a sequence having at least 95% sequence
 CC identity to NOVX or a sequence comprising one or more conservative
 CC substitutions in the amino acid sequence of NOVX. Also included are a
 CC composition comprising NOVX and a carrier, a kit comprising, in one or
 CC more containers, the composition, a method of identifying an agent that
 CC binds to NOVX, a method for identifying a potential therapeutic agent for
 CC use in treatment of a pathology related to aberrant expression or
 CC aberrant physiological interactions of NOVX, a method for screening for a
 CC modulator of activity of or of latency or predisposition to a pathology
 CC associated with NOVX, a method for modulating the activity of NOVX, a
 CC method of treating or preventing a pathology associated with NOVX or a
 CC pathological state in a mammal, an isolated nucleic acid molecule
 CC encoding a NOVX protein, a vector comprising the nucleic acid molecule,
 CC a cell comprising the vector, an antibody that immunospecifically binds
 CC to NOVX, a method for determining the presence or amount of NOVX or the
 CC nucleic acid molecule in a sample, a method for determining the presence
 CC of or predisposition to a disease associated with altered levels of
 CC expression of NOVX or the nucleic acid molecule in a first mammalian
 CC subject and a method of producing NOVX (comprising culturing the cell
 CC under conditions that lead to expression of the polypeptide). NOVX is
 CC useful in the manufacture of a medicament for treating a syndrome
 CC associated with a human disease associated with NOVX. The polypeptides

CC and nucleic acid molecules are useful in diagnosing, treating or
CC preventing diseases or conditions, e.g. autoimmune disease, Alzheimer's
CC disease, stroke, allergies, Parkinson's disease, Huntington's disease,
CC multiple sclerosis, anxiety, pain, diabetes, graft versus host disease,
CC pancreatitis, obesity, ulcers, anaemia, cancer, viral or bacterial and
CC parasitic infections (many more diseases and disorders are listed in the
CC specification). The present sequence represents a NOVX protein.
XX

SQ Sequence 424 AA;
Query Match 69.5%; Score 41; DB 8; Length 424;
Best Local Similarity 70.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 NYRCRGDDSK 10
|:|||||:
Db 198 NHRCRGDLTK 207

RESULT 13
ADA83857
ID ADA83857 standard; protein; 428 AA.
XX AC
XX ADA83857;
XX DT 20-NOV-2003 (first entry)
XX DE Human POM18 protein.
XX KW human; marker; expressed sequence tag; EST; arabidopsis; tumour;
XX KW stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;
XX KW vaccine.
XX OS Homo sapiens.
XX WO2002103028-A2.
XX PD 27-DEC-2002.
XX PF 30-MAY-2002; 2002WO-IB004189.
XX PR 30-MAY-2001; 2001US-0293999P.
XX PR 22-OCT-2001; 2001US-0330457P.
XX PR 19-FEB-2002; 2002US-0357144P.
XX PA (BIOM-) BIOMEDICAL CENT.

XX Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LL;
XX WPI; 2003-175241/17.
XX DR N-PSDB; ADA83856.
XX PT Determining if a nucleic acid is a marker for a phenotype/cell type of
XX PT interest, by global comparison of expressed sequence tags known to be
XX PT expressed in the phenotype/cell type with all ESTs expressed in normal
XX PT tissue.
XX PS Claim 29; Page 269-271; 516pp; English.

XX The invention relates to a novel method for determining if a nucleic acid
XX is a marker for a predetermined phenotype/cell type of interest from a
XX biological species. The method comprises performing a global comparison
XX of a group of expressed sequence tags (ESTs) known to be expressed in the
XX phenotype/cell type of interest with all ESTs expressed in normal tissue
XX in order to identify ESTs that are preferentially expressed in the
XX phenotype/cell of interest. A method of the invention is useful for
XX determining whether a nucleic acid is a marker for a predetermined
XX phenotype or cell type of interest from a biological species, preferably
XX Arabidopsis or human. The cell type of interest is an abnormal cell such
XX as a tumour cell, and the predetermined phenotype is a stress-induced
XX phenotype such as hyperosmotic stress or high salt conditions. A method
XX of the invention is also useful for determining the progression of colon
XX cancer in a human, for detecting a tumour cell, and for regulating or

CC preventing the growth of a tumour cell. An antibody of the invention is
CC useful for detecting the absence or presence of peptides encoded by
CC tumour-associated markers. A polypeptide of the invention is useful as an
CC immunogen for vaccinating an animal. The present sequence represents a
XX tumour-associated antigen of the invention.

SQ Sequence 428 AA;
Query Match 69.5%; Score 41; DB 6; Length 428;
Best Local Similarity 70.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 NYRCRGDDSK 10
|:|||||:
Db 197 NHRCRGDLTK 206

RESULT 14
ADR09234
ID ADR09234 standard; protein; 481 AA.
XX AC
XX ADR09234;
XX DT 04-NOV-2004 (first entry)
XX DE Human protein useful for treating neurological disease Seq 2740.
XX KW human; oligo-capping method; diagnostic marker; gene therapy;
XX KW osteoporosis; neurological disease; Alzheimer's disease;
XX KW Parkinson's disease; dementia; short memory; cancer;
XX KW sense or motor function; emotional reaction; fear response; panic;
XX KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
XX KW tranquiliser.
XX OS Homo sapiens.
XX EP1447413-A2.
XX PD 18-AUG-2004.
XX PF 12-FEB-2004; 2004EP-00003145.
XX PR 14-FEB-2003; 2003JP-00102207.
XX PR 09-MAY-2003; 2003JP-00131452.
XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;
XX Wakamatsu A, Ishii S, Nagai K, Irie R;
XX WPI; 2004-583265/57.
XX DR N-PSDB; ADR07278.
XX PT New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
XX PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX PS Claim 1; SEQ ID NO 2740; 2686pp; English.

XX This invention relates to novel, isolated full length human cDNA
XX molecules and the encoded proteins thereof. Specifically, it refers to
XX cDNA clones obtained by an oligo-capping method, where none of these
XX clones are identical to any known human mRNAs. The present invention
XX describes an immunoassay to identify agonists and antagonists, as well as
XX antibodies, antisense molecules and siRNAs that can all be used to bind
XX to and modulate expression of the cDNA molecules. As such, these
XX molecules are useful for diagnostic markers or therapeutic targets for
XX the various diseases or morbid states. In particular, they are useful in
XX gene therapy for treating osteoporosis, neurological disease, Alzheimer's
XX disease, Parkinson's disease, dementia, short memory and various cancers,
XX as well as for maintaining equilibrium of sense or motor function, and
XX for treating emotional reaction, fear response and panic. Accordingly,
XX they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,
XX cytostatic and tranquiliser activities. This polypeptide is a protein

CC encoded by a full length human cDNA sequence of the invention. NOTE: This
CC sequence is not given in the sequence listing of the specification but
CC can be obtained on CD-ROM from the European Patent Office, Vienna Sub-
CC office.

XX SQ Sequence 481 AA;

Query Match 69.5%; Score 41; DB 8; Length 481;
Best Local Similarity 70.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
|:|||||:|
Db 250 NHRCRGDLTK 259

RESULT 15
ADS10966
ID ADS10966 standard; protein; 481 AA.

XX AC ADS10966;

XX DT 16-DEC-2004 (first entry)

XX DE Human therapeutic protein - SEQ ID 1203.

XX KW antinflammatory; neuroprotective; antianaemic; cytostatic; vulnery;
XX KW inflammatory; haematopoesis; immunity; neurodegenerative; stem cell;
XX KW aplastic anaemia; cancer; wound healing; gene therapy.

XX OS Homo sapiens.

XX PN WO2004080148-A2.

XX PD 23-SEP-2004.

XX PF 30-SEP-2003; 2003WO-US030720.

XX PR 02-OCT-2002; 2002US-0416186P.

XX PA (NUVE-) NUVELO INC.

XX PI Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
XX PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Wang G, Zhou P;

XX WPI: 2004-668857/65.

XX DR N-PSDB; ADS10282.

XX PT New polynucleotide, useful in preparing a composition for diagnosing or
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
PT aplastic anemia or cancer for promoting wound healing.

XX PS Claim 20; SEQ ID NO 1203; 718pp; English.

XX CC The invention relates to a novel isolated polynucleotide and the encoded
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
CC neuroprotective, antianaemic, cytostatic and vulnery activities and may
CC be useful in preparing a composition for diagnosing or treating
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
CC disorders, such as aplastic anaemia or cancer, as well as for promoting
CC wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic protein
CC of the invention. The current sequence is not shown explicitly within the
CC specification but can be accessed from the WIPO web-site.

XX SQ Sequence 481 AA;

Query Match 69.5%; Score 41; DB 8; Length 481;
Best Local Similarity 70.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
|:|||||:|

Db 250 NHRCRGDLTK 259

RESULT 16

ADM04303
ID ADM04303 standard; protein; 489 AA.

XX AC ADM04303;

XX DT 20-MAY-2004 (first entry)

XX DE Human protein of the invention SEQ ID NO:2988.

XX KW human; gene therapy; diagnostic marker; pharmaceutical.

XX OS Homo sapiens.

XX PN EP1347046-A1.

XX PD 24-SEP-2003.

XX PF 12-APR-2002; 2002EP-00008400.

XX PR 22-MAR-2002; 2002JP-00137785.

XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX PI Isogai T, Sugiyama T, Otsuki T, Wakanatsu A, Sato H, Ishii S;
XX PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
XX PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

XX DR WPI: 2003-723558/69.

XX DR N-PSDB; ADM01860.

XX PT New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.

XX PS Claim 1; SEQ ID NO 2988; 305pp; English.

XX CC The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
CC protein sequence of the invention.

XX SQ Sequence 489 AA;

Query Match 69.5%; Score 41; DB 7; Length 489;
Best Local Similarity 70.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDDSK 10
|:|||||:|
Db 258 NHRCRGDLTK 267

RESULT 17

ABU31582
ID ABU31582 standard; protein; 400 AA.

XX AC ABU31582;

XX DT 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #17109.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

```

XX OS Klebsiella pneumoniae.
XX ID ABU45262 standard; protein; 400 AA.
XX AC ABU45262;
XX DT 19-JUN-2003 (first entry)
XX DE Protein encoded by Prokaryotic essential gene #30789.
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX OS Salmonella paratyphi.
XX PN WO200277183-A2.
XX PD 03-OCT-2002.
XX PF 21-MAR-2002; 2002WO-US009107.
XX PR 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX PR 25-OCT-2001; 2001US-0342923P.
XX PR 08-FEB-2002; 2002US-00072851.
XX PR 06-MAR-2002; 2002US-0362699P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX DR WPI; 2003-029926/02.
XX DR N-PSDB; ACA35452.
XX PT New antisense nucleic acids, useful for identifying proteins or screening
XX PT for homologous nucleic acids required for cellular proliferation to
XX PT isolate candidate molecules for rational drug discovery programs.
XX PS Claim 25; SEQ ID NO 59506; 1766pp; English.
XX CC The invention relates to an isolated nucleic acid comprising any one of
XX CC the 6213 antisense sequences given in the specification where expression
XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:
XX CC (1) a vector comprising a promoter operably linked to the nucleic acid
XX CC encoding a polypeptide whose expression is inhibited by the antisense
XX CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX CC antisense nucleic acid; (4) an antibody capable of specifically binding
XX CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX CC proliferation or the activity of a gene in an operon required for
XX CC proliferation; (7) identifying a compound that influences the activity of
XX CC the gene product or that has an activity against a biological pathway
XX CC required for proliferation, or that inhibits cellular proliferation; (8)
XX CC identifying a gene required for cellular proliferation or the biological
XX CC pathway in which a proliferation-required gene or its gene product lies
XX CC or a gene on which the test compound that inhibits proliferation of an
XX CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX CC compound's activity; (11) a culture comprising strains in which the gene
XX CC product is overexpressed or underexpressed; (12) determining the extent
XX CC to which each of the strains is present in a culture or collection of
XX CC strains; or (13) identifying the target of a compound that inhibits the
XX CC proliferation of an organism. The antisense nucleic acids are useful for
XX CC identifying proteins or screening for homologous nucleic acids required
XX CC for cellular proliferation to isolate candidate molecules for rational
XX CC drug discovery programs, or for screening homologous nucleic acids
XX CC required for proliferation in cells other than S. aureus, S. typhimurium,
XX CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
XX CC the target prokaryotic essential genes. Note: The sequence data for this
XX CC patent did not form part of the printed specification, but was obtained
XX CC in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 400 AA;

Query Match 67.8%; Score 40; DB 6; Length 400;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
:|||||
DB 39 FRCRGDD 45

RESULT 18

```

Query Match 67.8%; Score 40; DB 6; Length 400;
Best Local Similarity 85.7%; Pred. NO. 1.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
DB 39 FRCRGDD 45
:|||||

RESULT 19
ABU48051
ID ABU48051 standard; protein; 400 AA.
XX
AC ABU48051;
DT 19-JUN-2003 (first entry)
DE Protein encoded by Prokaryotic essential gene #33578.
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Salmomella typhi.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
DR N-PSDB; ACA51921.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 75975; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational

CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 400 AA;

Query Match 67.8%; Score 40; DB 6; Length 400;
Best Local Similarity 85.7%; Pred. NO. 1.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
DB 39 FRCRGDD 45
:|||||

RESULT 20
ABU15369
ID ABU15369 standard; protein; 400 AA.
XX
AC ABU15369;
DT 19-JUN-2003 (first entry)
DE Protein encoded by Prokaryotic essential gene #896.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Escherichia coli.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
DR N-PSDB; ACA19239.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 43293; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological

CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 400 AA;

Query Match 67.8%; Score 40; DB 6; Length 400;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
DB 39 FRCRGDD 45
:|||||

RESULT 21
ABO65513
ID ABO65513 standard; protein; 424 AA.
AC ABO65513;
XX
XX 29-JUL-2004 (first entry)
XX
DE Klebsiella pneumoniae polypeptide seqid 12030.
XX
KW Recombinant expression vector; transcription regulatory element;
KW Klebsiella pneumoniae protein; antibacterial; Vaccine.
XX
XX Klebsiella pneumoniae.
OS
XX
XX US6610836-B1.
XX
XX 26-AUG-2003.
XX
XX 27-JAN-2000; 2000US-00489039.
XX
XX 29-JAN-1999; 99US-0117747P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Breton GL, Osborne M;
XX
XX WPI; 2003-895346/82.
DR N-PSDB; ACH99064.
XX
XX New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
XX preparing a vaccine composition against Klebsiella pneumoniae.
XX
XX Disclosure; SEQ ID NO 12030; 932pp; English.
XX
XX The invention describes a new isolated nucleic acid encoding a Klebsiella
XX pneumoniae polypeptide. Also described are: a recombinant expression
XX vector comprising the nucleic acid, operably linked to a transcription
XX regulatory element; and a cell comprising the recombinant expression
XX vector. The nucleic acid is useful for preparing a vaccine composition
XX against Klebsiella pneumoniae. This is the amino acid sequence of a
XX Klebsiella pneumoniae polypeptide of the invention
XX
SQ Sequence 424 AA;

Query Match 67.8%; Score 40; DB 6; Length 400;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
DB 39 FRCRGDD 45
:|||||

RESULT 22
ADB74255
ID ADB74255 standard; protein; 705 AA.
XX
XX ADB74255;
XX
XX 04-DEC-2003 (first entry)
XX
XX Mycobacterium tuberculosis non-naturally occurring peptide #3.
XX
XX Non-naturally occurring peptide; anion pump protein; tuberculosis;
KW hypersensitivity reaction; tuberculostatic.
XX
XX Mycobacterium tuberculosis.
XX
XX US6583266-B1.
XX
XX 24-JUN-2003.
XX
XX 16-SEP-1994; 94US-00311731.
XX
XX 19-AUG-1993; 93US-00109181.
XX
XX 22-OCT-1993; 93US-00142558.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Smith DR, Mao J;
XX
XX WPI; 2003-656441/62.
DR N-PSDB; ADB74252.
XX
XX New Mycobacterium tuberculosis anion pump peptide useful for as
XX tuberculosis vaccine and diagnosis of tuberculosis infection.
XX
XX Disclosure; SEQ ID NO 4; 26pp; English.
XX
XX The invention relates to a non-naturally occurring peptide of
XX Mycobacterium tuberculosis comprising an amino acid sequence
XX corresponding to an anion pump protein. The invention also relates to a
XX non-naturally occurring nucleic acid corresponding to a DNA sequence of
XX Mycobacterium tuberculosis or Mycobacterium leprae. The new peptide is
XX useful as a vaccine against Mycobacterium tuberculosis or Mycobacterium
XX leprae or for screening for new tuberculosis drugs. Purified proteins
XX derived from the sequences of the invention may elicit a specific immune
XX response. The peptide may also be used to detect hypersensitivity
XX reactions of individuals exposed to Mycobacterium tuberculosis or
XX Mycobacterium leprae. The proteins and peptides may be affixed to solid
XX supports to detect antibodies typical of hypersensitivity reactions, from
XX a patient's sera. This sequence represents Mycobacterium tuberculosis non
XX -naturally occurring peptide of the invention. Note: The sequence data
XX for this patent did not form part of the printed specification but was
XX obtained in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html.
XX
XX Sequence 705 AA;
SQ

Query Match 67.8%; Score 40; DB 7; Length 705;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YRCRGDDSK 10
DB 383 YRCRADDT 391
:|||||

XX	RESULT 23	
XX	ABP72189	
XX	ID ABP72189 standard; protein; 1304 AA.	
XX	AC ABP72189;	
XX	DT 22-APR-2003 (first entry)	
XX	DE Plasmodium berghei modular secreted protein PbSR.	
XX	PbSR; protein secretion; malaria; diagnosis; vaccine; antimalarial;	
XX	KW protozoacide.	
XX	OS Plasmodium berghei.	
XX	Key Location/Qualifiers	
XX	FT Peptide 1..22	
XX	FT /label= Signal_peptide	
XX	FT Protein 23..1304	
XX	FT /label= Mature_protein	
XX	WO2003004524-A2.	
XX	PN 16-JAN-2003.	
XX	PD 02-JUL-2002; 2002WO-GB003045.	
XX	PF 02-JUL-2001; 2001GB-00016185.	
XX	PR (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.	
XX	PA Claudianos C, Crompton TK, Dessens JT, Sindén RE, Trueman HE;	
XX	PI WPI; 2003-210339/20.	
XX	DR N-PSDB; ABZ58196.	
XX	XX New secreted proteins from malarial parasites (e.g. Plasmodium falciparum), useful for detecting or diagnosing malaria, or as a vaccine or medicament for the treatment and/or prophylaxis of malaria.	
XX	Claim 1; Fig 1; 67pp; English.	
XX	CC The present sequence is the protein sequence of novel secreted protein PbSR from the mouse malaria parasite, Plasmodium berghei. The invention provides novel modular secreted proteins from Plasmodium falciparum (PfSR), P. berghei (PbSR) and Plasmodium yoelii (PySR) that are post-translationally modified in sporozoites. These include Limulus clotting factor, lipid binding, scavenger receptor cysteine-rich and pentraxin domains. Homologues were identified in Plasmodium knowlesi (PkSR), Plasmodium chabaudi (PcSR), Cryptosporidium parvum (CpSR), Toxoplasma gondii (TgSR) and Theileria parva (TpSR). PbSR, PfSR and PySR are from a unique and previously unrecognized family containing domains associated with binding and modulating host proteins involved in immunity. They are the first proteins from Plasmodium which are secreted and which show a gene disruption phenotype in both vertebrate and mosquito, making them highly useful for the production of malaria vaccines. Transgenic PbSR null mutants have attenuated growth in immunocompetent mice. They fail to produce sporozoites in Anopheles stephensi mosquitoes and consequently are dead-end parasites in the midgut of the mosquito. The novel Plasmodium proteins, and the nucleic acids encoding them, are used in claimed methods for the detection/diagnosis of malaria, and are also used in vaccine compositions. Agents capable of antagonising, inhibiting or interfering with the function or expression of the secreted protein are used in the treatment and/or prophylaxis of malaria	
XX	Sequence 1304 AA;	
XX	Query Match 67.8%; Score 40; DB 6; Length 1304;	
XX	Best Local Similarity 55.6%; Pred. No. 6.2e+02;	
XX	Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;	
XX	1 NVRCRGDDDS 9	
XX	:::	
XX	614 NFRCKGDEA 622	
XX	RESULT 24	
XX	ABB67864	
XX	ID ABB67864 standard; protein; 451 AA.	
XX	AC ABB67864;	
XX	DT 26-MAR-2002 (first entry)	
XX	DE Drosophila melanogaster polypeptide SEQ ID NO 30384.	
XX	Drosophila; developmental biology; cell signalling; insecticide;	
XX	KW pharmaceutical.	
XX	OS Drosophila melanogaster.	
XX	PN WO200171042-A2.	
XX	PD 27-SEP-2001.	
XX	PF 23-MAR-2001; 2001WO-US009231.	
XX	PR 23-MAR-2000; 2000US-0191637P.	
XX	PR 11-JUL-2000; 2000US-00614150.	
XX	PA (PEKE) PE CORP NY.	
XX	PI Venter JC, Adams M, Li PWD, Myers EW;	
XX	DR WPI; 2001-656860/75.	
XX	DR N-PSDB; ABL11967.	
XX	PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.	
XX	PS Disclosure; SEQ ID NO 30384; 2lpp + Sequence Listing; English.	
XX	CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences	
XX	Sequence 451 AA;	
XX	Query Match 66.1%; Score 39; DB 4; Length 451;	
XX	Best Local Similarity 75.0%; Pred. No. 3.2e+02;	
XX	Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	
XX	2 YRCRGDDDS 9	
XX	:::	
XX	3 YRCRGNES 10	
XX	RESULT 25	
XX	ABP72191	
XX	ID ABP72191 standard; protein; 1299 AA.	
XX	AC ABP72191;	
XX	DT 22-APR-2003 (first entry)	
XX	DE Plasmodium yoelii modular secreted protein PySR.	

XX PfSR; protein secretion; malaria; diagnosis; vaccine; antimalarial;
 KW protozoacide.
 XX
 XX Plasmodium yoelii.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..22 /label= Signal_peptide
 FT Protein 23..2399 /label= Mature_protein
 FT Misc-difference 175 /note= "encoded by ATK"
 FT
 XX WO2003004524-A2.
 XX
 XX 16-JAN-2003.
 XX
 XX 02-JUL-2002; 2002WO-GB003045.
 XX
 XX 02-JUL-2001; 2001GB-00016185.
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX Claudianos C, Crompton TK, Dessens JT, Sindén RE, Trueman HE;
 PI
 XX WPI; 2003-210339/20.
 DR N-PSDB; ABZ58198.
 XX
 XX New secreted proteins from malarial parasites (e.g. Plasmodium
 PT falciparum), useful for detecting or diagnosing malaria, or as a vaccine
 PT or medicament for the treatment and/or prophylaxis of malaria.
 XX
 XX Claim 1; Fig 1; 67pp; English.
 XX
 XX The present sequence is the protein sequence of novel secreted protein
 CC PySR from the mouse malaria parasite, Plasmodium yoelii. The invention
 CC provides novel modular secreted proteins from Plasmodium falciparum
 CC (PfSR), Plasmodium berghei (PbSR) and P. yoelii (PySR) that are post-
 CC translationally modified in sporozoites. These include Limulus clotting
 CC factor, lipid binding, scavenger receptor cysteine-rich and pentraxin
 CC domains. Homologues were identified in Plasmodium knowlesi (PkSR),
 CC Plasmodium chabaudi (PcSR), Cryptosporidium parvum (CpSR), Toxoplasma
 CC gondii (TgSR) and Theileria parva (TpSR). PbSR, PfSR and PySR are from a
 CC unique and previously unrecognized family containing domains associated
 CC with binding and modulating host proteins involved in immunity. They are
 CC the first proteins from Plasmodium which are secreted and which show a
 CC gene disruption phenotype in both vertebrate and mosquito, making them
 CC highly useful for the production of malaria vaccines. Transgenic PbSR
 CC null mutants have attenuated growth in immunocompetent mice. They fail to
 CC produce sporozoites in Anopheles stephensi mosquitoes and consequently
 CC are dead-end parasites in the midgut of the mosquito. The novel
 CC Plasmodium proteins, and the nucleic acids encoding them, are used in
 CC claimed methods for the detection/diagnosis of malaria, and are also used
 CC in vaccine compositions. Agents capable of antagonising, inhibiting or
 CC interfering with the function or expression of the secreted protein are
 CC used in the treatment and/or prophylaxis of malaria
 XX
 SQ Sequence 1299 AA;
 Query Match 66.1%; Score 39; DB 6; Length 1299;
 Best Local Similarity 62.5%; Pred. No. 9.2e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NYRCRGDD 8
 DB 614 NFRCKGDE 621
 RESULT 26
 AAW99087
 ID AAW99087 standard; protein; 822 AA.
 XX

AC AAW99087;
 XX 13-MAY-1999 (first entry)
 XX Human serine protease BSSP-3.
 XX Serine protease; BSSP-3; brain tissue.
 KW
 XX Homo sapiens.
 OS WO9905290-A1.
 PN 04-FEB-1999.
 PD 24-JUL-1998; 98WO-JP003324.
 PF 24-JUL-1997; 97JP-00213969.
 PR (SUNR) SUNTORY LTD.
 PA Tsuruoka N, Yamashiro K, Yamaguchi N;
 PI WPI; 1999-142942/12.
 DR N-PSDB; AAX19024.
 XX New serine protease expressed in brain tissue - used in screening for
 PT potential serine protease inhibitors for drug use.
 PT
 XX Claim 1; Page 61-65; 69pp; Japanese.
 PS The present sequence is a serine protease designated BSSP-3, which is
 CC isolated from human brain tissue. Transforms may be used to produce
 CC the enzyme or its partial sequences. Products from the present invention
 CC are used for screening for potential peptide or non-peptide serine
 CC protease inhibitors or expression regulators for use as drugs
 XX
 SQ Sequence 822 AA;
 Query Match 64.4%; Score 38; DB 2; Length 822;
 Best Local Similarity 75.0%; Pred. No. 8.6e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NYRCRGDD 8
 DB 183 NVRCRGDE 190
 RESULT 27
 AAW83361
 ID AAW83361 standard; protein; 875 AA.
 XX AAW83361;
 XX 17-FEB-1999 (first entry)
 DT Human neurotrypsin.
 DE
 XX Human; neurotrypsin; tumour inhibition; neurological disease;
 KW lung disease; gene therapy; drug development; stroke; brain injury;
 KW neurodegeneration; neuroinflammatory disease; multiple sclerosis;
 KW epilepsy; hypoxia; ischaemia; nerve transection; neuroangiogenesis;
 KW emphysema; bronchitis.
 XX Homo sapiens.
 OS WO9849322-A1.
 PN 05-NOV-1998.
 PD 24-APR-1998; 98WO-IB000625.
 PF 26-APR-1997; 97CH-00000966.
 PR
 XX

PA	(SOND/) SONDEREGGER P.
XX	Sonderegger P;
PI	
XX	
DR	WPI; 1999-009438/01.
XX	N-PSDB; AAV72589.
DR	
XX	New human and murine neurotysin - used, e.g. for inhibiting tumours,
PT	treatment of neurological or lung disease, including by gene therapy and
PT	in drug development.
XX	
XX	Claim 1; Page 20-24; 50pp; English.
PS	
XX	The present sequence represents human neurotysin. Neurotysin proteins
CC	and polynucleotides can be used: (i) to inhibit tumours, including
CC	metastases, e.g. of brain or retina; (ii) to minimise tissue damage
CC	caused by stroke or brain injury (having a protective effect on the
CC	pennumbra zone); (iii) to treat or prevent neurodegeneration,
CC	neuroinflammatory disease (e.g. multiple sclerosis) or epilepsy; (iv) to
CC	increase survival of damaged neurons (e.g. in cases of hypoxia,
CC	ischaemia, nerve transection) and to stimulate regeneration and/or
CC	restoration of synapses; (v) to treat or prevent retinal disorders (e.g.
CC	degeneration or neovascularisation); (vi) to prevent apoptosis (or other
CC	causes of cell death) in the nervous system; (vii) to regenerate brain
CC	and/or nervous tissue; (viii) to treat pain; (ix) to improve brain
CC	performance, including learning and memory; (x) to treat or prevent a
CC	wide range of psychiatric disorders; and (xi) to treat brain or lung
CC	injury associated with protease expression (specifically emphysema or
CC	bronchitis)
XX	
XX	Sequence 875 AA;
SQ	
	Query Match 64.4%; Score 38; DB 2; Length 875;
	Best Local Similarity 75.0%; Pred No. 9.1e+02;
	Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0
Qy	1 NVRCRGDD 8 236 NVRCRGDE 243
Dd	
RESULT 28	
ID	ADQ21226
ID	ADQ21226 standard; protein; 875 AA.
AC	ADQ21226;
XX	
DT	26-AUG-2004 (first entry)
XX	
XX	Human soft tissue sarcoma-upregulated protein - SEQ ID 4046.
DE	
DE	soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
KM	
OS	Homo sapiens.
XX	
PN	WO2004048938-A2.
XX	
PD	10-JUN-2004.
XX	
PF	26-NOV-2003; 2003WO-US038193.
XX	
PR	26-NOV-2002; 2002US-0429739P.
XX	
PA	(PROT-) PROTEIN DESIGN LABS INC.
XX	
PI	Aziz N, Ginsburg WM, Zlotnik A;
XX	
XX	WPI; 2004-441208/41.
XX	
PT	Early detection of soft tissue sarcoma comprises determining expression
PT	of a gene in a first soft tissue sample and a normal soft tissue sample
PT	and comparing the gene expression, also useful in treating soft tissue
PT	sarcoma.

XX The present invention describes the use of polypeptides related to
 CC urological disorders for identifying a compound capable of treating a
 CC urological disorder, identifying a subject having a urological disorder,
 CC or treating a subject having a urological disorder. Also described: (1) a
 CC method for identifying a compound capable of treating a urological
 CC disorder; (2) a method for identifying a subject having a urological
 CC disorder; and (3) a method for treating a subject having a urological
 CC disorder. The compound has urothelial and cytostatic activities. The
 CC polypeptides related to urological disorders are useful for identifying a
 CC compound capable of treating a urological disorder, identifying a subject
 CC having a urological disorder, or treating a subject having a urological
 CC disorder. Disorders include urinary incontinence and benign prostatic
 CC hyperplasia. The present sequence represents a human urological disorder
 CC related protein, which is used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 875 AA;

Query Match 64.4%; Score 38; DB 8; Length 875;
 Best Local Similarity 75.0%; Pred. No. 9.1e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NVRCRGDD 8
 Db 236 NVRCRGDE 243
 |||||

RESULT 30
 ABP42738
 ID ABP42738 standard; protein; 77 AA.
 XX
 AC ABP42738;
 XX
 DT 22-AUG-2002 (first entry)
 XX
 DE Human ovarian antigen HOVDU91, SEQ ID NO:3870.
 XX
 KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW Gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive.
 XX
 OS Homo sapiens.
 XX
 PN WO200200677-A1.
 XX
 PD 03-JAN-2002.
 XX
 PF 07-JUN-2001; 2001WO-US018569.
 XX
 PR 07-JUN-2000; 2000US-0209467P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Birse CE, Rosen CA;
 XX
 DR WPI; 2002-147878/19.
 DR N-PSDB; ABQ55815.
 XX
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.
 XX
 PS Claim 11; SEQ ID NO 3870; 2922pp; English.
 XX

CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), and toxic
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 77 AA;

Query Match 62.7%; Score 37; DB 5; Length 77;
 Best Local Similarity 60.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NVRCRGDDSK 10
 Db 41 NFFCRGPDGSK 50
 ||:|:|:|

RESULT 31
 AAU61299
 ID AAU61299 standard; protein; 92 AA.
 XX
 AC AAU61299;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DE Propionibacterium acnes immunogenic protein #22195.
 XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX
 PN WO200181581-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 20-APR-2001; 2001WO-US012865.
 XX
 PR 21-APR-2000; 2000US-0199047P.
 PR 02-JUN-2000; 2000US-0208841P.
 PR 07-JUL-2000; 2000US-0216747P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonmeuve J, Zhang Y, Jen S, Carter D;
 XX

DR WPI; 2001-616774/71.
 DR N-PSDB; AA359616.
 XX
 PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris.
 XX
 XX Example 1; SEQ ID NO 22494; 1069pp; English.
 XX
 XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 92 AA;
 Query Match 62.7%; Score 37; DB 4; Length 92;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 RCRGDD 8
 Db 74 RCRGDD 79
 RESULT 32
 ABM57818
 ID ABM57818 standard; protein; 92 AA.
 AC
 AC ABM57818;
 XX
 XX 20-OCT-2003 (first entry)
 DT
 DE Propionibacterium acnes predicted ORF-encoded polypeptide #22494.
 XX
 XX Acne vulgaris; antiseborrheic; dermatological; antibacterial;
 KW immunostimulant; immune response; vaccine.
 KW
 XX Propionibacterium acnes.
 OS
 XX
 XX WO2003033515-A1.
 PN
 XX 24-APR-2003.
 PD
 XX 11-OCT-2002; 2002WO-US032727.
 PF
 XX 15-OCT-2001; 2001US-00978825.
 PR
 XX (CORI-) CORIXA CORP.
 PA
 XX Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
 PI Zhang Y, Wang S, Jen S, Lodes WJ, Benson DR, Jones R, Carter D;
 PI Barth B, Vallieve-Douglass J;
 XX
 XX WPI; 2003-381789/36.
 DR
 DR N-PSDB; ACF64545.
 XX

PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX
 XX Example 1; SEQ ID NO 22494; 1481pp; English.
 XX
 XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising P. acnes polypeptides,
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the P. acnes polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 92 AA;
 Query Match 62.7%; Score 37; DB 6; Length 92;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 RCRGDD 8
 Db 74 RCRGDD 79
 RESULT 33
 AAM91935
 ID AAM91935 standard; protein; 113 AA.
 AC
 AC AAM91935;
 XX
 XX 05-NOV-2001 (first entry)
 DT
 XX Human digestive system antigen SEQ ID NO: 1284.
 DE
 XX Human; digestive system antigen; gene therapy; cancer; appendicitis;
 KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
 KW digestive system disorder; Meckel's diverticulum.
 XX
 XX Homo sapiens.
 OS
 XX WO200155314-A2.
 PN
 XX 02-AUG-2001.
 PD
 XX 17-JAN-2001; 2001WO-US001324.
 PF
 XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
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PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI; 2001-502630/55.
XX N-PSDB; AAK87708.
XX
XX Polynucleotides encoding digestive system antigens, useful for
PT diagnosing, treating, preventing and/or prognosing disorders of the
PT digestive system, particularly cancer and cancer metastases.
XX
XX Claim 11; SEQ ID NO 1284; 986pp; English.
PS
XX The present invention provides the protein and coding sequences of a
CC number of human digestive system antigens. These can be used in the

CC diagnosis, treatment and prevention of digestive system disorders,
CC including cancer, Meckel's diverticulum, bacterial or parasitic
CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
CC ulcerative colitis. The present sequence is a digestive system antigen of
CC the invention

XX
SQ Sequence 113 AA;

Query Match 62.7%; Score 37; DB 4; Length 113;

Best Local Similarity 62.5%; Pred. No. 1.8e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8

||:|:|

Db 10 NYQCEGED 17

RESULT 34

AAM38569

ID AAM38569 standard; protein; 113 AA.

XX AC AAM38569;

XX DT 19-OCT-2001 (first entry)

XX DE Human colorectal cancer antigen SEQ ID NO: 84.

XX KW Human; colorectal cancer; colorectal cancer antigen; gene therapy.

XX OS Homo sapiens.

XX PN WO200155350-A1.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US001350.

XX PR 31-JAN-2000; 2000US-0179065P.

XX PR 04-FEB-2000; 2000US-0180628P.

XX PR 24-FEB-2000; 2000US-0184664P.

XX PR 02-MAR-2000; 2000US-0186350P.

XX PR 16-MAR-2000; 2000US-0189874P.

XX PR 17-MAR-2000; 2000US-0190076P.

XX PR 18-APR-2000; 2000US-0198123P.

XX PR 19-MAY-2000; 2000US-0205515P.

XX PR 07-JUN-2000; 2000US-0209467P.

XX PR 28-JUN-2000; 2000US-0214886P.

XX PR 30-JUN-2000; 2000US-0215135P.

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PR 17-NOV-2000; 2000US-0249211P.

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PR 17-NOV-2000; 2000US-0249219P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI; 2001-457727/49.
DR N-PSDB; AA157547.
XX
XX Isolated polypeptide for treating, preventing and/ or prognosing
PT disorders related to the colon and rectum including colorectal cancers
PT and also for testing and detection e.g. diagnosis.
XX
XX Claim 11; SEQ ID NO 84; 522pp + Sequence Listing; English.
XX
XX The present invention provides the protein and coding sequences of a
CC number of colorectal cancer antigens. These are shown in AA157547-
CC AA157619 and AA157621-AA157641. These can be used in the diagnosis,
CC prevention and treatment of cancer of the colon and/or rectum. The
CC present sequence is a colorectal cancer antigen of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 113 AA;
Query Match 62.7%; Score 37; DB 4; Length 113;
Best Local Similarity 62.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
DB 10 NYQCEGED 17

RESULT 35
ABG97621
ID ABG97621 standard; protein; 113 AA.
XX
XX AC ABG97621;
XX
XX DT 18-DEC-2002 (first entry)
XX
XX DE Human colorectal cancer related protein #1.
XX
XX KW Human; colorectal cancer related protein; colon; rectum;
KW colorectal cancer metastasis; gastrointestinal disorder; cytostatic.

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XX Homo sapiens.
XX US2002119919-A1.
XX 29-AUG-2002.
XX
XX PF 17-JAN-2001; 2001US-00764855.
XX
XX PR 31-JAN-2000; 2000US-0179065P.
XX
XX (ROSE/) ROSEN C A.
XX (RUBE/) RUBEN S M.
XX (BARA/) BARASH S C.
XX
XX Rosen CA, Ruben SM, Barash SC;
PI
XX WPI; 2002-731367/79.
DR N-PSDB; ABS99724.
XX
XX New colorectal cancer polypeptide for diagnosing, prognosing, preventing,
PT and treating immune, hyperproliferative, liver, kidney, reproductive
PT disorders and for identifying modulators of therapeutic use.
XX
XX Claim 11; SEQ ID NO 84; 183pp; English.
XX
XX The present invention relates to the isolation of novel human colorectal
CC cancer related proteins, and polynucleotide sequences encoding them. The
CC sequences of the invention are useful in the diagnosis, treatment,
CC prevention and/or prognosis of the colon and/or rectum, including
CC colorectal cancer, colorectal cancer metastases, and gastrointestinal
CC disorders such as dysphagia, peptic oesophagitis, gastric reflux,
CC irritable bowel syndrome, and peritoneal diseases. The invention also
CC describes antibodies that bind colorectal cancer related proteins,
CC vectors, host cells, and recombinant and synthetic methods for producing
CC human colorectal cancer related polynucleotides, polypeptides, and/or
CC antibodies. ABG97621-ABG97693 represent human colorectal cancer related
CC proteins. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from the USPTO web site at seqdata.uspto.gov/psipsIDEntry.html
XX
XX SQ Sequence 113 AA;
Query Match 62.7%; Score 37; DB 5; Length 113;
Best Local Similarity 62.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYRCRGDD 8
DB 10 NYQCEGED 17

RESULT 36
ADB92877
ID ADB92877 standard; protein; 113 AA.
XX
XX AC ADB92877;
XX
XX DT 04-DEC-2003 (first entry)
XX
XX DE Human colorectal cancer related polypeptide #1.
XX
XX KW human; colorectal cancer; antigen; gene therapy;
KW gastrointestinal disorder; inflammatory disease; infection; cancer;
KW intestinal neoplasm; small intestine carcinoma; tumour;
KW small intestine non-Hodgkin's lymphoma; small bowel lymphoma; ulcer;
KW peptic ulcer; Bruton's disease; X linked infantile agammaglobulinaemia;
KW severe combined immunodeficiency; DiGeorge anomaly;
KW hyperproliferative disorder; acute lymphoblastic leukaemia;
KW acute lymphocytic leukaemia; urinary system disorder; cortical necrosis;
KW kidney infarction; cardiovascular disorder; carcinoid heart disease;
KW arrhythmia; respiratory disorder; non-allergic rhinitis; sinusitis;
KW musculoskeletal system disorder; Albers-Schonberg disease;

```

KW Marfan's syndrome; neurological disease; phenylketonuria;
KW Wernicke's encephalopathy; Alzheimer's disease; endocrine disorder;
KW Grave's disease; Cushing's syndrome; reproductive system disorder;
KW prostatitis; benign prostatic hypertrophy; benign prostatic hyperplasia;
KW thrombosis; atherosclerosis; myocardial infarction; ischaemic attack.

XX Homo sapiens.

OS US2003054420-A1.

PN 20-MAR-2003.

PD 11-FEB-2002; 2002US-00072349.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

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PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

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PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

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PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.

PR 14-AUG-2000; 2000US-0225759P.

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PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
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PR 08-NOV-2000; 2000US-0246603P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 06-DEC-2000; 2000US-0256719P.
PR 08-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.

PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 PR 17-JAN-2001; 2001US-00764855.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM, Barash SC;
 XX
 DR WPI; 2003-708345/67.
 DR N-PSDB; ADB92794.
 XX
 XX Novel colorectal cancer antigen useful for treating, preventing,
 PT diagnosing and/or prognosing gastrointestinal disorders, infections,
 PT cancers such as intestinal neoplasms, ulcers.
 XX
 PS Claim 11; SEQ ID NO 84; 179pp; English.
 XX
 CC The invention relates to a colorectal cancer antigen. The antigen is
 CC useful for chromosome identification, chromosome mapping, radiation
 CC hybrid mapping or gene therapy, or as hybridisation probes for
 CC differential identification of the tissues or cell types present in a
 CC biological sample. The antigen is useful for treating, preventing,
 CC diagnosing and/or prognosing gastrointestinal disorders, including
 CC inflammatory diseases and/or conditions, infections, cancers (e.g.
 CC intestinal neoplasms (carcinoid tumour of the small intestine, non-
 CC Hodgkin's lymphoma of the small intestine, small bowel lymphoma)) and
 CC ulcers (e.g. peptic ulcers). The antigen and its nucleic acid are useful
 CC to provide immunological probes for differential identification of the
 CC tissue. The antigen and its nucleic acid are useful for treating,
 CC preventing, diagnosing and/or prognosing diseases, disorders and/or
 CC conditions of the immune system e.g. Bruton's disease, X linked infantile
 CC agammaglobulinemia, severe combined immunodeficiencies, DiGeorge
 CC anomaly, etc. The antigen and its nucleic acid is useful for treating,
 CC preventing and/or diagnosing hyperproliferative disorders (e.g. acute

Query Match 62.7%; Score 37; DB 7; Length 113;
 Best Local Similarity 62.5%; Pred. No. 1.8e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NVRCRGDD 8
 ||:|:|
 Db 10 NVQCEGED 17

RESULT 37
 ABB11487
 ID ABB11487 standard; peptide; 140 AA.
 XX ABB11487;
 AC
 XX
 DT 11-JAN-2002 (first entry)
 XX
 DE Human secreted protein homologue, SEQ ID NO:1857.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
 KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KW antifungal; vulnary; antiulcer.
 XX
 OS Homo sapiens.
 XX
 XX WO200157188-A2.
 PN
 XX

PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US003800.
 XX
 PR 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Liu C, Drmanac RT;
 PI
 DR WPI; 2001-457740/49.
 DR N-PSDB; ABA08731.
 XX
 XX Human proteins and DNA encoding sequences useful for preventing, treating
 PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
 PT and cancer.
 XX
 PS Claim 20; Page 201; 1963pp; English.
 XX
 CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of identifying compounds which
 CC bind to polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, and hence
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g. myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g. asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness.
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention
 XX
 SQ Sequence 140 AA;
 Query Match 62.7%; Score 37; DB 4; Length 140;
 Best Local Similarity 85.7%; Pred. No. 2.2e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 CRGDDSK 10
 . . . |||:|
 Db 80 CRGEDSK 86

RESULT 38
 ABO65272
 ID ABO65272 standard; protein; 275 AA.
 XX

AC ABO65272;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Klebsiella pneumoniae polypeptide seqid 11789.
 XX
 KW Recombinant expression vector; transcription regulatory element;
 XX Klebsiella pneumoniae protein; antibacterial; Vaccine.
 XX
 OS Klebsiella pneumoniae.
 XX
 PN US6610836-B1.
 XX
 PD 26-AUG-2003.
 XX
 PF 27-JAN-2000; 2000US-00489039.
 XX
 PR 29-JAN-1999; 99US-0117747P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Breton GL, Osborne M;
 XX
 XX WPI; 2003-895346/82.
 DR N-PSDB; ACH98823.
 XX
 PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
 PT preparing a vaccine composition against Klebsiella pneumoniae.
 XX
 PS Disclosure; SEQ ID NO 11789; 932pp; English.
 XX
 CC The invention describes a new isolated nucleic acid encoding a Klebsiella
 CC pneumoniae polypeptide. Also described are: a recombinant expression
 CC vector comprising the nucleic acid, operably linked to a transcription
 CC regulatory element; and a cell comprising the recombinant expression
 CC vector. The nucleic acid is useful for preparing a vaccine composition
 CC against Klebsiella pneumoniae. This is the amino acid sequence of a
 CC Klebsiella pneumoniae polypeptide of the invention
 XX
 SQ Sequence 275 AA;
 XX
 Query Match 62.7%; Score 37; DB 7; Length 275;
 Best Local Similarity 66.7%; Pred. No. 4.3e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NVRCGGDS 9
 Db ||:||:|
 32 NWRCGGDS 40
 RESULT 39
 ABO66647
 ID ABO66647 standard; protein; 488 AA.
 XX
 AC ABO66647;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Klebsiella pneumoniae polypeptide seqid 13164.
 XX
 KW Recombinant expression vector; transcription regulatory element;
 KW Klebsiella pneumoniae protein; antibacterial; Vaccine.
 XX
 OS Klebsiella pneumoniae.
 XX
 PN US6610836-B1.
 XX
 PD 26-AUG-2003.
 XX
 PF 27-JAN-2000; 2000US-00489039.
 XX
 PR 29-JAN-1999; 99US-0117747P.
 XX

PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Breton GL, Osborne M;
 XX
 DR WPI; 2003-895346/82.
 DR N-PSDB; ABD00218.
 XX
 PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
 PT preparing a vaccine composition against Klebsiella pneumoniae.
 XX
 PS Disclosure; SEQ ID NO 13164; 932pp; English.
 XX
 CC The invention describes a new isolated nucleic acid encoding a Klebsiella
 CC pneumoniae polypeptide. Also described are: a recombinant expression
 CC vector comprising the nucleic acid, operably linked to a transcription
 CC regulatory element; and a cell comprising the recombinant expression
 CC vector. The nucleic acid is useful for preparing a vaccine composition
 CC against Klebsiella pneumoniae. This is the amino acid sequence of a
 CC Klebsiella pneumoniae polypeptide of the invention
 XX
 SQ Sequence 488 AA;
 XX
 Query Match 62.7%; Score 37; DB 7; Length 488;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 RCRGDD 8
 Db |||||
 102 RCRGDD 107
 RESULT 40
 ADD46237
 ID ADD46237 standard; protein; 1269 AA.
 XX
 AC ADD46237;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Rat Protein U49055, SEQ ID NO 11912.
 XX
 KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX
 OS Rattus norvegicus.
 XX
 PN WO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0342147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GENO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX
 DR WPI; 2003-268312/26.
 DR GENBANK; U49055.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell

CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX Sequence 1269 AA;
 SQ

Query Match 62.7%; Score 37; DB 7; Length 1269;
 Best Local Similarity 85.7%; Pred. No. 1.9e+03;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
 DB 100 YRCPGDD 106
 ||| |||

RESULT 41
 ADD46239
 ID ADD46239 standard; protein; 1272 AA.
 XX
 AC ADD46239;
 XX
 XX 29-JAN-2004 (first entry)
 DT
 XX Human Protein AB029039, SEQ ID NO 11914.
 DE

XX Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX

OS Homo sapiens.

XX WO2003016475-A2.

PN 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GEO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

DR GENBANK; AB029039.

XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 PT
 XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC that increases or decreases the expression of the polynucleotide sequence
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX Sequence 1272 AA;
 SQ

Query Match 62.7%; Score 37; DB 7; Length 1272;
 Best Local Similarity 85.7%; Pred. No. 2e+03;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YRCRGDD 8
 DB 100 YRCPGDD 106
 ||| |||

RESULT 42
 AAU49621
 ID AAU49621 standard; protein; 59 AA.
 XX

AC AAU49621;

XX 27-FEB-2002 (first entry)

DT
 XX Propionibacterium acnes immunogenic protein #10517.

DE
 XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.

XX Propionibacterium acnes.

XX WO200181581-A2.

XX 01-NOV-2001.

XX 20-APR-2001; 2001WO-US012865.

XX 21-APR-2000; 2000US-0199047P.

PR 02-JUN-2000; 2000US-0208841P.

PR 07-JUL-2000; 2000US-0216747P.

XX (CORI-) CORIXA CORP.

XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX WPI; 2001-616774/71.

DR N-PSDB; AAS959545.
 XX Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris.
 XX
 XX Example 1; SEQ ID NO 10816; 1069pp; English.
 PS
 CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 59 AA;
 Query Match 61.0%; Score 36; DB 4; Length 59;
 Best Local Similarity 85.7%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 YRCRGDD 8
 Db 25 YRCRTDD 31
 |||||
 |||||
 RESULT 43
 ABM46140
 ID ABM46140 standard; protein; 59 AA.
 XX
 AC ABM46140;
 XX
 DT 20-OCT-2003 (first entry)
 XX
 DE Propionibacterium acnes predicted ORF-encoded polypeptide #10816.
 XX
 KW Acne vulgaris; antiseborrheic; dermatological; antibacterial;
 KW immunostimulant; immune response; vaccine.
 XX
 OS Propionibacterium acnes.
 XX
 PN WO2003033515-A1.
 XX
 PD 24-APR-2003.
 XX
 PF 11-OCT-2002; 2002WO-US032727.
 XX
 PR 15-OCT-2001; 2001US-00978825.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Mitcham JL, Skeiky YAM, Persing DH, Bhatia A, Maisonneuve JL;
 PI Zhang Y, Wang S, Jen S, Lodes WJ, Benson DR, Jones R, Carter D;
 PI Barth B, Vallieue-Douglass J;
 XX
 DR WPI; 2003-381789/36.
 DR N-PSDB; ACF64474.
 XX
 PT New Propionibacterium acnes polypeptides and polynucleotides encoding the

PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX
 PS Example 1; SEQ ID NO 10816; 1481pp; English.
 XX
 CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC polynucleotide of the invention comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the P. acnes polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 59 AA;
 Query Match 61.0%; Score 36; DB 6; Length 59;
 Best Local Similarity 85.7%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 YRCRGDD 8
 Db 25 YRCRTDD 31
 |||||
 |||||
 RESULT 44
 ABM69291
 ID ABM69291 standard; protein; 405 AA.
 XX
 AC ABM69291;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Photobacterium luminescens protein sequence #2388.
 XX
 KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
 KW detection; food; gene expression; plant; animal; microorganism; toxin;
 KW antibiotic; biopesticide; virulence factor; disease model; plague;
 KW whooping cough.
 XX
 OS Photobacterium luminescens.
 XX
 PN WO200294867-A2.
 XX
 PD 28-NOV-2002.
 XX
 PF 07-FEB-2002; 2002WO-IB003040.
 XX
 PR 07-FEB-2001; 2001FR-00001659.
 XX
 PA (INSP) INST PASTEUR.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;

PI Buchrieser C;
 XX WPI; 2003-148459/14.
 XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
 PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.
 XX
 PS Claim 2; SEQ ID NO 2388; 1205pp; French.
 XX
 XX The invention relates to the isolation of genes and their encoded
 CC proteins from Photorhabdus luminescens. The isolated sequences are
 CC sources of probes and primers for detecting the genome of P. luminescens
 CC and related species; to study polymorphisms; for gene analysis and for
 CC detection/amplification of the genes. Antibodies (Ab) raised against the
 CC polypeptides encoded by the genes are used for detection/identification
 CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
 CC carry a gene-containing vector are used to select compounds that
 CC modulate, regulate, induce or inhibit expression of the genes in plants,
 CC animals or microorganisms other than P. luminescens and are able to alter
 CC response or sensitivity to toxins and antibiotics produced by P.
 CC luminescens. Cells transformed to express the genes are useful for
 CC recombinant production of the proteins, particularly toxins and
 CC antibacterials useful as insecticides, bactericides and fungicides. The
 CC genes, proteins, vectors containing the genes and Ab are also useful
 CC therapeutically (to treat microbial infection by bacteria or fungi that
 CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as
 CC biopesticides. Other uses of the genes and the proteins are as virulence
 CC factors and for identifying targets of human diseases for which P.
 CC luminescens is a model (particularly plague and whooping cough). This
 CC sequence represents one of the isolated P. luminescens proteins
 XX
 XX Sequence 405 AA;
 SQ
 Query Match 61.0%; Score 36; DB 6; Length 405;
 Best Local Similarity 71.4%; Pred. No. 9.2e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 YRCRGDD 8
 DB 39 FRCRGDE 45
 :|||||:
 RESULT 45
 ADN20343
 ID ADN20343 standard; protein; 466 AA.
 XX
 AC ADN20343;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Bacterial polypeptide #2996.
 XX
 KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX
 OS Bacteria.
 XX
 XX US2003233675-A1.
 PN
 XX 18-DEC-2003.
 PD
 XX 20-FEB-2003; 2003US-00369493.
 PF
 XX 21-FEB-2002; 2002US-0360039P.
 PR
 XX (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX WPI; 2004-061375/06.
 DR
 XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX
 PS Claim 1; SEQ ID NO 2996; 122pp; English.
 XX
 XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition. Improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 XX Sequence 466 AA;
 SQ
 Query Match 61.0%; Score 36; DB 8; Length 466;
 Best Local Similarity 71.4%; Pred. No. 1.1e+03;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 YRCRGDD 8
 DB 214 FRCRGED 220
 :|||||:
 RESULT 46
 ADN20289
 ID ADN20289 standard; protein; 470 AA.
 XX
 AC ADN20289;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Bacterial polypeptide #2942.
 XX
 KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX
 OS Bacteria.
 XX
 XX US2003233675-A1.
 PN
 XX 18-DEC-2003.
 PD
 XX

PF	20-FEB-2003; 2003US-00369493.
XX	
PR	21-FEB-2002; 2002US-0360039P.
XX	
PA	(CAOY/) CAO Y.
PA	(HINK/) HINKLE G J.
PA	(SLAT/) SLATER S C.
PA	(CHEN/) CHEN X.
PA	(GOLD/) GOLDMAN B S.
XX	
PI	Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
DR	WPI; 2004-061375/06.
XX	
PT	New recombinant DNA construct comprising a promoter positioned to provide
PT	for expression of a polynucleotide encoding a polypeptide from a
PT	microbial source, useful for producing plants with improved properties.
XX	
PS	Claim 1; SEQ ID NO 2942; 122pp; English.
XX	
CC	The invention relates to a recombinant DNA construct comprising a
CC	promoter functional in a plant cell, where the promoter is positioned to
CC	provide for expression of a polynucleotide encoding a polypeptide from a
CC	microbial source. The invention also relates to a transformed plant
CC	comprising the recombinant DNA construct and a method of producing a
CC	transformed plant having an improved property. The plant is a crop plant
CC	such as maize or soybean. The method of producing a transformed plant
CC	having an improved property comprises transforming a plant with the
CC	recombinant DNA construct and growing the transformed plant, where the
CC	polynucleotide or polypeptide is useful for improving plant properties.
CC	The recombinant DNA construct is useful for producing plants with
CC	improved plant properties, e.g. improved cold, heat or drought tolerance,
CC	tolerance to herbicides, extreme osmotic conditions, pathogens or pests.
CC	increased resistance to plant disease, better growth rate by modification
CC	of the cell cycle pathway with plant growth regulators, increased rate of
CC	homologous recombination, modified seed oil or protein yield and/or
CC	content, improved yield by modification of carbohydrate, nitrogen or
CC	phosphorus use and/or uptake, by modification of photosynthesis or by
CC	providing improved plant growth and development under at least one stress
CC	condition, improved lignin production or improved galactomannan
CC	production. This sequence represents a bacterial polypeptide used in the
CC	scope of the invention. Note: The sequence data for this patent did not
CC	form part of the printed specification but was obtained in electronic
CC	format from USPTO at seqdata.uspto.gov/sequence.html.
XX	
SQ	Sequence 470 AA;
Query Match	61.0%; Score 36; DB 8; Length 470;
Best Local Similarity	71.4%; Pred. No. 1.1e+03;
Matches	5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY	2 YRCRGDD 8
	: : : :
Db	214 FRCRGED 220
RESULT 47	
ID	ADM04173 standard; protein; 485 AA.
XX	
AC	ADM04173;
XX	
DT	20-MAY-2004 (first entry)
XX	
DE	Human protein of the invention SEQ ID NO:2858.
XX	
KW	human; gene therapy; diagnostic marker; pharmaceutical.
OS	Homo sapiens.
XX	
FN	EP1347046-A1.
XX	
PD	24-SEP-2003.

XX	12-APR-2002; 2002EP-00008400.
PF	
XX	
PR	22-MAR-2002; 2002JP-00137785.
XX	
PA	(REAS-) RES ASSOC BIOTECHNOLOGY.
XX	
PI	Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI	Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI	Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX	
DR	WPI; 2003-723558/69.
DR	N-PSDB; ADM01730.
XX	
PT	New polynucleotides and polypeptides are useful in gene therapy, for
PT	developing a diagnostic marker or medicines for regulating their
PT	expression and activity, or as a target of gene therapy.
XX	
PS	Claim 1; SEQ ID NO 2858; 305pp; English.
XX	
CC	The invention relates to a novel human polynucleotide and the encoded
CC	polypeptide. A polynucleotide of the invention may have a use in gene
CC	therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC	as a primer for synthesizing the polynucleotide or as a probe for
CC	detecting the polynucleotide. The polynucleotides ADM0316-ADM03758 are
CC	useful in gene therapy, for developing a diagnostic marker or medicines
CC	for regulating their expression and activity, or as a target of gene
CC	therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC	are useful as pharmaceutical agents. The present sequence represents a
CC	protein sequence of the invention.
XX	
SQ	Sequence 485 AA;
Query Match	61.0%; Score 36; DB 7; Length 485;
Best Local Similarity	60.0%; Pred. No. 1.1e+03;
Matches	6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY	1 NYRCRGDSDK 10
	: : : :
Db	469 NWRCPGTDS 478
RESULT 48	
AAY79209	
ID	AAY79209 standard; protein; 498 AA.
XX	
AC	AAY79209;
XX	
DT	19-JUN-2000 (first entry)
XX	
DE	Human transferase TRNSFS-1.
XX	
KW	Transferase; TRNSFS-1; human; antitumour; cancer;
KW	gastrointestinal disorder; developmental disorder; genetic disorder;
KW	neurological disorder; reproductive disorder; smooth muscle disorder;
KW	immunological disorder; inflammation; diagnosis; therapy;
KW	myristoyl CoA.protein N-myristoyltransferase.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Modified-site 64
FT	/note= "potential O-phosphorylation"
FT	Modified-site 68
FT	/note= "potential O-phosphorylation"
FT	Peptide 150..228
FT	/note= "myristoyl-CoA protein N-myristoyltransferase signature"
FT	Modified-site 166
FT	/note= "potential O-phosphorylation"
FT	Modified-site 220
FT	/note= "potential O-phosphorylation"
FT	Peptide 240..285

FT /note= "myristoyl-CoA protein N-myristoyltransferase
FT signature"
FT 240
FT Modified-site
FT /note= "potential O-phosphorylation"
FT 246. .254
FT Peptide
FT /note= "myristoyl-CoA protein N-myristoyltransferase
FT signature"
FT 258
FT Modified-site
FT /note= "potential O-phosphorylation"
FT 270
FT Modified-site
FT /note= "potential O-phosphorylation"
FT 286. .362
FT Peptide
FT /note= "myristoyl-CoA protein N-myristoyltransferase
FT signature"
FT 295
FT Modified-site
FT /note= "potential O-phosphorylation"
FT 319
FT Modified-site
FT /note= "potential N-glycosylation"
FT 325
FT Modified-site
FT /note= "potential O-phosphorylation"
FT 350
FT Modified-site
FT /note= "potential O-phosphorylation"
FT 350
FT Modified-site
FT /note= "potential O-phosphorylation"
FT 417
FT Modified-site
FT /note= "potential O-phosphorylation"
FT 436. .488
FT Peptide
FT /note= "myristoyl-CoA protein N-myristoyltransferase
FT signature"
FT 460
FT Modified-site
FT /note= "potential N-glycosylation"
FT 462
FT Modified-site
FT /note= "potential O-phosphorylation"
FT 468. .474
FT Peptide
FT /note= "myristoyl-CoA protein N-myristoyltransferase
FT signature"
FT 488
FT Modified-site
FT /note= "potential O-phosphorylation"
FT 490
FT Modified-site
FT /note= "potential O-phosphorylation"
FT 500014251-A2.
XX WO200014251-A2.
XX 16-MAR-2000.
XX
XX 09-SEP-1999; 99WO-US020989.
XX
XX 10-SEP-1998; 98US-00150657.
XX 04-NOV-1998; 98US-00186779.
XX 11-MAY-1999; 99US-0133642P.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Tang YT, Corley NC, Guegler KJ, Baughn MR, Lal P, Yue H;
XX Hillman JL, Azimzai Y;
XX
XX WPI; 2000-256996/22.
XX N-PSDB; AA294201.
XX
XX Human transferase proteins useful for preventing, diagnosing and treating
XX cancers and developmental, gastrointestinal, genetic, immunological,
XX neurological, reproductive and smooth muscle disorders.
XX
XX Claim 1; Page 78-79; 113pp; English.
XX
XX The present sequence is that of human transferase TRNSPS-1, 1 of 15
XX claimed novel human transferase proteins of the invention (see AAY79209-
XX 23). The sequence was deduced from a cDNA clone (see AA294201) isolated
XX from a caecal tissue library. It shows homology to human myristoyl-CoA
XX protein N-myristoyltransferase. TRNSPS-1 is expressed in reproductive,
XX nervous and smooth muscle tissues, especially those associated with
XX cancer and inflammation. The new human transferase proteins and the
XX polynucleotides encoding them can be used in the diagnosis, prevention

CC and treatment of cancer, developmental disorders, gastrointestinal
CC disorders, genetic disorders, immunological disorders, neurological
CC disorders, reproductive disorders, and smooth muscle disorders. The
CC polypeptides can also be used to raise antibodies, and to screen for
CC agonists and antagonists of transferase activity
XX
XX Sequence 498 AA;
SQ
Query Match 61.0%; Score 36; DB 3; Length 498;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 NYRCRGDSK 10
Db |::|||::
482 NWRCPGTQSE 491
RESULT 49
ADN95772
ID ADN95772 standard; protein; 498 AA.
XX AC ADN95772;
XX DT 01-JUL-2004 (first entry)
XX DE Human BEC/LEC-related protein sequence SeqID696.
XX
XX growth; differentiation; blood endothelial cell; BEC;
KW lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;
KW lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytostatic;
KW vasotropic; antiinflammatory; gene therapy; endothelial cell disorder;
KW inflammatory disease; cancer metastasis; lymphatic system; human.
XX
XX Homo sapiens.
XX WO2003080640-A1.
XX
XX 02-OCT-2003.
XX
XX 07-MAR-2003; 2003WO-US006900.
XX
XX 07-MAR-2002; 2002US-0363019P.
XX (LUDW-) LUDWIG INST CANCER RES.
XX (LICN) LICENTIA LTD.
XX
XX Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;
XX WPI; 2003-876899/81.
XX N-PSDB; ADN95773.
XX
XX Example 1; SEQ ID NO 696; 176pp; English.
XX
XX This invention relates to a method of differentially modulating the
XX growth or differentiation of blood endothelial cells (BEC) or lymphatic
XX endothelial cells (LEC) comprises contacting endothelial cells with a
XX composition comprising an agent that differentially modulates blood or
XX lymphatic endothelial cells. Treating hereditary lymphoedema comprises
XX identifying a human subject with lymphoedema and with a mutation in at
XX least one allele of a gene encoding a LEC protein, where the mutation
XX correlates with lymphoedema in human subjects, and with the proviso that
XX the LEC protein is not VEGFR-3; and administering to the subject a
XX composition comprising a lymphatic growth agent selected from VEGF-C or
XX VEGF-D polypeptides and polynucleotides. The invention may be useful for
XX the development of compounds with an antiangiogenic, cytostatic,
XX vasotropic or antiinflammatory activity or for gene therapy. The method
XX is useful in modulating the growth or differentiation of blood
XX endothelial cells or lymphatic endothelial cells, in treating hereditary
XX lymphoedema, in screening for an endothelial cell disorder or
XX predisposition to the disorder or in monitoring the efficacy or toxicity
XX of a drug on endothelial cells. The agent is useful in manufacturing a
XX medicament for the differential modulation of blood vessel endothelial
XX cell or lymphatic vessel endothelial cell growth or differentiation. The

CC lymphatic growth agent may also be used in manufacturing a medicament for
 CC the treatment of hereditary lymphoedema resulting from a mutation in a
 CC LEC gene or of other diseases involving the lymphatic vessels, such as
 CC various inflammatory diseases and cancer metastasis via the lymphatic
 CC system. The present sequence is that of a human LEC/BEC differentially
 CC expressed protein which is related to the method of the invention. Note:
 CC This sequence does not appear in the specification but was obtained by
 CC the indexer using the source data given in table 14 of the specification.

XX Sequence 498 AA;

Query Match 61.0%; Score 36; DB 7; Length 498;

Best Local Similarity 60.0%; Pred. NO. 1.1e+03;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NVRCRGDDSK 10

Db |:||| |::

482 NWRCPGTDSE 491

RESULT 50

ADP23807

ID ADP23807 standard; protein; 498 AA.

XX

AC ADP23807;

XX

DT 18-NOV-2004 (first entry)

XX

DE PRO polypeptide SEQ ID NO:985.

XX

KW PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;

KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;

KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.

XX

OS Unidentified.

XX

PN WO2004041170-A2.

XX

PD 21-MAY-2004.

XX

PF 30-OCT-2003; 2003WO-US034312.

XX

PR 01-NOV-2002; 2002US-0423394P.

XX

PA (GETH) GENENTECH INC.

XX

PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;

PI Wu TD;

XX

WPI; 2004-419628/39.

DR

N-PSDB; ADP23806.

XX

PT New PRO polypeptides and polynucleotides, useful for treating e.g.
 PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
 PT renal disease, or demyelinating diseases of the central or peripheral
 PT nervous system.

XX

PS Claim 7; SEQ ID NO 985; 2940pp; English.

XX

CC The invention relates to a novel isolated nucleic acid and the PRO
 CC polypeptide encoded by it. A protein of the invention has

CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,

CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,

CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide

CC of the invention may have a use in gene therapy. The PRO polypeptide, its

CC agonist, antagonist, or antibody that specifically binds to the

CC polypeptide is useful for treating an immune related disorder such as

CC systemic lupus erythematous, rheumatoid arthritis, osteoarthritis,

CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an

CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic

CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune

CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal

CC disease, a demyelinating disease of the central or peripheral nervous

CC

CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein
 CC of the invention.

XX Sequence 498 AA;

Query Match 61.0%; Score 36; DB 8; Length 498;

Best Local Similarity 60.0%; Pred. NO. 1.1e+03;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NVRCRGDDSK 10

Db |:||| |::

482 NWRCPGTDSE 491

Search completed: September 7, 2005, 19:54:56

Job time : 86.093 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 7, 2005, 19:48:00 ; Search time 132.558 Seconds
(without alignments)
59.419 Million cell updates/sec

Title: US-10-812-238B-2

Perfect score: 109

Sequence: 1 EGVQNYRCRGDDSKVQEAR 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1774312 seqs, 393823214 residues

Total number of hits satisfying chosen parameters: 1774312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Published Applications AA:*

1:	/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2:	/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3:	/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4:	/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5:	/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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7:	/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8:	/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9:	/cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10:	/cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11:	/cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12:	/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13:	/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14:	/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15:	/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16:	/cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17:	/cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18:	/cgn2_6/ptodata/1/pubpaa/US10F_NEW_PUB.pep.*
19:	/cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20:	/cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21:	/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	109	100.0	20	17 US-10-812-238A-2	Sequence 2, Appli
2	109	100.0	311	16 US-10-655-601-2	Sequence 2, Appli
3	109	100.0	311	17 US-10-812-238A-13	Sequence 13, Appl
4	73	67.0	13	17 US-10-812-238A-23	Sequence 23, Appl
5	59	54.1	10	17 US-10-812-238A-20	Sequence 20, Appl
6	59	54.1	221	15 US-10-287-226-346	Sequence 346, App
7	59	54.1	221	15 US-10-287-226-348	Sequence 348, App
8	59	54.1	284	18 US-10-764-425-157	Sequence 157, App
9	59	54.1	285	16 US-10-655-601-1	Sequence 1, Appli
10	59	54.1	289	16 US-10-643-795A-136	Sequence 136, App
11	59	54.1	289	17 US-10-948-518-136	Sequence 136, App

55	50.5	10	17	US-10-812-238A-22	Sequence 22, Appl
53	48.6	10	17	US-10-812-238A-21	Sequence 21, Appl
49	45.0	847	15	US-10-369-493-13157	Sequence 13157, A
46	45.0	1327	15	US-10-369-493-13172	Sequence 13172, A
46	42.2	74	16	US-10-425-115-262985	Sequence 262985,
46	42.2	304	15	US-10-424-599-228315	Sequence 228315,
45	41.3	135	15	US-10-316-194-17	Sequence 17, Appl
45	41.3	135	17	US-10-732-180-17	Sequence 17, Appl
45	41.3	822	9	US-09-147-947-6	Sequence 6, Appli
45	41.3	875	16	US-10-757-262-34	Sequence 34, Appl
45	41.3	875	16	US-10-723-860-4046	Sequence 4046, Ap
45	41.3	875	17	US-10-843-299-2	Sequence 2, Appli
44	40.4	99	16	US-10-437-963-108989	Sequence 108989,
44	40.4	191	15	US-10-114-270-104	Sequence 104, App
44	40.4	485	15	US-10-108-260A-2858	Sequence 2858, Ap
44	40.4	498	14	US-10-427-631-1	Sequence 1, Appli
44	40.4	1100	15	US-10-369-493-13176	Sequence 13176, A
44	40.4	1907	9	US-09-832-292-39	Sequence 39, Appl
44	40.4	3293	16	US-10-437-963-168323	Sequence 168323,
43.5	39.9	130	15	US-10-424-599-202541	Sequence 202541,
43	39.4	193	16	US-10-767-701-36687	Sequence 36687, A
43	39.4	237	15	US-10-291-172-610	Sequence 610, App
43	39.4	237	15	US-10-221-278-610	Sequence 610, App
43	39.4	363	14	US-10-156-761-13203	Sequence 13203, A
43	39.4	421	15	US-10-210-281-12	Sequence 12, Appl
43	39.4	424	15	US-10-210-281-10	Sequence 10, Appl
43	39.4	428	14	US-10-157-031-139	Sequence 139, App
43	39.4	489	15	US-10-108-260A-2988	Sequence 2988, Ap
43	39.4	505	15	US-10-369-493-21996	Sequence 21996, A
43	39.4	557	9	US-09-815-242-12804	Sequence 12804, A
43	39.4	565	15	US-10-282-122A-43871	Sequence 43871, A
43	39.4	565	17	US-10-857-625-554	Sequence 554, App
43	39.4	566	14	US-10-282-287-4	Sequence 4, Appli
42	38.5	130	15	US-10-282-122A-78271	Sequence 78271, A
42	38.5	137	15	US-10-104-047-3193	Sequence 3193, Ap
42	38.5	173	16	US-10-767-701-33785	Sequence 33785, A
42	38.5	208	16	US-10-437-963-135805	Sequence 135805,
42	38.5	305	18	US-10-898-775-28	Sequence 28, Appl
42	38.5	554	15	US-10-437-963-135808	Sequence 135808,
42	38.5	1166	14	US-10-032-585-7638	Sequence 7638, Ap
41	37.6	56	15	US-10-424-599-268486	Sequence 268486,
41	37.6	119	16	US-10-425-115-337109	Sequence 337109,
41	37.6	130	15	US-10-282-122A-68446	Sequence 68446, A
41	37.6	201	15	US-10-434-817-12	Sequence 12, Appl
41	37.6	201	20	US-11-086-903-12	Sequence 12, Appl
41	37.6	236	15	US-10-434-817-7	Sequence 7, Appli
41	37.6	236	20	US-11-086-903-7	Sequence 7, Appli
41	37.6	255	15	US-10-434-817-2	Sequence 2, Appli
41	37.6	255	20	US-11-086-903-2	Sequence 2, Appli
41	37.6	306	16	US-10-767-701-39559	Sequence 39559, A
41	37.6	396	14	US-10-065-133A-92	Sequence 92, Appl
41	37.6	396	14	US-10-065-133A-95	Sequence 95, Appl
41	37.6	396	16	US-10-734-373-92	Sequence 92, Appl
41	37.6	396	16	US-10-734-373-95	Sequence 95, Appl
41	37.6	396	18	US-10-181-585B-64	Sequence 64, Appl
41	37.6	396	18	US-10-181-585B-67	Sequence 67, Appl
41	37.6	752	16	US-10-381-530-28	Sequence 28, Appl
41	37.6	757	14	US-10-065-133A-107	Sequence 107, App
41	37.6	757	16	US-10-734-373-107	Sequence 107, App
41	37.6	757	18	US-10-181-585B-72	Sequence 72, Appl
41	37.6	1150	16	US-10-437-963-147798	Sequence 147798,
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40.5	37.2	255	16	US-10-437-963-116185	Sequence 116185,
40.5	37.2	353	16	US-10-437-963-178169	Sequence 178169,
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40	36.7	42	16	US-10-425-115-328990	Sequence 328990,
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40	36.7	51	16	US-10-437-963-204484	Sequence 204484,
40	36.7	79	16	US-10-437-963-131923	Sequence 131923,
40	36.7	84	16	US-10-437-963-154748	Sequence 154748,
40	36.7	94	15	US-10-289-762-1290	Sequence 1290, Ap
40	36.7	102	15	US-10-424-599-260014	Sequence 260014,

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86	40	36.7	112	15	US-10-424-599-275302	Sequence 275302,	159	39.5	36.2	211	15	US-10-236-031B-14	Sequence 14, Appl
87	40	36.7	113	15	US-10-282-122A-50965	Sequence 50965, A	160	39.5	36.2	211	15	US-10-072-012-335	Sequence 335, App
88	40	36.7	112	15	US-10-282-122A-76429	Sequence 76429, A	161	39.5	36.2	211	15	US-10-072-012-336	Sequence 336, App
89	40	36.7	115	15	US-10-276-774-1857	Sequence 1857, Ap	162	39.5	36.2	211	15	US-10-344-487-13	Sequence 13, Appl
90	40	36.7	147	15	US-10-424-599-269282	Sequence 269282,	163	39.5	36.2	211	15	US-10-601-953-896	Sequence 896, App
91	40	36.7	231	15	US-10-424-599-239306	Sequence 239306,	164	39.5	36.2	247	14	US-10-106-698-6273	Sequence 6273, Ap
92	40	36.7	226	18	US-10-724-972A-5260	Sequence 5260, Ap	165	39.5	36.2	247	15	US-10-264-049-3053	Sequence 3053, Ap
93	40	36.7	259	15	US-10-424-599-222209	Sequence 222209,	166	39.5	36.2	286	15	US-10-282-122A-69355	Sequence 69355, A
94	40	36.7	286	15	US-10-424-599-173051	Sequence 173051,	166	39.5	36.2	286	15	US-10-369-493-1571	Sequence 493-1571, Ap
95	40	36.7	301	15	US-10-369-493-15738	Sequence 15738, A	168	39	35.8	43	16	US-10-437-963-17113	Sequence 157113,
96	40	36.7	301	15	US-10-369-493-16124	Sequence 16124, A	169	39	35.8	51	16	US-10-435-115-309902	Sequence 309902,
97	40	36.7	302	15	US-10-369-493-15371	Sequence 15371, A	170	39	35.8	74	9	US-09-764-877-2043	Sequence 2043, Ap
98	40	36.7	371	15	US-10-425-114-42592	Sequence 42592, A	171	39	35.8	74	15	US-10-242-515-2043	Sequence 2043, Ap
99	40	36.7	386	14	US-10-065-133A-86	Sequence 86, Appl	172	39	35.8	77	16	US-10-437-963-170560	Sequence 170560,
100	40	36.7	386	14	US-10-065-133A-89	Sequence 89, Appl	173	39	35.8	99	16	US-10-437-963-149116	Sequence 149116,
101	40	36.7	396	16	US-10-734-373-86	Sequence 86, Appl	174	39	35.8	115	15	US-10-424-599-165388	Sequence 165388,
102	40	36.7	396	16	US-10-734-373-89	Sequence 89, Appl	175	39	35.8	117	15	US-10-424-599-249919	Sequence 249919,
103	40	36.7	396	18	US-10-181-585B-54	Sequence 54, Appl	176	39	35.8	122	11	US-09-864-408A-8608	Sequence 8608, Ap
104	40	36.7	396	18	US-10-181-585B-54	Sequence 54, Appl	177	39	35.8	127	16	US-10-467-253-9	Sequence 9, Appl
105	40	36.7	400	15	US-10-282-122A-43293	Sequence 43293, A	178	39	35.8	131	15	US-10-282-122A-50058	Sequence 50058, A
106	40	36.7	400	15	US-10-282-122A-59506	Sequence 59506, A	179	39	35.8	132	9	US-09-738-626-4098	Sequence 4098, Ap
107	40	36.7	400	15	US-10-282-122A-73186	Sequence 73186, A	180	39	35.8	132	16	US-10-494-674-16	Sequence 16, Appl
108	40	36.7	400	15	US-10-282-122A-75975	Sequence 75975, A	181	39	35.8	161	16	US-10-767-701-54578	Sequence 54578, A
109	40	36.7	401	14	US-10-156-761-9009	Sequence 9009, Ap	182	39	35.8	173	9	US-09-205-658-216	Sequence 216, App
110	40	36.7	421	16	US-10-437-963-204884	Sequence 204884,	183	39	35.8	173	10	US-09-963-693-216	Sequence 216, App
111	40	36.7	422	16	US-10-739-930-6688	Sequence 6688, Ap	184	39	35.8	185	15	US-10-282-122A-63885	Sequence 63885, A
112	40	36.7	434	14	US-10-167-127-13	Sequence 13, Appl	185	39	35.8	214	14	US-10-002-631C-250	Sequence 250, App
113	40	36.7	440	15	US-10-369-493-3576	Sequence 3576, Ap	186	39	35.8	234	15	US-10-424-599-179999	Sequence 179999,
114	40	36.7	482	16	US-10-425-115-210789	Sequence 210789,	187	39	35.8	253	15	US-10-282-122A-63937	Sequence 63937, A
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116	40	36.7	497	16	US-10-437-963-111779	Sequence 111779,	189	39	35.8	297	15	US-10-282-122A-51933	Sequence 51933, A
117	40	36.7	531	16	US-10-259-194A-150	Sequence 150, App	190	39	35.8	301	9	US-09-815-242-11200	Sequence 11200, A
118	40	36.7	531	16	US-10-425-115-359488	Sequence 359488,	191	39	35.8	325	15	US-10-104-047-3498	Sequence 3498, Ap
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121	40	36.7	564	16	US-10-767-701-46229	Sequence 46229, A	194	39	35.8	435	15	US-10-425-114-43540	Sequence 43540, A
122	40	36.7	662	15	US-10-424-599-208782	Sequence 208782,	195	39	35.8	447	13	US-10-047-676A-10	Sequence 10, Appl
123	40	36.7	669	16	US-10-425-115-215599	Sequence 215599,	196	39	35.8	447	16	US-10-790-914-10	Sequence 10, Appl
124	40	36.7	730	14	US-10-067-632-58	Sequence 58, Appl	197	39	35.8	461	15	US-10-417-700A-21	Sequence 21, Appl
125	40	36.7	757	14	US-10-073-377-23	Sequence 23, Appl	198	39	35.8	462	17	US-10-732-923-6182	Sequence 6182, Ap
126	40	36.7	757	14	US-10-073-377-25	Sequence 25, Appl	199	39	35.8	462	17	US-10-732-923-6187	Sequence 6187, Ap
127	40	36.7	757	14	US-10-073-377-27	Sequence 27, Appl	200	39	35.8	466	15	US-10-369-493-2996	Sequence 2996, Ap
128	40	36.7	757	14	US-10-073-377-29	Sequence 29, Appl	201	39	35.8	470	15	US-10-369-493-2942	Sequence 2942, Ap
129	40	36.7	757	14	US-10-073-377-31	Sequence 31, Appl	202	39	35.8	487	15	US-10-424-599-269280	Sequence 269280,
130	40	36.7	757	14	US-10-073-377-33	Sequence 33, Appl	203	39	35.8	487	15	US-10-425-114-51705	Sequence 51705, A
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132	40	36.7	757	14	US-10-073-377-37	Sequence 37, Appl	205	39	35.8	550	15	US-10-108-260A-4334	Sequence 4334, Ap
133	40	36.7	757	14	US-10-073-377-39	Sequence 39, Appl	206	39	35.8	557	9	US-09-815-242-12165	Sequence 12165, A
134	40	36.7	757	14	US-10-073-377-43	Sequence 43, Appl	207	39	35.8	563	9	US-09-815-242-5464	Sequence 5464, Ap
135	40	36.7	757	14	US-10-073-377-43	Sequence 43, Appl	208	39	35.8	565	16	US-10-408-765A-1726	Sequence 1726, Ap
136	40	36.7	757	14	US-10-073-377-45	Sequence 45, Appl	209	39	35.8	572	15	US-10-425-114-43039	Sequence 43039, A
137	40	36.7	757	14	US-10-073-377-47	Sequence 47, Appl	210	39	35.8	602	15	US-10-094-749-3150	Sequence 3150, Ap
138	40	36.7	757	14	US-10-065-133A-104	Sequence 104, App	211	39	35.8	615	17	US-10-741-600-1522	Sequence 1522, Ap
139	40	36.7	757	16	US-10-381-530-10	Sequence 10, Appl	212	39	35.8	631	15	US-10-424-599-266585	Sequence 266585,
140	40	36.7	757	16	US-10-734-373-104	Sequence 104, App	213	39	35.8	654	15	US-10-369-493-5125	Sequence 5125, Ap
141	40	36.7	757	18	US-10-181-585B-69	Sequence 69, Appl	214	39	35.8	662	17	US-10-741-600-1523	Sequence 1523, Ap
142	40	36.7	823	14	US-10-167-127-15	Sequence 15, Appl	215	39	35.8	662	17	US-10-741-600-1524	Sequence 1524, Ap
143	40	36.7	891	17	US-10-732-923-14985	Sequence 14985, A	216	39	35.8	670	14	US-10-156-761-14107	Sequence 14107, A
144	40	36.7	967	17	US-10-732-923-14984	Sequence 14984, A	217	39	35.8	690	15	US-10-369-493-22730	Sequence 22730,
145	40	36.7	1896	17	US-10-732-923-1758	Sequence 1758, Ap	218	39	35.8	693	16	US-10-437-963-149803	Sequence 149803,
146	40	36.7	5560	15	US-10-263-929-142	Sequence 142, App	219	39	35.8	694	16	US-10-425-115-210914	Sequence 210914,
147	40	36.7	8523	18	US-10-840-512-162	Sequence 162, App	220	39	35.8	702	17	US-10-741-600-1526	Sequence 1526, Ap
148	39.5	36.2	77	16	US-10-425-115-230658	Sequence 230658,	221	39	35.8	754	17	US-10-741-600-1525	Sequence 1525, Ap
149	39.5	36.2	77	16	US-10-425-115-230659	Sequence 230659,	222	39	35.8	801	9	US-09-815-242-5518	Sequence 5518, Ap
150	39.5	36.2	78	16	US-10-437-963-139394	Sequence 139394,	223	39	35.8	801	9	US-09-815-242-12519	Sequence 12519, A
151	39.5	36.2	126	14	US-10-002-631C-46	Sequence 46, Appl	224	39	35.8	801	15	US-10-282-122A-44225	Sequence 44225, A
152	39.5	36.2	137	10	US-09-866-050A-174	Sequence 174, App	225	39	35.8	809	15	US-10-282-122A-61637	Sequence 61637, A
153	39.5	36.2	194	9	US-09-935-301-999	Sequence 999, App	226	39	35.8	898	15	US-10-257-174-43	Sequence 43, Appl
154	39.5	36.2	210	9	US-09-935-390A-36	Sequence 36, Appl	227	39	35.8	912	13	US-10-047-542-75	Sequence 75, Appl
155	39.5	36.2	211	10	US-09-471-749-7	Sequence 7, Appl	228	39	35.8	917	13	US-10-047-542-76	Sequence 76, Appl
156	39.5	36.2	211	14	US-10-176-847-84	Sequence 84, Appl	229	39	35.8	917	13	US-10-047-542-87	Sequence 87, Appl
157	39.5	36.2	211	14	US-10-068-486A-2	Sequence 2, Appl	230	39	35.8	917	14	US-10-025-524-2	Sequence 2, Appl

231	39	35.8	924	13	US-10-047-542-67	Sequence 67, Appl	304	34.9	347	10	US-09-907-613-148	Sequence 148, App
232	39	35.8	924	14	US-10-025-524-28	Sequence 28, Appl	305	34.9	347	10	US-09-907-942-148	Sequence 148, App
233	39	35.8	924	15	US-10-723-860-1976	Sequence 1976, Ap	306	34.9	347	10	US-09-904-859-148	Sequence 148, App
234	39	35.8	1004	15	US-10-114-270-32	Sequence 32, Appl	307	34.9	347	10	US-09-909-204-148	Sequence 148, App
235	39	35.8	1229	16	US-10-437-963-133251	Sequence 133251,	308	34.9	347	10	US-09-904-820-148	Sequence 148, App
236	39	35.8	2742	16	US-10-437-963-139002	Sequence 139002,	309	34.9	347	10	US-09-904-786-148	Sequence 148, App
237	39	35.8	3389	15	US-10-016-248-47	Sequence 47, Appl	310	34.9	347	10	US-09-906-646-148	Sequence 148, App
238	39	35.8	3389	16	US-10-408-768A-2286	Sequence 2286, Ap	311	34.9	347	10	US-09-906-700-148	Sequence 148, App
239	39	35.8	3508	15	US-10-016-248-46	Sequence 46, Appl	312	34.9	347	10	US-09-903-786-148	Sequence 148, App
240	38.5	35.3	89	14	US-10-029-386-29445	Sequence 29445, A	313	34.9	347	10	US-09-903-903-148	Sequence 148, App
241	38.5	35.3	114	9	US-09-738-626-6692	Sequence 6692, Ap	314	34.9	347	10	US-09-903-749A-148	Sequence 148, App
242	38.5	35.3	159	15	US-10-108-260A-4046	Sequence 4046, Ap	315	34.9	347	10	US-09-904-119-148	Sequence 148, App
243	38.5	35.3	256	17	US-10-732-923-8967	Sequence 8967, Ap	316	34.9	347	10	US-09-904-956-148	Sequence 148, App
244	38.5	35.3	274	18	US-10-491-467-49	Sequence 49, Appl	317	34.9	347	10	US-09-903-736-148	Sequence 148, App
245	38.5	35.3	553	16	US-10-425-115-352266	Sequence 352266,	318	34.9	347	10	US-09-907-794-148	Sequence 148, App
246	38.5	35.3	645	14	US-10-156-761-12752	Sequence 12752, A	319	34.9	347	10	US-09-903-943-148	Sequence 148, App
247	38.5	35.3	870	16	US-10-437-963-116415	Sequence 116415,	320	34.9	347	10	US-09-904-462-148	Sequence 148, App
248	38.5	35.3	897	15	US-10-259-194A-304	Sequence 304, App	321	34.9	347	10	US-09-907-925-148	Sequence 148, App
249	38.5	35.3	974	16	US-10-437-963-150927	Sequence 150927,	322	34.9	347	10	US-09-902-652-148	Sequence 148, App
250	38.5	35.3	993	16	US-10-437-963-182980	Sequence 182980,	323	34.9	347	10	US-09-903-520-148	Sequence 148, App
251	38.5	35.3	1081	16	US-10-437-963-178760	Sequence 178760,	324	34.9	347	10	US-09-905-056-148	Sequence 148, App
252	38.5	35.3	1275	15	US-10-282-122A-53272	Sequence 53272, A	325	34.9	347	10	US-09-905-064-148	Sequence 148, App
253	38.5	35.3	1287	18	US-10-756-149-5772	Sequence 5772, Ap	326	34.9	347	10	US-09-904-553-148	Sequence 148, App
254	38.5	35.3	1561	17	US-10-805-684-45	Sequence 45, Appl	327	34.9	347	10	US-09-905-381-148	Sequence 148, App
255	38.5	35.3	1893	17	US-10-479-764-15	Sequence 15, Appl	328	34.9	347	10	US-09-904-485-148	Sequence 148, App
256	38	34.9	22	9	US-09-864-761-34955	Sequence 34955, A	329	34.9	347	10	US-09-905-348-148	Sequence 148, App
257	38	34.9	43	15	US-10-424-599-238960	Sequence 238960,	330	34.9	347	10	US-09-905-088-148	Sequence 148, App
258	38	34.9	71	15	US-10-424-599-283295	Sequence 283295,	331	34.9	347	10	US-09-907-575-148	Sequence 148, App
259	38	34.9	77	15	US-10-264-049-3870	Sequence 3870, Ap	332	34.9	347	10	US-09-905-075-148	Sequence 148, App
260	38	34.9	85	16	US-10-437-963-124176	Sequence 124176,	333	34.9	347	10	US-09-902-759-148	Sequence 148, App
261	38	34.9	94	16	US-10-425-115-303573	Sequence 303573,	334	34.9	347	10	US-09-903-634-148	Sequence 148, App
262	38	34.9	96	16	US-10-437-963-201926	Sequence 201926,	335	34.9	347	10	US-09-902-713-148	Sequence 148, App
263	38	34.9	108	15	US-10-108-260A-3952	Sequence 3952, Ap	336	34.9	347	10	US-09-907-979-148	Sequence 148, App
264	38	34.9	116	15	US-10-282-122A-51355	Sequence 51355, A	337	34.9	347	10	US-09-902-615-148	Sequence 148, App
265	38	34.9	129	16	US-10-451-467A-214	Sequence 214, App	338	34.9	347	10	US-09-284-320-4	Sequence 4, Appli
266	38	34.9	136	14	US-10-062-831-131	Sequence 131, App	339	34.9	347	10	US-09-903-925-148	Sequence 148, App
267	38	34.9	136	14	US-10-062-598-131	Sequence 131, App	340	34.9	347	10	US-09-906-760A-148	Sequence 148, App
268	38	34.9	151	15	US-10-074-978A-404	Sequence 404, App	341	34.9	347	10	US-09-903-823-148	Sequence 148, App
269	38	34.9	151	16	US-10-425-115-269918	Sequence 269918,	342	34.9	347	10	US-09-907-652-148	Sequence 148, App
270	38	34.9	152	17	US-10-732-923-22004	Sequence 22004, A	343	34.9	347	10	US-09-902-572A-148	Sequence 148, App
271	38	34.9	159	16	US-10-425-115-346856	Sequence 346856,	344	34.9	347	10	US-09-903-979-148	Sequence 148, App
272	38	34.9	164	9	US-09-863-824-4	Sequence 4, Appli	345	34.9	347	10	US-09-905-125-148	Sequence 148, App
273	38	34.9	164	18	US-10-950-177-4	Sequence 4, Appli	346	34.9	347	10	US-09-906-815A-148	Sequence 148, App
274	38	34.9	168	16	US-10-767-701-54860	Sequence 54860, A	347	34.9	347	10	US-09-905-449-148	Sequence 148, App
275	38	34.9	172	15	US-10-282-122A-54254	Sequence 54254, A	348	34.9	347	10	US-09-903-806-148	Sequence 148, App
276	38	34.9	182	17	US-10-491-823-96	Sequence 96, Appl	349	34.9	347	10	US-09-904-992-148	Sequence 148, App
277	38	34.9	206	13	US-10-087-192-1548	Sequence 14771, Ap	350	34.9	347	10	US-09-904-838-148	Sequence 148, App
278	38	34.9	212	16	US-10-437-963-147771	Sequence 147771,	351	34.9	347	10	US-09-906-777-148	Sequence 148, App
279	38	34.9	228	16	US-10-437-963-143729	Sequence 143729,	352	34.9	347	10	US-09-903-603A-148	Sequence 148, App
280	38	34.9	240	16	US-10-490-318-15	Sequence 15, Appl	353	34.9	347	10	US-09-904-532-148	Sequence 148, App
281	38	34.9	250	15	US-10-282-122A-58270	Sequence 58270, A	354	34.9	347	10	US-09-904-766-148	Sequence 148, App
282	38	34.9	268	15	US-10-424-599-152408	Sequence 152408,	355	34.9	347	10	US-09-904-920A-148	Sequence 148, App
283	38	34.9	303	14	US-10-032-201B-268	Sequence 268, App	356	34.9	347	10	US-09-904-877A-148	Sequence 148, App
284	38	34.9	303	17	US-10-472-928-2968	Sequence 2968, Ap	357	34.9	347	10	US-09-903-562-148	Sequence 148, App
285	38	34.9	305	16	US-10-425-115-283662	Sequence 283662,	358	34.9	347	10	US-09-906-618-148	Sequence 148, App
286	38	34.9	307	16	US-10-322-281-690	Sequence 690, App	359	34.9	347	10	US-09-907-728-148	Sequence 148, App
287	38	34.9	318	16	US-10-425-115-308664	Sequence 308664,	360	34.9	347	10	US-09-904-805-148	Sequence 148, App
288	38	34.9	322	15	US-10-369-493-10753	Sequence 10753, A	361	34.9	347	10	US-09-904-938A-148	Sequence 148, App
289	38	34.9	326	15	US-10-282-122A-51926	Sequence 51926, A	362	34.9	347	10	US-09-906-722A-148	Sequence 148, App
290	38	34.9	338	15	US-10-425-114-58760	Sequence 58760, A	363	34.9	347	10	US-09-908-576-148	Sequence 148, App
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296	38	34.9	347	9	US-09-902-853-148	Sequence 148, App	369	34.9	347	10	US-10-232-224-114	Sequence 114, App
297	38	34.9	347	9	US-09-907-841-148	Sequence 148, App	370	34.9	347	10	US-10-216-159A-114	Sequence 114, App
298	38	34.9	347	9	US-09-904-011-148	Sequence 148, App	371	34.9	347	10	US-10-218-849-114	Sequence 114, App
299	38	34.9	347	10	US-09-903-640-148	Sequence 148, App	372	34.9	347	10	US-10-227-873-114	Sequence 114, App
300	38	34.9	347	10	US-09-904-093-148	Sequence 148, App	373	34.9	347	10	US-10-227-883-114	Sequence 114, App
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302	38	34.9	347	10	US-09-906-743-148	Sequence 148, App	375	34.9	347	10	US-10-230-434-114	Sequence 114, App
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419 38 34.9 347 14 US-10-219-471-114 Sequence 114, App 492 38 34.9 367 16 US-10-739-930-7243 Sequence 7243, Ap
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422 38 34.9 347 14 US-10-219-482-114 Sequence 114, App 495 38 34.9 391 15 US-10-074-978A-402 Sequence 402, App
423 38 34.9 347 14 US-10-230-433-114 Sequence 114, App 496 38 34.9 391 15 US-10-425-114-42060 Sequence 42060, A
424 38 34.9 347 14 US-10-230-435-114 Sequence 114, App 497 38 34.9 407 15 US-10-282-122A-71177 Sequence 71177, A
425 38 34.9 347 14 US-10-227-876-114 Sequence 114, App 498 38 34.9 411 11 US-09-939-853A-92 Sequence 92, Appl
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429 38 34.9 347 14 US-10-230-183-114 Sequence 114, App
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431 38 34.9 347 14 US-10-230-306-114 Sequence 114, App
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437 38 34.9 347 14 US-10-232-222-114 Sequence 114, App
438 38 34.9 347 14 US-10-223-084-24 Sequence 24, Appl
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441 38 34.9 347 14 US-10-219-070-114 Sequence 114, App
442 38 34.9 347 14 US-10-219-472-114 Sequence 114, App
443 38 34.9 347 14 US-10-219-527-114 Sequence 114, App
444 38 34.9 347 14 US-10-227-877-114 Sequence 114, App
445 38 34.9 347 14 US-10-223-087-24 Sequence 24, Appl
446 38 34.9 347 14 US-10-223-083-24 Sequence 24, Appl
447 38 34.9 347 14 US-10-216-166-114 Sequence 114, App
448 38 34.9 347 14 US-10-218-612-114 Sequence 114, App
449 38 34.9 347 14 US-10-223-089-24 Sequence 24, Appl
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ALIGNMENTS

RESULT 1

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US-10-812-238A-2
; Sequence 2, Application US/10812238A
; Publication No. US20050002904A1
; GENERAL INFORMATION:
; APPLICANT: Humt-soe, Joseph O.
; TITLE OF INVENTION: Uses of Vascular Endothelial Growth Factor
; FILE REFERENCE: D6563
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,164
; PRIOR FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 2
; LENGTH: 20
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; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: peptide used to raise anti-VCIP-RGD antibody
US-10-812-238A-2

Query Match 100.0%; Score 109; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGYQNYRCRGDDSKVQEAR 20
Db 1 EGYQNYRCRGDDSKVQEAR 20
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RESULT 2
US-10-655-601-2
; Sequence 2, Application US/10655601
; Publication No. US20040137522A1
; GENERAL INFORMATION:
; APPLICANT: Feany, Mel B.
; TITLE OF INVENTION: Genes and Proteins Altering Tau-Related Neuropathy
; FILE REFERENCE: 7570/73251
; CURRENT APPLICATION NUMBER: US/10/655,601
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-655-601-2

Query Match 100.0%; Score 109; DB 16; Length 311;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGYQNYRCRGDDSKVQEAR 20
Db 173 EGYQNYRCRGDDSKVQEAR 192
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RESULT 3
US-10-812-238A-13
; Sequence 13, Application US/10812238A
; Publication No. US20050002904A1
; GENERAL INFORMATION:
; APPLICANT: Wary, Kishore, K.
; TITLE OF INVENTION: Uses of Vascular Endothelial Growth Factor
; TITLE OF INVENTION: and Type I Collagen Inducible Protein (VCIP)
; FILE REFERENCE: D6563
; CURRENT APPLICATION NUMBER: US/10/812,238A
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,164
; PRIOR FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 13
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: human VCIP
US-10-812-238A-13

Query Match 100.0%; Score 109; DB 17; Length 311;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGYQNYRCRGDDSKVQEAR 20

Db 173 EGYQNYRCRGDDSKVQEAR 192
|||||

RESULT 4
US-10-812-238A-23
; Sequence 23, Application US/10812238A
; Publication No. US20050002904A1
; GENERAL INFORMATION:
; APPLICANT: Wary, Kishore, K.
; APPLICANT: Humtsoe, Joseph O.
; TITLE OF INVENTION: Uses of Vascular Endothelial Growth Factor
; TITLE OF INVENTION: and Type I Collagen Inducible Protein (VCIP)
; FILE REFERENCE: D6563
; CURRENT APPLICATION NUMBER: US/10/812,238A
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,164
; PRIOR FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 23
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: a peptide containing RGD sequence
US-10-812-238A-23

Query Match 67.0%; Score 73; DB 17; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NYRCRGDDSKVQES 18
Db 1 NYRCRGDDSKVQES 13
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RESULT 5
US-10-812-238A-20
; Sequence 20, Application US/10812238A
; Publication No. US20050002904A1
; GENERAL INFORMATION:
; APPLICANT: Wary, Kishore, K.
; TITLE OF INVENTION: Uses of Vascular Endothelial Growth Factor
; TITLE OF INVENTION: and Type I Collagen Inducible Protein (VCIP)
; FILE REFERENCE: D6563
; CURRENT APPLICATION NUMBER: US/10/812,238A
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,164
; PRIOR FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: a peptide containing RGD sequence
US-10-812-238A-20

Query Match 54.1%; Score 59; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NYRCRGDDSK 15
Db 1 NYRCRGDDSK 10
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RESULT 6
US-10-287-226-346
; Sequence 346, Application US/10287226

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; Publication No. US2004008675A1
; GENERAL INFORMATION:
; APPLICANT: Agee, Michele L.,
; APPLICANT: Alsobrook, John P.,
; APPLICANT: Berghs, Constance,
; APPLICANT: Boldog, Ference,
; APPLICANT: Burgess, Catherine E.,
; APPLICANT: Chant, John S.,
; APPLICANT: Chaudhuri, Amitabha,
; APPLICANT: DiPippo, Vincent A.,
; APPLICANT: Edinger, Shlomit R.,
; APPLICANT: Eisen, Andrew,
; APPLICANT: Ellerman, Karen,
; APPLICANT: Gangolli, Esha A.,
; APPLICANT: Gorman, Linda,
; APPLICANT: Gerlach, Valerie,
; APPLICANT: Ji, Weizhen,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Khrantsov, Nikolai,
; APPLICANT: Li, Li,
; APPLICANT: Malyankar, Uriel M.,
; APPLICANT: MacDougall, John R.,
; APPLICANT: Mezes, Peter S.,
; APPLICANT: Miller, Charles E.,
; APPLICANT: Millet, Isabelle,
; APPLICANT: Ooi, Chean Eng,
; APPLICANT: Ort, Tatiana,
; APPLICANT: Padigaru, Muralidhara,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Rastelli, Luca,
; APPLICANT: Rieger, Daniel K.,
; APPLICANT: Rothenberg, Mark E.,
; APPLICANT: Shenoy, Suresh G.,
; APPLICANT: Spaderna, Steven K.,
; APPLICANT: Spytek, Kimberley A.,
; APPLICANT: Taupier, Jr., Raymond J.,
; APPLICANT: Vernet, Corine A.M.,
; APPLICANT: Zerhusen, Bryan D.,
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-480C
; CURRENT APPLICATION NUMBER: US/10/287,226
; CURRENT FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: 60/334,421
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,392
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/360,148
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/364,000
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/404,821
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/334,526
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,409
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/364,227
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/334,027
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/331,641
; PRIOR FILING DATE: 2001-11-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 673
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 346
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-226-346
, Query Match      54.1%; Score 59; DB 15; Length 221;

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Best Local Similarity 50.0%; Pred. No. 0.68;
Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EGYIONVRCRGGDSKVQEAR 20
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Db 82 DGYIEYTCRGNARVKEGR 101

RESULT 7
US-10-287-226-348
; Sequence 348, Application US/10287226
; Publication No. US2004008675A1
; GENERAL INFORMATION:
; APPLICANT: Agee, Michele L.,
; APPLICANT: Alsobrook, John P.,
; APPLICANT: Berghs, Constance,
; APPLICANT: Boldog, Ference,
; APPLICANT: Burgess, Catherine E.,
; APPLICANT: Chant, John S.,
; APPLICANT: Chaudhuri, Amitabha,
; APPLICANT: DiPippo, Vincent A.,
; APPLICANT: Edinger, Shlomit R.,
; APPLICANT: Eisen, Andrew,
; APPLICANT: Ellerman, Karen,
; APPLICANT: Gangolli, Esha A.,
; APPLICANT: Gorman, Linda,
; APPLICANT: Gerlach, Valerie,
; APPLICANT: Ji, Weizhen,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Khrantsov, Nikolai,
; APPLICANT: Li, Li,
; APPLICANT: Malyankar, Uriel M.,
; APPLICANT: MacDougall, John R.,
; APPLICANT: Mezes, Peter S.,
; APPLICANT: Miller, Charles E.,
; APPLICANT: Millet, Isabelle,
; APPLICANT: Ooi, Chean Eng,
; APPLICANT: Ort, Tatiana,
; APPLICANT: Padigaru, Muralidhara,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Rastelli, Luca,
; APPLICANT: Rieger, Daniel K.,
; APPLICANT: Rothenberg, Mark E.,
; APPLICANT: Shenoy, Suresh G.,
; APPLICANT: Spaderna, Steven K.,
; APPLICANT: Spytek, Kimberley A.,
; APPLICANT: Taupier, Jr., Raymond J.,
; APPLICANT: Vernet, Corine A.M.,
; APPLICANT: Zerhusen, Bryan D.,
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-480C
; CURRENT APPLICATION NUMBER: US/10/287,226
; CURRENT FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: 60/334,421
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,392
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/360,148
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/364,000
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/404,821
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/334,526
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,409
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/364,227
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/334,027
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/331,641
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 673
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 346
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-226-346
, Query Match      54.1%; Score 59; DB 15; Length 221;

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; PRIOR FILING DATE: 2001-11-20
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 673

; SOFTWARE: CuraseqList version 0.1

; SEQ ID NO 348

; LENGTH: 221

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-287-226-348

Query Match 54.1%; Score 59; DB 15; Length 221;
Best Local Similarity 50.0%; Pred. No. 0.68; Length 221;
Matches 10; Conservative 5; Mismatches 0; Indels 5; Gaps 0;

Qy 1 EGYIONRCRGDDSKVQEAR 20

:|||: |||: :|||

Db 82 DGYIEYICRGNAERVKEGR 101

RESULT 8

US-10-764-425-157

; Sequence 157, Application US/10764425

; Publication No. US20040146921A1

; GENERAL INFORMATION:

; APPLICANT: Bayer Pharmaceuticals Corporation

; APPLICANT: Eveleigh, Deepa

; APPLICANT: Bigwood, Douglas

; APPLICANT: Taylor, Ian

; TITLE OF INVENTION: EXPRESSION PROFILES FOR COLON CANCER AND METHODS OF USE

; FILE REFERENCE: 5151

; CURRENT APPLICATION NUMBER: US/10764,425

; CURRENT FILING DATE: 2004-01-23

; PRIOR APPLICATION NUMBER: 60/442,582

; PRIOR FILING DATE: 2003-01-24

; NUMBER OF SEQ ID NOS: 191

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 157

; LENGTH: 284

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-764-425-157

Query Match 54.1%; Score 59; DB 18; Length 284;
Best Local Similarity 50.0%; Pred. No. 0.88; Length 284;
Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EGYIONRCRGDDSKVQEAR 20

:|||: |||: :|||

Db 145 DGYIEYICRGNAERVKEGR 164

RESULT 9

US-10-655-601-1

; Sequence 1, Application US/10655601

; Publication No. US20040137522A1

; GENERAL INFORMATION:

; APPLICANT: Feany, Mel B.

; APPLICANT: Shulman, Joshua M.

; TITLE OF INVENTION: Genes and Proteins Altering Tau-Related Neuropathy

; FILE REFERENCE: 7570/73251

; CURRENT APPLICATION NUMBER: US/10/655,601

; CURRENT FILING DATE: 2003-09-05

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 285

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-655-601-1

Query Match 54.1%; Score 59; DB 16; Length 285;
Best Local Similarity 50.0%; Pred. No. 0.88; Length 285;
Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EGYIONRCRGDDSKVQEAR 20

:|||: |||: :|||

Db 146 DGYIEYICRGNAERVKEGR 165

RESULT 10

US-10-643-795A-136

; Sequence 136, Application US/10643795A

; Publication No. US20040241703A1

; GENERAL INFORMATION:

; APPLICANT: FREDERIC J. DESAUVAGE

; APPLICANT: GRETCHEN FRANTZ

; APPLICANT: KENNETH J. HILLAN

; APPLICANT: PAUL POLAKIS

; APPLICANT: ANDREW POLSON

; APPLICANT: VICTORIA SMITH

; APPLICANT: SUSAN D. SPENCER

; APPLICANT: THOMAS D. WU

; APPLICANT: ZEMIN ZHANG

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND

; FILE REFERENCE: P5026R1-US

; CURRENT APPLICATION NUMBER: US/10/643,795A

; CURRENT FILING DATE: 2003-08-19

; PRIOR APPLICATION NUMBER: US 60/404,809

; PRIOR FILING DATE: 2002-08-19

; PRIOR APPLICATION NUMBER: US 60/405,645

; PRIOR FILING DATE: 2002-08-21

; PRIOR APPLICATION NUMBER: US 60/413,192

; PRIOR FILING DATE: 2002-09-23

; PRIOR APPLICATION NUMBER: US 60/419,008

; PRIOR FILING DATE: 2002-10-15

; PRIOR APPLICATION NUMBER: US 60/426,847

; PRIOR FILING DATE: 2002-11-15

; PRIOR APPLICATION NUMBER: US 60/484,959

; PRIOR FILING DATE: 2003-07-02

; NUMBER OF SEQ ID NOS: 158

; SEQ ID NO 136

; LENGTH: 289

; TYPE: PRT

; ORGANISM: Homo sapien

US-10-643-795A-136

Query Match 54.1%; Score 59; DB 16; Length 289;
Best Local Similarity 50.0%; Pred. No. 0.89; Length 289;
Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EGYIONRCRGDDSKVQEAR 20

:|||: |||: :|||

Db 150 DGYIEYICRGNAERVKEGR 169

RESULT 11

US-10-948-518-136

; Sequence 136, Application US/10948518

; Publication No. US20050064492A1

; GENERAL INFORMATION:

; APPLICANT: FREDERIC J. DESAUVAGE

; APPLICANT: GRETCHEN FRANTZ

; APPLICANT: KENNETH J. HILLAN

; APPLICANT: PAUL POLAKIS

; APPLICANT: ANDREW POLSON

; APPLICANT: VICTORIA SMITH

; APPLICANT: SUSAN D. SPENCER

; APPLICANT: THOMAS D. WU

; APPLICANT: ZEMIN ZHANG

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND

; FILE REFERENCE: P5026R1-US

; CURRENT APPLICATION NUMBER: US/10/948,518

; CURRENT FILING DATE: 2004-09-22

; PRIOR APPLICATION NUMBER: US/10/643,795

```

RESULT 15
US-10-369-493-13172
; Sequence 13172, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICRO-
; TITLE OF INVENTION: PLANTS WITH IMPRO-
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369.

```

10

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VAP amino acid
; OTHER INFORMATION: sequence of Imabill
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(135)
US-10-732-180-17

Query Match          41.3%; Score 45; DB 17; Length 135;
Best Local Similarity 53.3%; Pred. No. 58;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      2 GYIVNRCRGDDSKV 16
      |||:|||||
Db      119 GYDSHYRCGTDVTV 133

RESULT 20
US-09-147-947-6
; Sequence 6, Application US/09147947A
; Patent No. US20020160490A1
; GENERAL INFORMATION:
; APPLICANT: TSURUOKA, No. US20020160490A1uo
; APPLICANT: YAMAGUCHI, Kyoto
; TITLE OF INVENTION: No. US20020160490A1om1
; FILE REFERENCE: 001560-349
; CURRENT APPLICATION NUMBER: US/09/147,947A
; CURRENT FILING DATE: 1997-03-24
; EARLIER APPLICATION NUMBER: PCT/JP98/03324
; EARLIER FILING DATE: 1998-07-24
; EARLIER APPLICATION NUMBER: JP 9/213969
; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 6
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; OTHER INFORMATION:
US-09-147-947-6

Query Match          41.3%; Score 45; DB 9; Length 822;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      3 YIVNRCRGDDSKV 16
      |||:|||||
Db      180 YWSNRCRGDEINI 193

RESULT 21
US-10-757-262-34
; Sequence 34, Application US/10757262
; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Eliasoof, Scott D.
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 2245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; TITLE OF INVENTION: 55053
; FILE REFERENCE: MPI03-007PIRNONMIM
; CURRENT APPLICATION NUMBER: US/10/757,262

; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 875
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-757-262-34

Query Match          41.3%; Score 45; DB 16; Length 875;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      3 YIVNRCRGDDSKV 16
      |||:|||||
Db      233 YWSNRCRGDEINI 246

RESULT 22
US-10-723-860-4046
; Sequence 4046, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Gineburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 4046
; LENGTH: 875
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-4046

Query Match          41.3%; Score 45; DB 16; Length 875;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      3 YIVNRCRGDDSKV 16
      |||:|||||
Db      233 YWSNRCRGDEINI 246

RESULT 23
US-10-843-299-2
; Sequence 2, Application US/10843299
```


; Publication No. US20050032694A1
; GENERAL INFORMATION:
; APPLICANT: SONDEREGGER, Peter
; TITLE OF INVENTION: NEUROTRYPsin
; FILE REFERENCE: 030708-035
; CURRENT APPLICATION NUMBER: US/10/843,299
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/403,724
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/IB98/00625
; PRIOR FILING DATE: 1998-04-24
; PRIOR APPLICATION NUMBER: CH 0966/97
; PRIOR FILING DATE: 1997-04-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 875
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-843-299-2

Query Match 41.3%; Score 45; DB 17; Length 875;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 YIQNYRCRGDSDKV 16
| | | | | :
Db 233 YWSNVRCRGDENI 246

RESULT 24
US-10-437-963-108989
; Sequence 108989, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yinhua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 108989
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_13190C.1.pep
US-10-437-963-108989

Query Match 40.4%; Score 44; DB 16; Length 99;
Best Local Similarity 44.4%; Pred. No. 61;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 EGYIQNYRCRGDSDKVQOE 18
: | | | | :
Db 18 KGVAQDYSMYGHDAKLA 35

RESULT 25
US-10-114-270-104
; Sequence 104, Application US/10114270
; Publication No. US20040030110A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesh

; APPLICANT: Miller, Charles E.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Patturajan, Meera
; APPLICANT: Liu, Ziaohong
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Li, Li
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Gorman, Linda
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Smithson, Glenda
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shinkete, Richard A.
; APPLICANT: Gangolli, Bsha A.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Ji, Weizhen
; APPLICANT: Anderson, David W.
; APPLICANT: Liete, Mario W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Stone, David J.
; APPLICANT: MacDougall, John R.
; APPLICANT: Rothenberg, Mark E.
; TITLE OF INVENTION: No. US20040030110A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-322C
; CURRENT APPLICATION NUMBER: US/10/114,270
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/281,086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; Remaining Prior Application data removed - See File Wrapper. or PALM.
; NUMBER OF SEQ ID NOS: 470
; SEQ ID NO 104
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-270-104

Query Match 40.4%; Score 44; DB 15; Length 191;
Best Local Similarity 43.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IQNYRCRGDSDKVQEA 19
: | | | | :
Db 137 LQYRCREDAIYQA 152

RESULT 26
US-10-108-260A-2858
; Sequence 2858, Application US/10108260A
; Publication No. US20040005560A1

; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560a1e1 full length cdna
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2858
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-2858

Query Match 40.4%; Score 44; DB 15; Length 485;
Best Local Similarity 53.8%; Pred. No. 3.1e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 YIQNYRCRGDDSK 15
|:|:|:|:|:
Db 466 YLYNWRCPGTDSE 478

RESULT 27
US-10-427-631-1
; Sequence 1, Application US/10427631
; Publication No. US20030175923A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; TANG, Y. Tom;
; APPLICANT: CORLEY, Neil C.; GUEGLER, Karl J.;
; APPLICANT: BAUGHN, Mariah R.; LAL, Preeti G.;
; APPLICANT: YUE, Henry; HILLMAN, Jennifer L.;
; APPLICANT: AZIMZAI, Yalda
; TITLE OF INVENTION: HUMAN TRANSFERASE PROTEINS
; FILE REFERENCE: PF-0592-1 DIV
; CURRENT APPLICATION NUMBER: US/10/427,631
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US 09/786,240
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: PCT/US99/20989
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: US 60/172,220
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: US 60/155,248
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 60/133,642
; PRIOR FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030175923A1 1632930CD1
US-10-427-631-1

Query Match 40.4%; Score 44; DB 14; Length 498;
Best Local Similarity 53.8%; Pred. No. 3.1e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 YIQNYRCRGDDSK 15
|:|:|:|:|:
Db 479 YLYNWRCPGTDSE 491

RESULT 28
US-10-369-493-13176
; Sequence 13176, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 13176
; LENGTH: 1100
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
US-10-369-493-13176

Query Match 40.4%; Score 44; DB 15; Length 1100;
Best Local Similarity 46.7%; Pred. No. 7.1e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 GYIQNYRCRGDDSKV 16
|:|:|:|:|:
Db 59 GFQKRCHGQDIEI 73

RESULT 29
US-09-832-292-39
; Sequence 39, Application US/09832292
; Patent No. US20020177205A1
; GENERAL INFORMATION:
; APPLICANT: RYAZANOV, Alexey
; TITLE OF INVENTION: MAMMALIAN ALPHA-KINASE PROTEINS, NUCLEIC ACIDS AND
; FILE REFERENCE: 601-1-098CIP
; CURRENT APPLICATION NUMBER: US/09/832,292
; CURRENT FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 09/632,131
; PRIOR FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 1907
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-292-39

Query Match 40.4%; Score 44; DB 9; Length 1907;
Best Local Similarity 43.8%; Pred. No. 1.2e+03;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IQNYRCRGDDSKVQEA 19
|:|:|:|:|:
Db 339 LQLYRCREDAAIYQA 354

RESULT 30
US-10-437-963-168323
; Sequence 168323, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B

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; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 168323
; LENGTH: 3993
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_66849C.1.pep
US-10-437-963-168323

Query Match      40.4%; Score 44; DB 16; Length 3993;
Best Local Similarity 42.9%; Pred. No. 2.6e+03;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 4 IQNYRCRGDSDSKVQ 17
   :||:| |||:::
Db 132 VQNFPCASDDSEIK 145

RESULT 31
US-10-424-599-202541
; Sequence 202541, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 202541
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(130)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_2491C.1.pep
US-10-424-599-202541

Query Match      39.9%; Score 43.5; DB 15; Length 130;
Best Local Similarity 56.2%; Pred. No. 96;
Matches 9; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 3 YIQNYRCRG-DDSKVQ 17
   ||: : |||:| |||
Db 91 YIKGFACRGSNNKSVQ 106

RESULT 32
US-10-767-701-36687
; Sequence 36687, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 36687
; LENGTH: 193
; TYPE: PRT

; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(193)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C10059_1.pep
US-10-767-701-36687

Query Match      39.4%; Score 43; DB 16; Length 193;
Best Local Similarity 53.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 GYIQNYRCRGDSDS 14
   ||: || |||:
Db 89 GYVTNYAVDGDGA 101

RESULT 33
US-10-291-172-610
; Sequence 610, Application US/10291172
; Publication No. US20030228584A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20030228584A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/291,172
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 610
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-172-610

Query Match      39.4%; Score 43; DB 15; Length 237;
Best Local Similarity 58.3%; Pred. No. 2.1e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 IQNYRCRGDSDSK 15
   :||:| |||:|
Db 3 LDNHRCRGDLTK 14

RESULT 34
US-10-221-278-610
; Sequence 610, Application US/10221278
; Publication No. US20040034208A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20040034208A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/221,278
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
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; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 610
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-221-278-610

Query Match 39.4%; Score 43; DB 15; Length 237;
Best Local Similarity 58.3%; Pred. No. 2.1e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 IQNYRCRGDDSK 15
:|:|||||:
Db 3 LDNHRCRGDLTK 14

RESULT 35
US-10-156-761-13203
; Sequence 13203, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 13203
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-13203

Query Match 39.4%; Score 43; DB 14; Length 363;
Best Local Similarity 46.7%; Pred. No. 3.2e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 YIQNYRCRGDDSKVQ 17
|::|||::|:
Db 182 YLRGRTTGDGTVE 196

RESULT 36
US-10-210-281-12
; Sequence 12, Application US/10210281
; Publication No. US20040030096A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Zhong, Mei
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Pena, Carol E.A.

; APPLICANT: Burgess, Catherine E.
; APPLICANT: Sciore, Paul
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J., Jr.
; APPLICANT: Casman, Stacie
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc L.
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
; TITLE OF INVENTION: THE SAME
; FILE REFERENCE: 21402-416D
; CURRENT APPLICATION NUMBER: US/10/210,281
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: 60/309,501
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/310,291
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/361,775
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 60/310,951
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/361,832
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/312,203
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/313,201
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/313,702
; PRIOR FILING DATE: 2001-08-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 12
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-210-281-12

Query Match 39.4%; Score 43; DB 15; Length 421;
Best Local Similarity 58.3%; Pred. No. 3.8e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 IQNYRCRGDDSK 15
:|:|||||:
Db 195 LDNHRCRGDLTK 206

RESULT 37
US-10-210-281-10
; Sequence 10, Application US/10210281
; Publication No. US20040030096A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Zhong, Mei
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Sciore, Paul
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J., Jr.
; APPLICANT: Casman, Stacie
; APPLICANT: Rothenberg, Mark E.

```
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc L.
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS
; TITLE OF INVENTION: THE SAME
; FILE REFERENCE: 21402-416D
; CURRENT APPLICATION NUMBER: US/10/210,281
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: 60/309,501
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/310,291
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/361,775
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 60/310,951
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/361,832
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/312,203
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/313,201
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/313,702
; PRIOR FILING DATE: 2001-08-20
; REMAINING Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 10
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-210-281-10

Query Match          39.4%; Score 43; DB 15; Length 424;
Best Local Similarity 58.3%; Pred. No. 3.8e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      4 IONYRCRGDSDK 15
       :|:|||||:|
Db      196 LDNHRRCGDLTK 207

RESULT 38
US-10-157-031-139
; Sequence 139, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobahev, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 139
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-031-139

Query Match          39.4%; Score 43; DB 14; Length 428;
Best Local Similarity 58.3%; Pred. No. 3.8e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      4 IONYRCRGDSDK 15
       :|:|||||:|

; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc L.
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS
; TITLE OF INVENTION: THE SAME
; FILE REFERENCE: 21402-416D
; CURRENT APPLICATION NUMBER: US/10/210,281
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: 60/309,501
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/310,291
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/361,775
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 60/310,951
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/361,832
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/312,203
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/313,201
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/313,702
; PRIOR FILING DATE: 2001-08-20
; REMAINING Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 10
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-210-281-10

Query Match          39.4%; Score 43; DB 15; Length 489;
Best Local Similarity 58.3%; Pred. No. 4.4e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      4 IONYRCRGDSDK 15
       :|:|||||:|
Db      256 LDNHRRCGDLTK 267

RESULT 40
US-10-369-493-21996
; Sequence 21996, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 21996
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-21996

Query Match          39.4%; Score 43; DB 15; Length 505;
Best Local Similarity 72.7%; Pred. No. 4.5e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      10 RGDSDKVQEAR 20
       :|:|||||:|
Db      487 RSDAKVEEAR 497

RESULT 41
US-09-815-242-12804
; Sequence 12804, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
```

RESULT 42
US-10-282-122A-43871
; Sequence 43871, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625

QY 1 EGYIONYRCRGDDSKVQE 18

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; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 135805
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(208)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_37445C.1.pap
US-10-437-963-135805

Query Match      38.5%; Score 42; DB 16; Length 208;
Best Local Similarity 43.8%; Pred. No. 2.6e+02;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      3 YIQNYRCRGDDSKVQE 18
Db      93 FMFDYSCGGDDSGTEE 108

RESULT 49
US-10-898-775-28
; Sequence 28, Application US/10898775
; Publication No. US20050142647A1
; GENERAL INFORMATION:
; APPLICANT: WASSELL, PAUL
; APPLICANT: SOE, JORN BORCH
; APPLICANT: MIKKELSON, JORN DALGAARD
; APPLICANT: KRISTENSEN, ANNA CECILIE JENTOFT
; TITLE OF INVENTION: METHOD
; FILE REFERENCE: 674509-2058
; CURRENT APPLICATION NUMBER: US/10/898,775
; CURRENT FILING DATE: 2004-07-26
; PRIOR APPLICATION NUMBER: GB 0416023.0
; PRIOR FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: PCT/IB04/00655
; PRIOR FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: GB 0330016.7
; PRIOR FILING DATE: 2003-12-24
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 28
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Streptomyces coelicolor
US-10-898-775-28

Query Match      38.5%; Score 42; DB 18; Length 305;
Best Local Similarity 61.5%; Pred. No. 3.9e+02;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      8 RCRGDDSKVQEAR 20
Db      258 RCRDDGAVHEFR 270

RESULT 50
US-10-437-963-135808
; Sequence 135808, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 135808
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(473)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_37448C.1.pap
US-10-437-963-135808

Query Match      38.5%; Score 42; DB 16; Length 473;
Best Local Similarity 43.8%; Pred. No. 6.1e+02;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      3 YIQNYRCRGDDSKVQE 18
Db      150 FMFDYSCGGDDSGTEE 165

Search completed: September 7, 2005, 20:02:58
Job time : 143.558 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 7, 2005, 19:44:24 ; Search time 25.1163 Seconds
(without alignments)
59.443 Million cell updates/sec

Title: US-10-812-238B-2

Perfect score: 109

Sequence: 1 EGVQNYRCRGDDSKVQEAR 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS-COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109	100.0	233	4	US-09-360-376-55
2	66	60.6	282	4	US-09-360-376-54
3	65	59.6	283	3	US-08-992-035A-3
4	65	59.6	283	4	US-09-360-376-53
5	59	54.1	285	3	US-08-992-035A-1
6	46.5	42.7	705	4	US-08-311-731A-4
7	44	40.4	416	4	US-09-949-016-8237
8	44	40.4	498	4	US-09-786-240-1
9	43	39.4	505	4	US-09-538-092-359
10	42	38.5	167	4	US-09-252-991A-29214
11	42	38.5	342	4	US-09-248-796A-18072
12	41	37.6	132	4	US-09-543-681A-7222
13	41	37.6	201	3	US-09-015-734-12
14	41	37.6	201	4	US-09-015-311-12
15	41	37.6	236	3	US-09-015-734-7
16	41	37.6	236	4	US-09-015-311-7
17	41	37.6	255	3	US-09-015-734-2
18	41	37.6	255	4	US-09-015-311-2
19	41	37.6	272	4	US-09-489-039A-13748
20	41	37.6	396	4	US-09-506-286B-92
21	41	37.6	396	4	US-09-506-286B-95
22	41	37.6	396	4	US-10-065-133A-92
23	41	37.6	396	4	US-10-065-133A-95
24	41	37.6	757	4	US-09-506-286B-107
25	41	37.6	757	4	US-10-065-133A-107
26	40.5	37.2	145	4	US-09-022-540-13372
27	40.5	37.2	314	4	US-09-252-991A-20336

28	40	36.7	94	4	US-09-198-452A-1290	Sequence 1290, Ap
29	40	36.7	256	3	US-09-134-001C-5278	Sequence 5278, Ap
30	40	36.7	396	4	US-09-506-286B-86	Sequence 86, Appl
31	40	36.7	396	4	US-09-506-286B-89	Sequence 89, Appl
32	40	36.7	396	4	US-10-065-133A-86	Sequence 86, Appl
33	40	36.7	396	4	US-10-065-133A-89	Sequence 89, Appl
34	40	36.7	424	4	US-09-489-039A-12030	Sequence 12030, A
35	40	36.7	501	4	US-09-270-767-41177	Sequence 41177, A
36	40	36.7	710	4	US-09-270-767-56393	Sequence 56393, A
37	40	36.7	710	4	US-09-252-991A-19287	Sequence 19287, A
38	40	36.7	730	1	US-08-121-713D-58	Sequence 58, Appl
39	40	36.7	730	1	US-08-835-268-58	Sequence 58, Appl
40	40	36.7	730	2	US-09-060-692-58	Sequence 58, Appl
41	40	36.7	730	3	US-08-833-391-58	Sequence 58, Appl
42	40	36.7	730	3	US-09-060-610-58	Sequence 58, Appl
43	40	36.7	730	5	PCT-US94-10151A-58	Sequence 58, Appl
44	40	36.7	757	4	US-09-506-286B-104	Sequence 104, Appl
45	40	36.7	757	4	US-10-065-133A-104	Sequence 104, Appl
46	40	36.7	980	4	US-09-252-991A-30838	Sequence 30838, A
47	39.5	36.2	99	4	US-09-621-976-4220	Sequence 4220, Ap
48	39.5	36.2	137	3	US-09-188-930-174	Sequence 174, Appl
49	39.5	36.2	137	4	US-09-312-283C-174	Sequence 174, Appl
50	39.5	36.2	225	4	US-09-673-395A-354	Sequence 354, Appl
51	39.5	36.2	413	4	US-09-270-767-44418	Sequence 44418, A
52	39.5	36.2	456	3	US-09-134-001C-3659	Sequence 3659, Ap
53	39.5	36.2	1238	4	US-09-252-991A-26363	Sequence 26363, A
54	39	35.8	106	4	US-09-673-395A-363	Sequence 263, Appl
55	39	35.8	169	4	US-09-252-991A-19373	Sequence 19373, A
56	39	35.8	317	4	US-09-270-767-42366	Sequence 42366, A
57	39	35.8	447	3	US-09-627-376-10	Sequence 10, Appl
58	39	35.8	447	4	US-10-047-678B-10	Sequence 10, Appl
59	39	35.8	621	2	US-08-419-652-4	Sequence 4, Appl
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61	39	35.8	660	2	US-08-419-652-3	Sequence 3, Appl
62	39	35.8	662	1	US-08-248-532-2	Sequence 2, Appl
63	39	35.8	662	2	US-08-419-652-2	Sequence 2, Appl
64	39	35.8	662	2	US-08-685-118-4	Sequence 4, Appl
65	39	35.8	662	2	US-08-915-495-4	Sequence 4, Appl
66	39	35.8	662	2	US-08-914-520-4	Sequence 4, Appl
67	39	35.8	662	3	US-08-789-350-2	Sequence 2, Appl
68	39	35.8	662	4	US-09-949-016-6624	Sequence 6624, Ap
69	39	35.8	683	4	US-09-949-016-10092	Sequence 10092, A
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71	39	35.8	917	1	US-08-481-130-2	Sequence 2, Appl
72	39	35.8	917	1	US-08-656-984A-2	Sequence 2, Appl
73	39	35.8	917	1	US-08-485-604-2	Sequence 2, Appl
74	39	35.8	917	2	US-08-487-595-2	Sequence 2, Appl
75	39	35.8	924	1	US-08-481-130-28	Sequence 28, Appl
76	39	35.8	924	1	US-08-656-984A-28	Sequence 28, Appl
77	39	35.8	924	1	US-08-485-604-28	Sequence 28, Appl
78	39	35.8	924	2	US-08-487-595-28	Sequence 28, Appl
79	38.5	35.3	383	4	US-09-248-796A-18954	Sequence 18954, A
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81	38	34.9	120	4	US-09-513-999C-6407	Sequence 6407, Ap
82	38	34.9	136	4	US-09-690-454-131	Sequence 131, Appl
83	38	34.9	213	4	US-09-252-991A-22600	Sequence 22600, A
84	38	34.9	265	4	US-09-583-110-3445	Sequence 3445, Ap
85	38	34.9	284	4	US-09-134-000C-3594	Sequence 3594, Ap
86	38	34.9	346	3	US-09-034-916-2	Sequence 2, Appl
87	38	34.9	347	4	US-09-907-794A-148	Sequence 148, Appl
88	38	34.9	347	4	US-09-905-125A-148	Sequence 148, Appl
89	38	34.9	347	4	US-09-902-775A-148	Sequence 148, Appl
90	38	34.9	347	4	US-09-906-700-148	Sequence 148, Appl
91	38	34.9	347	4	US-09-903-603A-148	Sequence 148, Appl
92	38	34.9	347	4	US-09-904-920A-148	Sequence 148, Appl
93	38	34.9	347	4	US-09-909-064-148	Sequence 148, Appl
94	38	34.9	347	4	US-09-905-361A-148	Sequence 148, Appl
95	38	34.9	347	4	US-09-906-618-148	Sequence 148, Appl
96	38	34.9	369	4	US-09-949-016-10311	Sequence 10311, A
97	38	34.9	380	4	US-09-252-991A-28929	Sequence 28929, A
98	38	34.9	427	3	US-09-134-001C-5143	Sequence 5143, Ap
99	38	34.9	440	4	US-09-270-767-60249	Sequence 60249, A
100	38	34.9	456	1	US-08-464-164-2	Sequence 2, Appl

101	38	34.9	456	1	US-08-338-057-2	Sequence 2, Appli	174	36	33.0	35	3	US-09-082-279B-144	Sequence 144, App
102	38	34.9	456	2	US-08-668-416-2	Sequence 2, Appli	175	36	33.0	35	3	US-09-082-279B-145	Sequence 145, App
103	38	34.9	463	3	US-09-252-991A-31367	Sequence 31367, A	176	36	33.0	35	3	US-09-082-279B-146	Sequence 146, App
104	38	34.9	503	4	US-09-270-767-37684	Sequence 37684, A	177	36	33.0	35	3	US-09-082-279B-147	Sequence 147, App
105	38	34.9	503	4	US-09-270-767-52901	Sequence 52901, A	178	36	33.0	35	3	US-09-082-279B-148	Sequence 148, App
106	38	34.9	503	4	US-09-248-796A-17110	Sequence 17110, A	179	36	33.0	35	3	US-09-082-279B-149	Sequence 149, App
107	38	34.9	532	4	US-09-252-991A-21005	Sequence 21005, A	180	36	33.0	35	3	US-08-474-349A-228	Sequence 228, App
108	38	34.9	572	5	PC7-US91-08177-11	Sequence 11, Appl	181	36	33.0	35	3	US-09-315-304B-22	Sequence 22, Appl
109	38	34.9	625	4	US-09-252-991A-28537	Sequence 28537, A	182	36	33.0	35	3	US-09-315-304B-138	Sequence 138, App
110	38	34.9	923	4	US-09-717-926-2	Sequence 2, Appli	183	36	33.0	35	3	US-09-315-304B-139	Sequence 139, App
111	37.5	34.4	304	4	US-09-252-991A-26325	Sequence 26325, A	184	36	33.0	35	3	US-09-315-304B-140	Sequence 140, App
112	37.5	34.4	511	4	US-09-252-991A-26396	Sequence 26396, A	185	36	33.0	35	3	US-09-315-304B-141	Sequence 141, App
113	37.5	34.4	1269	3	US-08-781-891-74	Sequence 74, Appl	186	36	33.0	35	3	US-09-315-304B-142	Sequence 142, App
114	37.5	34.4	1269	4	US-08-168-166-74	Sequence 22, Appl	187	36	33.0	35	3	US-09-315-304B-143	Sequence 143, App
115	37.5	34.4	1409	4	US-09-949-001-22	Sequence 74, Appl	188	36	33.0	35	3	US-09-315-304B-144	Sequence 144, App
116	37.5	34.4	1432	3	US-08-781-891-71	Sequence 71, Appl	189	36	33.0	35	3	US-09-315-304B-145	Sequence 145, App
117	37.5	34.4	1432	4	US-09-618-166-71	Sequence 71, Appl	190	36	33.0	35	3	US-09-315-304B-146	Sequence 146, App
118	37.5	34.4	1432	4	US-09-949-001-16	Sequence 16, Appl	191	36	33.0	35	3	US-09-315-304B-147	Sequence 147, App
119	37	33.9	129	4	US-09-732-210-1649	Sequence 1649, Ap	192	36	33.0	35	3	US-09-315-304B-148	Sequence 148, App
120	37	33.9	130	4	US-09-711-164-320	Sequence 320, App	193	36	33.0	35	3	US-09-315-304B-149	Sequence 149, App
121	37	33.9	130	4	US-09-492-709A-318	Sequence 318, App	194	36	33.0	35	4	US-09-834-784-22	Sequence 22, Appl
122	37	33.9	132	4	US-09-489-039A-11034	Sequence 11034, A	195	36	33.0	35	4	US-09-834-784-138	Sequence 138, App
123	37	33.9	159	4	US-09-252-991A-16672	Sequence 16672, A	196	36	33.0	35	4	US-09-834-784-139	Sequence 139, App
124	37	33.9	185	4	US-09-328-352-7477	Sequence 7477, Ap	197	36	33.0	35	4	US-09-834-784-140	Sequence 140, App
125	37	33.9	191	4	US-09-602-777A-350	Sequence 350, App	198	36	33.0	35	4	US-09-834-784-141	Sequence 141, App
126	37	33.9	236	4	US-09-479-040-25	Sequence 25, Appl	199	36	33.0	35	4	US-09-834-784-142	Sequence 142, App
127	37	33.9	275	4	US-09-489-039A-11789	Sequence 11789, A	200	36	33.0	35	4	US-09-834-784-143	Sequence 143, App
128	37	33.9	332	4	US-09-585-858-50	Sequence 50, Appl	201	36	33.0	35	4	US-09-834-784-144	Sequence 144, App
129	37	33.9	332	4	US-10-270-878-50	Sequence 50, Appl	202	36	33.0	35	4	US-09-834-784-145	Sequence 145, App
130	37	33.9	341	4	US-09-252-991A-16890	Sequence 16890, A	203	36	33.0	35	4	US-09-834-784-146	Sequence 146, App
131	37	33.9	357	4	US-09-248-796A-21669	Sequence 21669, A	204	36	33.0	35	4	US-09-834-784-147	Sequence 147, App
132	37	33.9	362	4	US-09-252-991A-31016	Sequence 31016, A	205	36	33.0	35	4	US-09-834-784-148	Sequence 148, App
133	37	33.9	391	4	US-09-252-991A-16725	Sequence 16725, A	206	36	33.0	35	4	US-09-834-784-149	Sequence 149, App
134	37	33.9	400	1	US-08-447-500-6	Sequence 6, Appli	207	36	33.0	35	4	US-09-515-965A-22	Sequence 22, Appl
135	37	33.9	400	1	US-08-454-097-6	Sequence 6, Appli	208	36	33.0	35	4	US-09-515-965A-138	Sequence 138, App
136	37	33.9	400	1	US-08-453-866-6	Sequence 6, Appli	209	36	33.0	35	4	US-09-515-965A-139	Sequence 139, App
137	37	33.9	400	3	US-08-185-359-6	Sequence 6, Appli	210	36	33.0	35	4	US-09-515-965A-140	Sequence 140, App
138	37	33.9	403	4	US-09-252-991A-25048	Sequence 25048, A	211	36	33.0	35	4	US-09-515-965A-141	Sequence 141, App
139	37	33.9	437	4	US-09-262-537-8	Sequence 2, Appli	212	36	33.0	35	4	US-09-515-965A-142	Sequence 142, App
140	37	33.9	464	3	US-09-056-783-2	Sequence 2, Appli	213	36	33.0	35	4	US-09-515-965A-143	Sequence 143, App
141	37	33.9	488	4	US-09-489-039A-13164	Sequence 13164, A	214	36	33.0	35	4	US-09-515-965A-144	Sequence 144, App
142	37	33.9	583	4	US-09-270-767-43661	Sequence 43661, A	215	36	33.0	35	4	US-09-515-965A-145	Sequence 145, App
143	37	33.9	754	3	US-09-276-400-8	Sequence 8, Appli	216	36	33.0	35	4	US-09-515-965A-146	Sequence 146, App
144	37	33.9	754	3	US-09-448-076-8	Sequence 8, Appli	217	36	33.0	35	4	US-09-515-965A-147	Sequence 147, App
145	37	33.9	754	3	US-09-702-572-8	Sequence 8, Appli	218	36	33.0	35	4	US-09-515-965A-148	Sequence 148, App
146	37	33.9	944	4	US-09-270-767-46843	Sequence 46843, A	219	36	33.0	35	4	US-09-515-965A-149	Sequence 149, App
147	37	33.9	946	4	US-09-502-540-16817	Sequence 16817, A	220	36	33.0	35	4	US-09-350-641C-22	Sequence 22, Appl
148	37	33.9	1123	4	US-09-262-537-4	Sequence 4, Appli	221	36	33.0	35	4	US-09-350-641C-138	Sequence 138, App
149	37	33.9	1177	4	US-09-262-537-2	Sequence 2, Appli	222	36	33.0	35	4	US-09-350-641C-139	Sequence 139, App
150	37	33.9	1403	4	US-09-263-537-6	Sequence 6, Appli	223	36	33.0	35	4	US-09-350-641C-140	Sequence 140, App
151	37	33.9	1658	2	US-08-609-049A-13	Sequence 13, Appl	224	36	33.0	35	4	US-09-350-641C-141	Sequence 141, App
152	37	33.9	1858	3	US-09-170-996-13	Sequence 13, Appl	225	36	33.0	35	4	US-09-350-641C-142	Sequence 142, App
153	37	33.9	1886	4	US-09-355-160D-2	Sequence 2, Appli	226	36	33.0	35	4	US-09-350-641C-143	Sequence 143, App
154	37	33.9	1886	4	US-10-092-219-2	Sequence 2, Appli	227	36	33.0	35	4	US-09-350-641C-144	Sequence 144, App
155	37	33.9	1726	2	US-08-609-049A-30	Sequence 30, Appl	228	36	33.0	35	4	US-09-350-641C-145	Sequence 145, App
156	37	33.9	1726	3	US-09-170-996-30	Sequence 30, Appl	229	36	33.0	35	4	US-09-350-641C-146	Sequence 146, App
157	36.5	33.5	451	4	US-09-489-039A-12702	Sequence 12702, A	230	36	33.0	35	4	US-09-350-641C-147	Sequence 147, App
158	36.5	33.5	724	4	US-09-710-279-3082	Sequence 3082, Ap	231	36	33.0	35	4	US-09-350-641C-148	Sequence 148, App
159	36	33.0	28	3	US-09-082-279B-18	Sequence 18, Appl	232	36	33.0	35	4	US-09-350-641C-149	Sequence 149, App
160	36	33.0	28	3	US-08-474-349A-224	Sequence 224, App	233	36	33.0	35	4	US-09-350-841A-22	Sequence 22, Appl
161	36	33.0	28	3	US-09-315-304B-18	Sequence 18, Appl	234	36	33.0	35	4	US-09-350-841A-138	Sequence 138, App
162	36	33.0	28	4	US-09-834-784-18	Sequence 18, Appl	235	36	33.0	35	4	US-09-350-841A-139	Sequence 139, App
163	36	33.0	28	4	US-09-515-965A-18	Sequence 18, Appl	236	36	33.0	35	4	US-09-350-841A-140	Sequence 140, App
164	36	33.0	28	4	US-09-350-641C-18	Sequence 18, Appl	237	36	33.0	35	4	US-09-350-841A-141	Sequence 141, App
165	36	33.0	28	4	US-09-350-841A-18	Sequence 18, Appl	238	36	33.0	35	4	US-09-350-841A-142	Sequence 142, App
166	36	33.0	35	3	US-08-488-264A-210	Sequence 210, App	239	36	33.0	35	4	US-09-350-841A-143	Sequence 143, App
167	36	33.0	35	3	US-09-082-279B-22	Sequence 22, Appl	240	36	33.0	35	4	US-09-350-841A-144	Sequence 144, App
168	36	33.0	35	3	US-09-082-279B-138	Sequence 138, App	241	36	33.0	35	4	US-09-350-841A-145	Sequence 145, App
169	36	33.0	35	3	US-09-082-279B-139	Sequence 139, App	242	36	33.0	35	4	US-09-350-841A-146	Sequence 146, App
170	36	33.0	35	3	US-09-082-279B-140	Sequence 140, App	243	36	33.0	35	4	US-09-350-841A-147	Sequence 147, App
171	36	33.0	35	3	US-09-082-279B-141	Sequence 141, App	244	36	33.0	35	4	US-09-350-841A-148	Sequence 148, App
172	36	33.0	35	3	US-09-082-279B-142	Sequence 142, App	245	36	33.0	35	4	US-09-350-841A-149	Sequence 149, App
173	36	33.0	35	3	US-09-082-279B-143	Sequence 143, App	246	36	33.0	37	3	US-08-919-597-210	Sequence 210, App

247	36	33.0	37	3	US-08-919-597-211	Sequence 211, App	320	36	33.0	401	4	US-09-270-767-56710	Sequence 56710, A
248	36	33.0	37	3	US-08-919-597-212	Sequence 212, App	321	36	33.0	437	1	US-08-487-037-2	Sequence 2, Appli
249	36	33.0	37	4	US-08-470-896-210	Sequence 210, App	322	36	33.0	437	1	US-08-487-037-3	Sequence 3, Appli
250	36	33.0	37	4	US-08-470-896-211	Sequence 211, App	323	36	33.0	448	1	US-08-295-411-3	Sequence 3, Appli
251	36	33.0	37	4	US-08-470-896-212	Sequence 212, App	324	36	33.0	448	1	US-08-955-471-3	Sequence 3, Appli
252	36	33.0	42	3	US-08-486-099-121	Sequence 121, App	325	36	33.0	448	5	PCT-US92-10068-1	Sequence 1, Appli
253	36	33.0	42	3	US-08-484-223B-121	Sequence 121, App	326	36	33.0	448	5	PCT-US92-10242-3	Sequence 3, Appli
254	36	33.0	42	3	US-08-919-597-121	Sequence 121, App	327	36	33.0	475	4	US-09-902-540-15337	Sequence 15337, A
255	36	33.0	42	3	US-08-475-668A-121	Sequence 121, App	328	36	33.0	475	4	US-09-252-991A-26966	Sequence 26966, A
256	36	33.0	42	3	US-08-485-551A-121	Sequence 121, App	329	36	33.0	488	1	US-08-487-037-1	Sequence 1, Appli
257	36	33.0	42	3	US-08-471-913A-121	Sequence 121, App	330	36	33.0	488	4	US-09-367-777-44	Sequence 44, Appli
258	36	33.0	42	3	US-08-485-264A-121	Sequence 121, App	331	36	33.0	488	4	US-09-367-791A-27	Sequence 27, Appli
259	36	33.0	42	3	US-09-082-279B-17	Sequence 17, Appli	332	36	33.0	496	4	US-09-949-016-9524	Sequence 9524, Ap
260	36	33.0	42	3	US-08-474-349A-121	Sequence 121, App	333	36	33.0	521	4	US-09-252-991A-27321	Sequence 27321, A
261	36	33.0	42	3	US-09-315-304B-17	Sequence 17, Appli	334	36	33.0	527	2	US-08-659-939-4	Sequence 4, Appli
262	36	33.0	42	4	US-08-470-896-121	Sequence 121, App	335	36	33.0	527	2	US-08-850-041-4	Sequence 4, Appli
263	36	33.0	42	4	US-08-485-546A-121	Sequence 121, App	336	36	33.0	527	3	US-08-896-500-4	Sequence 4, Appli
264	36	33.0	42	4	US-08-474-784-17	Sequence 17, Appli	337	36	33.0	527	3	US-08-476-397-4	Sequence 4, Appli
265	36	33.0	42	4	US-09-515-965A-17	Sequence 17, Appli	338	36	33.0	527	3	US-08-973-720-4	Sequence 4, Appli
266	36	33.0	42	4	US-09-350-641C-17	Sequence 17, Appli	339	36	33.0	527	3	US-08-923-558-2	Sequence 2, Appli
267	36	33.0	42	4	US-09-350-841A-17	Sequence 17, Appli	340	36	33.0	527	3	US-09-262-927-4	Sequence 4, Appli
268	36	33.0	42	4	US-08-487-266A-121	Sequence 121, App	341	36	33.0	527	3	US-09-486-553-2	Sequence 2, Appli
269	36	33.0	48	3	US-08-486-099-16	Sequence 16, Appli	342	36	33.0	527	4	US-09-570-383-4	Sequence 4, Appli
270	36	33.0	48	3	US-08-360-107A-16	Sequence 16, Appli	343	36	33.0	527	4	US-09-395-336-4	Sequence 4, Appli
271	36	33.0	48	3	US-08-484-223B-16	Sequence 16, Appli	344	36	33.0	534	4	US-09-252-991A-32086	Sequence 32086, A
272	36	33.0	48	3	US-08-919-597-16	Sequence 16, Appli	345	36	33.0	569	1	US-08-306-231-3	Sequence 3, Appli
273	36	33.0	48	3	US-08-475-668A-16	Sequence 16, Appli	346	36	33.0	574	6	5223254-2	Patent No. 5223254
274	36	33.0	48	3	US-08-485-551A-16	Sequence 16, Appli	347	36	33.0	574	6	5223254-2	Patent No. 5223254
275	36	33.0	48	3	US-08-471-913A-16	Sequence 16, Appli	348	36	33.0	592	4	US-09-919-039-141	Sequence 141, App
276	36	33.0	48	3	US-08-485-264A-16	Sequence 16, Appli	349	36	33.0	594	2	US-08-659-939-2	Sequence 2, Appli
277	36	33.0	48	3	US-08-474-349A-16	Sequence 16, Appli	350	36	33.0	594	2	US-08-850-041-2	Sequence 2, Appli
278	36	33.0	48	4	US-08-255-208A-33	Sequence 33, Appli	351	36	33.0	594	2	US-08-467-963C-6	Sequence 6, Appli
279	36	33.0	48	4	US-08-470-896-16	Sequence 16, Appli	352	36	33.0	594	2	US-08-838-189D-6	Sequence 6, Appli
280	36	33.0	48	4	US-08-485-546A-16	Sequence 16, Appli	353	36	33.0	594	3	US-08-852-344D-6	Sequence 6, Appli
281	36	33.0	48	4	US-08-487-266A-16	Sequence 16, Appli	354	36	33.0	594	3	US-08-896-500-2	Sequence 2, Appli
282	36	33.0	50	4	US-08-255-208A-16	Sequence 16, Appli	355	36	33.0	594	3	US-08-476-397-2	Sequence 2, Appli
283	36	33.0	127	3	US-08-346-026-4	Sequence 4, Appli	356	36	33.0	594	3	US-08-973-720-2	Sequence 2, Appli
284	36	33.0	141	4	US-09-732-210-1657	Sequence 1657, App	357	36	33.0	594	3	US-08-344-639E-6	Sequence 6, Appli
285	36	33.0	142	4	US-09-732-210-519	Sequence 519, App	358	36	33.0	594	3	US-09-262-927-2	Sequence 2, Appli
286	36	33.0	159	4	US-09-248-796A-19824	Sequence 19824, A	359	36	33.0	594	3	US-08-467-969A-6	Sequence 6, Appli
287	36	33.0	167	4	US-09-270-767-45525	Sequence 45525, A	360	36	33.0	594	3	US-08-467-961A-6	Sequence 6, Appli
288	36	33.0	171	4	US-09-248-796A-19456	Sequence 19456, A	361	36	33.0	594	3	US-08-001-554A-6	Sequence 6, Appli
289	36	33.0	180	4	US-09-302-540-13416	Sequence 13416, A	362	36	33.0	594	4	US-09-570-383-2	Sequence 2, Appli
290	36	33.0	235	3	US-09-029-785-1	Sequence 1, Appli	363	36	33.0	594	4	US-09-395-336-2	Sequence 2, Appli
291	36	33.0	235	4	US-08-382-430-3	Sequence 3, Appli	364	36	33.0	632	4	US-09-949-016-8152	Sequence 8152, Ap
292	36	33.0	241	1	US-08-330-978-4	Sequence 4, Appli	365	36	33.0	637	4	US-09-949-016-8152	Sequence 10668, A
293	36	33.0	241	1	US-08-474-042-4	Sequence 4, Appli	366	36	33.0	643	4	US-09-538-092-844	Sequence 844, App
294	36	33.0	241	1	US-08-484-558-4	Sequence 4, Appli	367	36	33.0	651	4	US-09-248-796A-18743	Sequence 18743, A
295	36	33.0	241	1	US-08-774-592-4	Sequence 4, Appli	368	36	33.0	668	4	US-09-270-767-41490	Sequence 41490, A
296	36	33.0	247	3	US-08-944-483-49	Sequence 49, Appli	369	36	33.0	681	6	5194595-19	Patent No. 5194595
297	36	33.0	252	4	US-09-248-796A-18740	Sequence 18740, A	370	36	33.0	681	6	5194595-19	Patent No. 5194595
298	36	33.0	254	1	US-08-330-978-3	Sequence 3, Appli	371	36	33.0	749	4	US-09-562-737-95	Sequence 95, Appli
299	36	33.0	254	1	US-08-474-042-3	Sequence 3, Appli	372	36	33.0	783	4	US-08-780-562-7	Sequence 7, Appli
300	36	33.0	254	1	US-08-484-558-3	Sequence 3, Appli	373	36	33.0	804	4	US-09-116-676-10	Sequence 10, Appli
301	36	33.0	254	1	US-08-774-592-3	Sequence 3, Appli	374	36	33.0	819	4	US-09-949-016-11044	Sequence 11044, A
302	36	33.0	272	1	US-08-282-951-6	Sequence 6, Appli	375	36	33.0	837	4	US-09-949-016-6515	Sequence 6515, Ap
303	36	33.0	280	4	US-09-601-478-5	Sequence 5, Appli	376	36	33.0	883	4	US-08-982-430-1	Sequence 1, Appli
304	36	33.0	280	4	US-09-601-478-8	Sequence 8, Appli	377	36	33.0	894	2	US-08-599-455B-2	Sequence 2, Appli
305	36	33.0	280	4	US-09-442-013-13	Sequence 13, Appli	378	36	33.0	894	3	US-09-069-781B-2	Sequence 2, Appli
306	36	33.0	280	4	US-09-513-365A-1	Sequence 1, Appli	379	36	33.0	894	3	US-08-618-957A-12	Sequence 12, Appli
307	36	33.0	280	4	US-09-513-365A-6	Sequence 6, Appli	380	36	33.0	894	3	US-09-137-132-2	Sequence 2, Appli
308	36	33.0	306	1	US-08-330-978-1	Sequence 1, Appli	381	36	33.0	894	3	US-08-864-564A-2	Sequence 2, Appli
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310	36	33.0	306	1	US-08-484-558-1	Sequence 1, Appli	383	36	33.0	894	4	US-08-708-123D-2	Sequence 2, Appli
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313	36	33.0	320	4	US-09-252-991A-21360	Sequence 21360, A	386	36	33.0	894	4	US-08-638-524B-2	Sequence 2, Appli
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315	36	33.0	326	4	US-09-543-681A-4563	Sequence 4563, Ap	388	36	33.0	895	3	US-08-827-962-19	Sequence 19, Appli
316	36	33.0	349	4	US-09-502-540-13240	Sequence 13240, A	389	36	33.0	895	3	US-08-827-962-21	Sequence 21, Appli
317	36	33.0	359	4	US-09-572-758A-2	Sequence 2, Appli	390	36	33.0	896	2	US-08-640-389A-10	Sequence 10, Appli
318	36	33.0	362	4	US-09-252-991A-24409	Sequence 24409, A	391	36	33.0	896	2	US-08-640-389A-10	Sequence 10, Appli
319	36	33.0	367	4	US-09-252-991A-28477	Sequence 28477, A	392	36	33.0	896	3	US-08-618-957A-12	Sequence 12, Appli

393	36	33.0	896	4	US-09-357-914-33	Sequence 33, Appl	466	35	32.1	132	4	US-09-732-210-1658	Sequence 1658, Ap
394	36	33.0	896	4	US-08-780-562-3	Sequence 3, Appli	467	35	32.1	142	4	US-09-270-767-37079	Sequence 37079, A
395	36	33.0	896	4	US-10-095-929-10	Sequence 10, Appl	468	35	32.1	142	4	US-09-270-767-52296	Sequence 52296, A
396	36	33.0	898	2	US-08-693-697-36	Sequence 36, Appl	469	35	32.1	143	4	US-09-152-060-107	Sequence 107, App
397	36	33.0	898	4	US-08-588-189-3	Sequence 3, Appli	470	35	32.1	145	4	US-09-270-767-39255	Sequence 39255, A
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400	36	33.0	906	4	US-09-357-914-32	Sequence 32, Appl	473	35	32.1	159	4	US-09-713-273A-6	Sequence 6, Appli
401	36	33.0	906	4	US-10-095-929-9	Sequence 9, Appli	474	35	32.1	168	4	US-09-270-767-37245	Sequence 37245, A
402	36	33.0	908	2	US-08-693-697-33	Sequence 33, Appl	475	35	32.1	168	4	US-09-270-767-52462	Sequence 52462, A
403	36	33.0	908	2	US-08-588-526-3	Sequence 3, Appli	476	35	32.1	172	4	US-09-252-991A-22192	Sequence 22192, A
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406	36	33.0	958	2	US-08-640-389A-8	Sequence 8, Appli	479	35	32.1	188	4	US-09-583-110-3036	Sequence 3036, Ap
407	36	33.0	958	4	US-08-618-957A-8	Sequence 8, Appli	480	35	32.1	194	4	US-09-107-433-2363	Sequence 2363, Ap
408	36	33.0	958	4	US-10-095-929-8	Sequence 8, Appli	481	35	32.1	214	2	US-08-846-790A-1	Sequence 1, Appli
409	36	33.0	960	1	US-08-355-888A-8	Sequence 8, Appli	482	35	32.1	214	3	US-08-935-333-1	Sequence 1, Appli
410	36	33.0	960	2	US-08-588-190-3	Sequence 3, Appli	483	35	32.1	229	4	US-09-252-991A-22195	Sequence 22195, A
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412	36	33.0	960	2	US-08-640-389A-3	Sequence 3, Appli	485	35	32.1	260	2	US-09-193-877-3	Sequence 3, Appli
413	36	33.0	960	3	US-08-693-696-8	Sequence 8, Appli	486	35	32.1	281	3	US-08-808-148-4	Sequence 4, Appli
414	36	33.0	960	3	US-08-618-957A-3	Sequence 3, Appli	487	35	32.1	281	3	US-09-583-110-3563	Sequence 3563, Ap
415	36	33.0	960	4	US-09-357-914-8	Sequence 8, Appli	488	35	32.1	292	4	US-09-107-433-4868	Sequence 4868, Ap
416	36	33.0	960	4	US-10-095-929-3	Sequence 3, Appli	489	35	32.1	293	4	US-09-248-796A-18514	Sequence 18514, A
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418	36	33.0	1162	3	US-08-827-962-15	Sequence 15, Appl	491	35	32.1	303	4	US-09-248-796A-16452	Sequence 16452, A
419	36	33.0	1162	3	US-08-827-962-20	Sequence 20, Appl	492	35	32.1	334	3	US-09-267-031-2	Sequence 2, Appli
420	36	33.0	1162	3	US-08-803-346-1	Sequence 1, Appli	493	35	32.1	337	2	US-08-861-464-12	Sequence 12, Appl
421	36	33.0	1162	3	US-09-069-781B-43	Sequence 43, Appl	494	35	32.1	337	2	US-08-396-001-12	Sequence 12, Appl
422	36	33.0	1162	3	US-09-137-132-43	Sequence 43, Appl	495	35	32.1	337	3	US-09-323-433A-12	Sequence 12, Appl
423	36	33.0	1162	3	US-08-864-564A-43	Sequence 43, Appl	496	35	32.1	337	4	US-09-826-752-12	Sequence 12, Appl
424	36	33.0	1162	4	US-09-410-410-43	Sequence 43, Appl	497	35	32.1	358	4	US-09-107-433-3157	Sequence 3157, Ap
425	36	33.0	1162	4	US-08-708-123D-43	Sequence 43, Appl	498	35	32.1	365	1	US-08-447-500-4	Sequence 4, Appli
426	36	33.0	1162	4	US-08-638-524B-43	Sequence 43, Appl	499	35	32.1	365	1	US-08-453-866-4	Sequence 4, Appli
427	36	33.0	1165	2	US-08-640-389A-11	Sequence 11, Appl	500	35	32.1	365	1	US-08-453-866-4	Sequence 4, Appli
428	36	33.0	1165	2	US-08-599-455B-4	Sequence 4, Appli							
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443	36	33.0	5179	4	US-09-538-092-1258	Sequence 1258, Ap							
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445	35.5	32.6	162	3	US-09-199-637A-162	Sequence 162, App							
446	35.5	32.6	175	4	US-09-949-016-10743	Sequence 10743, A							
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449	35.5	32.6	269	4	US-09-949-016-6121	Sequence 6121, Ap							
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454	35.5	32.6	573	4	US-09-949-016-10415	Sequence 10415, A							
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457	35	32.1	93	2	US-08-479-078-11	Sequence 11, Appl							
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460	35	32.1	99	1	US-08-473-981A-12	Sequence 12, Appl							
461	35	32.1	99	2	US-08-474-087-12	Sequence 12, Appl							
462	35	32.1	100	4	US-09-621-976-4269	Sequence 4269, Ap							
463	35	32.1	118	4	US-09-489-039A-7782	Sequence 7782, Ap							
464	35	32.1	130	4	US-09-732-210-1645	Sequence 1645, Ap							
465	35	32.1	132	4	US-09-732-210-1655	Sequence 1655, Ap							

US-09-360-376-55

US-09-360-376-55

Sequence 55, Application US/09360376

Patent No. 6495739

GENERAL INFORMATION:

APPLICANT: Lasener, Michael

APPLICANT: Ruesinsky, Diane

TITLE OF INVENTION: PLANT PHOSPHATIDIC ACID PHOSPHATASES

FILE REFERENCE: 17026/01/US

CURRENT APPLICATION NUMBER: US/09/360,376

CURRENT FILING DATE: 1999-07-23

PRIOR APPLICATION NUMBER: US 09/122,315

PRIOR FILING DATE: 1998-07-24

NUMBER OF SEQ ID NOS: 55

SOFTWARE: PatentIn version 3.0

SEQ ID NO 55

LENGTH: 233

TYPE: PRT

ORGANISM: Homo sapiens

US-09-360-376-55

Query Match 100.0%; Score 109; DB 4; Length 233;

Best Local Similarity 100.0%; Pred. No. 1.5e-09;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGYIONVRCRGDSDSKVQEAR 20

Db 173 EGYIONVRCRGDSDSKVQEAR 192

RESULT 2

US-09-360-376-54

Sequence 54, Application US/09360376

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; Patent No. 6495739
; GENERAL INFORMATION:
; APPLICANT: Lassner, Michael
; APPLICANT: Ruezinsky, Diane
; TITLE OF INVENTION: PLANT PHOSPHATIDIC ACID PHOSPHATASES
; FILE REFERENCE: 17026/01/US
; CURRENT APPLICATION NUMBER: US/09/360,376
; CURRENT FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: US 09/122,315
; PRIOR FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 54
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-360-376-54

Query Match 60.6%; Score 66; DB 4; Length 282;
Best Local Similarity 50.0%; Pred. No. 0.012;
Matches 10; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 EGYIQRRCRGDDSKVQEAR 20
   :|||:|:|:|:|:|:|:|:|
Db 145 DGYIENFVCGNEQKVEGR 164

RESULT 3
US-08-992-035A-3
; Sequence 3, Application US/08992035A
; Patent No. 6242179
; GENERAL INFORMATION:
; APPLICANT: Shah, Purvi
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: HUMAN PHOSPHATASES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/992,035A
; FILING DATE: December 17, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0433 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 283 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 1487873
US-08-992-035A-3
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Query Match 59.6%; Score 65; DB 3; Length 283;
Best Local Similarity 50.0%; Pred. No. 0.017;
Matches 10; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 EGYIQRRCRGDDSKVQEAR 20
   :|||:|:|:|:|:|:|:|:|
Db 145 DGYIEDYICQNEEKVKEGR 164

RESULT 4
US-09-360-376-53
; Sequence 53, Application US/09360376
; Patent No. 6495739
; GENERAL INFORMATION:
; APPLICANT: Lassner, Michael
; APPLICANT: Ruezinsky, Diane
; TITLE OF INVENTION: PLANT PHOSPHATIDIC ACID PHOSPHATASES
; FILE REFERENCE: 17026/01/US
; CURRENT APPLICATION NUMBER: US/09/360,376
; CURRENT FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: US 09/122,315
; PRIOR FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 53
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-360-376-53

Query Match 59.6%; Score 65; DB 4; Length 283;
Best Local Similarity 50.0%; Pred. No. 0.017;
Matches 10; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 EGYIQRRCRGDDSKVQEAR 20
   :|||:|:|:|:|:|:|:|:|
Db 145 DGYIEDYICQNEEKVKEGR 164

RESULT 5
US-08-992-035A-1
; Sequence 1, Application US/08992035A
; Patent No. 6242179
; GENERAL INFORMATION:
; APPLICANT: Shah, Purvi
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: HUMAN PHOSPHATASES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/992,035A
; FILING DATE: December 17, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0433 US
```

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BLADNOT06
CLONE: 1719418
US-08-992-035A-1

Query Match 54.1%; Score 59; DB 3; Length 285;
Best Local Similarity 50.0%; Pred. No. 0.16;
Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EGYQNYRCRGDDSKVQEAR 20
146 DGVEYYICRGNAERVKEGR 165

RESULT 6

US-08-311-731A-4
Sequence 4, Application US/08311731A
Patent No. 6583266
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:

CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 705 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: MYCOBACTERIUM TUBERCULOSIS
US-08-311-731A-4

Query Match 42.7%; Score 46.5; DB 4; Length 705;
Best Local Similarity 50.0%; Pred. No. 40;
Matches 8; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 EGYQNYRCRGDDSKV 16

DB 378 DGMV-TYRCRADDTGV 392
:|:: |||| |::|

RESULT 7

US-09-949-016-8237
Sequence 8237, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8237
LENGTH: 416
TYPE: PRT
ORGANISM: Human
US-09-949-016-8237

Query Match 40.4%; Score 44; DB 4; Length 416;
Best Local Similarity 53.8%; Pred. No. 56;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 YIQNYRCRGDDSK 15
|:|::| |::|

DB 397 YLYNWRCPGTDSE 409

RESULT 8

US-09-786-240-1
Sequence 1, Application US/09786240
Patent No. 6558935
GENERAL INFORMATION:
APPLICANT: INCYTE PHARMACEUTICALS, INC.
APPLICANT: TANG, Y. Tom
APPLICANT: CORLEY, Neil C.
APPLICANT: GUEGLER, Karl J.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: LAL, Preeti
APPLICANT: YUE, Henry
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: AZIMZAI, Yalda
TITLE OF INVENTION: HUMAN TRANSFERASE PROTEINS
FILE REFERENCE: PF-0592 PCT
CURRENT APPLICATION NUMBER: US/09/786,240
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 09/150,657; unassigned; 09/186,779; unassigned; 60/133,642
PRIOR FILING DATE: 1998-09-10; 1998-09-10; 1998-11-04; 1998-11-04; 1999-05-11
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PERL Program
SEQ ID NO 1
LENGTH: 498
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. 6558935 1632930CDI
US-09-786-240-1

Query Match 40.4%; Score 44; DB 4; Length 498;
Best Local Similarity 53.8%; Pred. No. 68;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;


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; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,734
; FILING DATE: 29-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 201 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-09-015-734-12

Query Match 37.6%; Score 41; DB 3; Length 201;
Best Local Similarity 53.8%; Pred. No. 78;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 7 YRCRGDDSKVQEA 19
Db 91 YRCRNDNLSEA 103

RESULT 14
US-09-015-311-12
; Sequence 12, Application US/09515311
; Patent No. 6582701
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL EQUINE FC EPSILON RECEPTOR ALPHA
; TITLE OF INVENTION: CHAIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,734
; FILING DATE: 29-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-09-015-734-7

Query Match 37.6%; Score 41; DB 3; Length 236;
Best Local Similarity 53.8%; Pred. No. 92;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 7 YRCRGDDSKVQEA 19
Db 72 YRCRNDNLSEA 84

RESULT 16
US-09-515-311-7
; Sequence 7, Application US/09515311
; Patent No. 6582701
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
```


;; TITLE OF INVENTION: NOVEL EQUINE FC EPSILON RECEPTOR ALPHA
;; TITLE OF INVENTION: CHAIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Heska Corporation
;; STREET: 1825 Sharp Point Drive
;; CITY: Fort Collins
;; STATE: Colorado
;; COUNTRY: USA
;; ZIP: 80525
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WordPerfect for Windows, Version 7.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/515,311
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/015,734
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Verser, Carol Talkington
;; REGISTRATION NUMBER: 37,459
;; REFERENCE/DOCKET NUMBER: DI-4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 970/493-7272
;; TELEFAX: 970/484-9505
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 236 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: Protein
US-09-515-311-7
Query Match 37.6%; Score 41; DB 4; Length 236;
Best Local Similarity 53.8%; Pred. No. 92;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 7 YRCRGDDSKVQEA 19
Db 72 YRCRNDLNLSEA 84
RESULT 17
US-09-015-734-2
; Sequence 2, Application US/09015734
; Patent No. 6057127
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL EQUINE FC EPSILON RECEPTOR ALPHA
; TITLE OF INVENTION: CHAIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,734
; FILING DATE: 29-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

;; NAME: Verser, Carol Talkington
;; REGISTRATION NUMBER: 37,459
;; REFERENCE/DOCKET NUMBER: DI-4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 970/493-7272
;; TELEFAX: 970/484-9505
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 255 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: Protein
US-09-015-734-2
Query Match 37.6%; Score 41; DB 3; Length 255;
Best Local Similarity 53.8%; Pred. No. 1e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 7 YRCRGDDSKVQEA 19
Db 91 YRCRNDLNLSEA 103
RESULT 18
US-09-515-311-2
; Sequence 2, Application US/09515311
; Patent No. 6582701
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL EQUINE FC EPSILON RECEPTOR ALPHA
; TITLE OF INVENTION: CHAIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/515,311
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/015,734
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-09-515-311-2
Query Match 37.6%; Score 41; DB 4; Length 255;
Best Local Similarity 53.8%; Pred. No. 1e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 7 YRCRGDDSKVQEA 19

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Db 91 YRCRNDLNLSEA 103

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/489039A
; PATENT NO. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13748
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13748

Query Match 37.6%; Score 41; DB 4; Length 272;
Best Local Similarity 50.0%; Pred. NO. 1.1e+02;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 6 NYRCRGDDSKVQEA 19
| | | | | | | | | |
Db 210 NVRFKGDAAKKA 223

RESULT 20
US-09-506-286B-92
; Sequence 92, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; CURRENT FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-09-506-286B-92

Query Match 37.6%; Score 41; DB 4; Length 396;
Best Local Similarity 38.9%; Pred. NO. 1.6e+02;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 YIQNYRCRGDDSKVQEAR 20
| | | | | | | | | |
Db 194 YRYTYRCQRGDTQIQTRR 211

RESULT 21
US-09-506-286B-95
; Sequence 95, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/09/506,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 95
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-09-506-286B-95

Query Match 37.6%; Score 41; DB 4; Length 396;
Best Local Similarity 38.9%; Pred. NO. 1.6e+02;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 YIQNYRCRGDDSKVQEAR 20
| | | | | | | | | |
Db 194 YRYTYRCQRGDTQIQTRR 211

RESULT 22
US-10-065-133A-92
; Sequence 92, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-92

Query Match 37.6%; Score 41; DB 4; Length 396;
Best Local Similarity 38.9%; Pred. NO. 1.6e+02;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 YIQNYRCRGDDSKVQEAR 20
| | | | | | | | | |
Db 194 YRYTYRCQRGDTQIQTRR 211

RESULT 23
US-10-065-133A-95
; Sequence 95, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 95
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-95

Query Match 37.6%; Score 41; DB 4; Length 396;
Best Local Similarity 38.9%; Pred. NO. 1.6e+02;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
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; NAME/KEY: misc feature
; LOCATION: (707)..(707)
; OTHER INFORMATION: The 'Xaa' at location 707 stands for Arg, or Lys.
US-10-065-133A-107

Query Match      37.6%; Score 41; DB 4; Length 757;
Best Local Similarity 38.9%; Pred. NO. 3.2e+02;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 YIQNYRCRGDDSKVQEAR 20
      | |||: |||: |
      555 YRYTYRCQGDYQIOTFR 572

Db

RESULT 26
US-09-902-540-13372
; Sequence 13372, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(13849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13372
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13372

Query Match      37.2%; Score 40.5; DB 4; Length 145;
Best Local Similarity 52.6%; Pred. NO. 66;
Matches 10; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 2 GYIQNYRCRGDDSKVQEAR 20
      | |||: |||: |
      45 GSIQTWR-NSDEEKVQEMR 62

Db

RESULT 27
US-09-252-991A-20336
; Sequence 20336, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20336
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20336

Query Match      37.2%; Score 40.5; DB 4; Length 314;
Best Local Similarity 42.9%; Pred. NO. 1.5e+02;
Matches 9; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 EGYIQNYRC-RGDDSKVQEAR 20
      :|||: |
      :|||: |||: |

```

```
Db 172 DGYVTNLNVHRGDYARVGEAK 192

RESULT 28
US-09-198-452A-1290
; Sequence 1290, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1290
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1290

Query Match 36.7%; Score 40; DB 4; Length 94;
Best Local Similarity 63.6%; Pred. No. 50;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GYQNYRCRGD 12
Db 9 GYRNRRCRGD 19

RESULT 29
US-09-134-001C-5278
; Sequence 5278, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5278
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5278

Query Match 36.7%; Score 40; DB 3; Length 256;
Best Local Similarity 47.1%; Pred. No. 1.4e+02;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 GYQNYRCRGD 18
Db 87 GYQTRKRKDRGRLE 103

RESULT 30
US-09-506-286B-86
; Sequence 86, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; CURRENT FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 86
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-09-506-286B-86

Query Match 36.7%; Score 40; DB 4; Length 396;
Best Local Similarity 38.9%; Pred. No. 2.3e+02;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 3 YIQNYRCRGD 20
Db 194 YRYTYRCHRGDTQITRR 211

RESULT 31
US-09-506-286B-89
; Sequence 89, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; CURRENT FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-09-506-286B-89

Query Match 36.7%; Score 40; DB 4; Length 396;
Best Local Similarity 38.9%; Pred. No. 2.3e+02;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 3 YIQNYRCRGD 20
Db 194 YRYTYRCHRGDTQITRR 211

RESULT 32
US-10-065-133A-86
; Sequence 86, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86
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; CURRENT FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-09-506-286B-86

Query Match 36.7%; Score 40; DB 4; Length 396;
Best Local Similarity 38.9%; Pred. No. 2.3e+02;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 3 YIQNYRCRGD 20
Db 194 YRYTYRCHRGDTQITRR 211

RESULT 31
US-09-506-286B-89
; Sequence 89, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; CURRENT FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-09-506-286B-89

Query Match 36.7%; Score 40; DB 4; Length 396;
Best Local Similarity 38.9%; Pred. No. 2.3e+02;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 3 YIQNYRCRGD 20
Db 194 YRYTYRCHRGDTQITRR 211

RESULT 32
US-10-065-133A-86
; Sequence 86, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86
```

; LENGTH: 396
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-86

Query Match 36.7%; Score 40; DB 4; Length 396;
Best Local Similarity 38.9%; Pred. No. 2.3e+02;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 3 YIQNYRCRGDDSKVQBAR 20
| ||| |:::|
Db 194 YRYTYRCHRGDTQIQTR 211

RESULT 33

US-10-065-133A-89
; Sequence 89, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:

; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-89

Query Match 36.7%; Score 40; DB 4; Length 396;
Best Local Similarity 38.9%; Pred. No. 2.3e+02;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 3 YIQNYRCRGDDSKVQBAR 20
| ||| |:::|
Db 194 YRYTYRCHRGDTQIQTR 211

RESULT 34

US-09-489-039A-12030
; Sequence 12030, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12030
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12030

Query Match 36.7%; Score 40; DB 4; Length 424;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 YRCRGDD 13
: |||||
Db 63 FRCRGDD 69

RESULT 35

US-09-270-767-41177
; Sequence 41177, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homberger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41177
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41177

Query Match 36.7%; Score 40; DB 4; Length 501;
Best Local Similarity 60.0%; Pred. No. 3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 YRCRGDDSKV 16
|||: |||:
Db 485 YRCKGDSSLI 494

RESULT 36

US-09-270-767-56393
; Sequence 56393, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:

; APPLICANT: Homberger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56393
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-56393

Query Match 36.7%; Score 40; DB 4; Length 501;
Best Local Similarity 60.0%; Pred. No. 3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 YRCRGDDSKV 16
|||: |||:
Db 485 YRCKGDSSLI 494

RESULT 37

US-09-252-991A-19287
; Sequence 19287, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19287
; LENGTH: 710
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19287

Query Match 36.7%; Score 40; DB 4; Length 710;
Best Local Similarity 38.9%; Pred. No. 4.3e+02;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 EGYIYNYRCRGDDSKVQE 18
DB 523 QGIAQGHRRQGTDRRLQQ 540

RESULT 38

US-08-121-713D-58
; Sequence 58, Application US/08121713D
; Patent No. 5639856

; GENERAL INFORMATION:

; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy

; TITLE OF INVENTION: The Semaphorin Gene Family

; NUMBER OF SEQUENCES: 100

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 Bush Street, Suite 3200

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/121,713D

; FILING DATE: 13-SEP-1993

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Osman, Richard A.

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: B94-002-1

; TELEPHONE: (415)343-4341

; TELEFAX: (415) 343-4342

; TELEX:

; INFORMATION FOR SEQ ID NO: 58:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 730 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-121-713D-58

Query Match 36.7%; Score 40; DB 1; Length 730;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 GYIYNYRCRGDD 13

DB 648 GFLFSRRCRGED 659

RESULT 39

US-08-835-268-58

; Sequence 58, Application US/08835268

; Patent No. 5807826

; GENERAL INFORMATION:

; APPLICANT: Goodman, Corey S.

; APPLICANT: Kolodkin, Alex L.

; APPLICANT: Matthes, David

; APPLICANT: Bentley, David R.

; APPLICANT: O'Connor, Timothy

; TITLE OF INVENTION: The Semaphorin Gene Family

; NUMBER OF SEQUENCES: 100

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 Bush Street, Suite 3200

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/835,268

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/121,713

; FILING DATE: 13-SEP-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Osman, Richard A.

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: B94-002-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415)343-4341

; TELEFAX: (415) 343-4342

; TELEX:

; INFORMATION FOR SEQ ID NO: 58:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 730 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-835-268-58

Query Match 36.7%; Score 40; DB 1; Length 730;

Best Local Similarity 50.0%; Pred. No. 4.4e+02;

Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 GYIYNYRCRGDD 13

DB 648 GFLFSRRCRGED 659

RESULT 40

US-09-060-692-58

; Sequence 58, Application US/09060692

; Patent No. 5935865

; GENERAL INFORMATION:

; APPLICANT: Goodman, Corey S.

; APPLICANT: Kolodkin, Alex L.

; APPLICANT: Matthes, David

; APPLICANT: Bentley, David R.

; APPLICANT: O'Connor, Timothy

; TITLE OF INVENTION: The Semaphorin Gene Family

; NUMBER OF SEQUENCES: 100

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 Bush Street, Suite 3200

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94104

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,692
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 730 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-060-692-58

Query Match 36.7%; Score 40; DB 2; Length 730;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 GYIQNYRCRGDD 13
|:::|||||
Db 648 GFLFSRRCRGDD 659

RESULT 41
US-08-833-391-58
; Sequence 58, Application US/08833391
; Patent No. 6013781
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,391
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
```

```
;
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 730 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-833-391-58

Query Match 36.7%; Score 40; DB 3; Length 730;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 GYIQNYRCRGDD 13
|:::|||||
Db 648 GFLFSRRCRGDD 659

RESULT 42
US-09-060-610-58
; Sequence 58, Application US/09060610
; Patent No. 6344544
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,610
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/835,268
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 730 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-060-610-58

Query Match 36.7%; Score 40; DB 3; Length 730;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 GYIQNYRCRGDD 13
|:::|||||
```

Db 648 GFLFSRRCRGED 659

RESULT 43
PCT-US94-10151A-58
; Sequence 58, Application PC/TUS9410151A
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR HOBBACH TEST ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10151A
; FILING DATE: 13-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Oman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: FP-58750-PC/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299 FHT UR
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 730 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-10151A-58

Query Match 36.7%; Score 40; DB 5; Length 730;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 GYIQNYRCRGDD 13
|::: |||||
Db 648 GFLFSRRCRGED 659

RESULT 44
US-09-506-286B-104
; Sequence 104, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: The University of Pittsburgh, of the Commonwealth
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; CURRENT FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 757
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8

; FEATURE:
; OTHER INFORMATION: At amino acid location 489, Xaa = unknown
US-09-506-286B-104

Query Match 36.7%; Score 40; DB 4; Length 757;
Best Local Similarity 38.9%; Pred. No. 4.6e+02;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 3 YIQNYRCRGDDSKVQEAR 20
|::: |||||
Db 555 YRYTYRCHRGDTQIOTRR 572

RESULT 45
US-10-065-133A-104
; Sequence 104, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
; LENGTH: 757
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
; NAME/KEY: misc feature
; LOCATION: (489)..(489)
; OTHER INFORMATION: The 'Xaa' at location 489 stands for Thr or Ser
US-10-065-133A-104

Query Match 36.7%; Score 40; DB 4; Length 757;
Best Local Similarity 38.9%; Pred. No. 4.6e+02;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 3 YIQNYRCRGDDSKVQEAR 20
|::: |||||
Db 555 YRYTYRCHRGDTQIOTRR 572

RESULT 46
US-09-252-991A-30838
; Sequence 30838, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30838
; LENGTH: 980
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30838

Query Match 36.7%; Score 40; DB 4; Length 980;
Best Local Similarity 43.8%; Pred. No. 6.1e+02;

Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 5 QNYRCRGDDSKVQEAR 20
| | | | : |
Db 901 QRYCGRQGENSVHALR 916

RESULT 47

US-09-621-976-4220
; Sequence 4220, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4220
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -26..-1
US-09-621-976-4220

Query Match 36.2%; Score 39.5; DB 4; Length 99;
Best Local Similarity 69.2%; Pred. No. 63;
Matches 9; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 8 RCRGDDSKVQEAR 20
| | | | : |
Db 41 RCGGDD-KVKAR 52

RESULT 48

US-09-188-930-174
; Sequence 174, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 174
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Human
US-09-188-930-174

Query Match 36.2%; Score 39.5; DB 3; Length 137;
Best Local Similarity 69.2%; Pred. No. 89;
Matches 9; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 8 RCRGDDSKVQEAR 20
| | | | : |
Db 46 RCGGDD-KVKAR 57

RESULT 49

US-09-312-283C-174

; Sequence 174, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-174

Query Match 36.2%; Score 39.5; DB 4; Length 137;
Best Local Similarity 69.2%; Pred. No. 89;
Matches 9; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 8 RCRGDDSKVQEAR 20
| | | | : |
Db 46 RCGGDD-KVKAR 57

RESULT 50

US-09-673-395A-354
; Sequence 354, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12
; CURRENT APPLICATION NUMBER: US/09/673,395A
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 637
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 354
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-673-395A-354

Query Match 36.2%; Score 39.5; DB 4; Length 225;
Best Local Similarity 69.2%; Pred. No. 1.5e+02;
Matches 9; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 8 RCRGDDSKVQEAR 20
| | | | : |
Db 120 RCGGDD-KVKAR 131

Search completed: September 7, 2005, 19:58:02
Job time : 31.1163 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 7, 2005, 19:43:14 ; Search time 70.2326 Seconds
(without alignments)
145.824 Million cell updates/sec

Title: US-10-812-238B-2

Perfect score: 109

Sequence: 1 EGYIQNYRCRGDDSKVQEAR 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Uniprot_01.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	109	100.0	311	1 LPP3_HUMAN	O14495 h lipid pho
2	105	96.3	312	1 LPP3_MOUSE	Q99JY8 mus musculus
3	105	96.3	312	1 LPP3_RAT	P97544 rattus norv
4	105	96.3	312	2 Q6IMX4	Q6IMX4 rattus norv
5	74	67.9	307	2 Q68F34	Q68F34 xenopus lae
6	71	65.1	307	2 Q6AX87	Q6AX87 xenopus lae
7	70	64.2	167	2 Q95L84	Q95L84 oryctolagus
8	66	60.6	282	1 LPPI_RAT	O08564 rattus norv
9	66	60.6	282	2 Q6P766	Q6P766 rattus norv
10	65	59.6	283	1 LPPI_MOUSE	Q61469 mus musculus
11	62	56.9	285	1 LPPI_CAVPO	O88956 cavia porce
12	59	54.1	284	1 LPPI_HUMAN	O14494 homo sapien
13	53	48.6	284	2 Q6GF13	Q6GF13 xenopus lae
14	52	47.7	504	1 Y787_METJA	Q58197 methanococc
15	51	46.8	252	2 Q95ZL6	Q95ZL6 caenorhabdi
16	51	46.8	252	2 Q95ZL7	Q95ZL7 caenorhabdi
17	51	46.8	2736	2 Q7RTC3	Q7RTC3 plasmodium
18	50	45.9	276	1 LPP2_MOUSE	Q8dax2 mus musculus
19	50	45.9	276	1 LPP2_RAT	Q8k593 rattus norv
20	48	44.0	130	2 Q83ER2	Q83ER2 coxiella bu
21	48	44.0	217	2 Q7R7R7	Q7R7R7 plasmodium
22	48	44.0	269	2 Q7R8M3	Q7R8M3 plasmodium
23	48	44.0	283	2 Q6P897	Q6P897 xenopus tro
24	48	44.0	283	2 Q7PPD6	Q7PPD6 anopheles g
25	47	43.1	343	2 Q6FYZZ	Q6FYZZ bartonella
26	46.5	42.7	705	2 Q50468	Q50468 mycobacteri
27	46.5	42.7	705	2 P96283	P96283 mycobacteri
28	46.5	42.7	705	2 Q7TXK7	Q7TXK7 mycobacteri
29	46	42.2	130	2 Q6CZY4	Q6CZY4 erwinia car
30	46	42.2	340	2 Q7YU44	Q7YU44 drosophila
31	46	42.2	340	2 Q9VNT9	Q9VNT9 drosophila

32	46	42.2	776	2	Q73RY0	Q73RY0 mycobacteri
33	46	42.2	1325	2	Q95Z20	Q95Z20 caenorhabdi
34	45.5	41.7	179	2	Q20683	Q20683 caenorhabdi
35	45.5	41.7	1086	2	Q6XNK7	Q6XNK7 emericella
36	45	41.3	130	2	Q7MYG5	Q7MYG5 photorhabdu
37	45	41.3	300	2	Q7RA96	Q7RA96 plasmodium
38	45	41.3	304	2	Q7RCS6	Q7RCS6 plasmodium
39	45	41.3	314	2	Q7RS76	Q7RS76 plasmodium
40	45	41.3	344	2	Q9AEN7	Q9AEN7 rhizobium s
41	45	41.3	344	2	Q92KY2	Q92KY2 rhizobium s
42	45	41.3	505	2	Q96I80	Q96I80 homo sapien
43	45	41.3	607	2	P73606	P73606 synechocyst
44	45	41.3	875	1	NETR_HUMAN	P56730 homo sapien
45	44	40.4	63	2	Q9BS83	Q9BS83 homo sapien
46	44	40.4	121	2	Q9Q0W8	Q9Q0W8 methanosarc
47	44	40.4	172	2	Q897T4	Q897T4 clostridium
48	44	40.4	338	2	Q8SSM8	Q8SSM8 encephalito
49	44	40.4	385	1	DIAC_HUMAN	Q01459 homo sapien
50	44	40.4	485	2	Q8CFK1	Q8CFK1 mus musculu
51	44	40.4	498	1	NMT2_HUMAN	Q60551 homo sapien
52	44	40.4	529	1	NMT2_MOUSE	Q70311 mus musculu
53	44	40.4	529	2	Q700Q7	Q700Q7 rattus norv
54	44	40.4	918	2	Q6BOV5	Q6BOV5 debaryomyce
55	44	40.4	1193	2	Q7Z8L8	Q7Z8L8 cochliobolu
56	44	40.4	1907	2	Q96L96	Q96L96 homo sapien
57	43.5	39.9	339	2	Q90709	Q90709 cowpea aphl
58	43.5	39.9	476	2	Q6B8Q6	Q6B8Q6 gracilaria
59	43.5	39.9	635	2	Q8TUQ1	Q8TUQ1 methanosarc
60	43	39.4	37	2	Q8P0M2	Q8P0M2 streptococc
61	43	39.4	150	2	Q6TUT7	Q6TUT7 yaba monkey
62	43	39.4	151	2	Q8PRK4	Q8PRK4 xanthomonas
63	43	39.4	190	2	Q8K3W6	Q8K3W6 oryza sativ
64	43	39.4	206	2	Q8PKC5	Q8PKC5 xanthomonas
65	43	39.4	239	2	O44730	O44730 caenorhabdi
66	43	39.4	274	2	Q6AHQ6	Q6AHQ6 caenorhabdi
67	43	39.4	310	2	Q7RFC4	Q7RFC4 plasmodium
68	43	39.4	319	2	Q8UDV8	Q8UDV8 agrobacteri
69	43	39.4	341	1	YSX3_CAEBL	Q10022 caenorhabdi
70	43	39.4	342	2	Q6AHQ7	Q6AHQ7 caenorhabdi
71	43	39.4	356	2	Q919T1	Q919T1 influenza a
72	43	39.4	363	2	Q82BN3	Q82BN3 streptomyce
73	43	39.4	369	2	Q7CV30	Q7CV30 agrobacteri
74	43	39.4	371	2	Q6KNX8	Q6KNX8 arabidopsis
75	43	39.4	394	2	Q8EVB5	Q8EVB5 mycoplasma
76	43	39.4	403	2	Q6MQE4	Q6MQE4 bdellovibri
77	43	39.4	428	2	Q8TBF1	Q8TBF1 homo sapien
78	43	39.4	489	2	Q8N9B8	Q8N9B8 homo sapien
79	43	39.4	505	1	SMI1_YEAST	P32566 saccharomyc
80	43	39.4	542	1	HNA2_CUCSA	P49295 cucumis sat
81	43	39.4	565	2	Q8NY08	Q8NY08 staphylococ
82	43	39.4	565	2	Q99WC5	Q99WC5 staphylococ
83	43	39.4	565	2	Q7A7C7	Q7A7C7 staphylococ
84	43	39.4	565	2	Q6GC10	Q6GC10 staphylococ
85	43	39.4	565	2	Q6GJ15	Q6GJ15 staphylococ
86	43	39.4	605	2	Q8PZF0	Q8PZF0 methanosarc
87	43	39.4	639	2	Q7QUK1	Q7QUK1 giardia lam
88	43	39.4	750	2	Q26I88	Q26I88 plasmodium
89	43	39.4	850	2	Q7RIR5	Q7RIR5 plasmodium
90	43	39.4	1150	2	P79045	P79045 emericella
91	43	39.4	1315	2	O8I2E4	O8I2E4 plasmodium
92	43	39.4	1322	2	Q6UDM4	Q6UDM4 plasmodium
93	43	39.4	1324	2	Q6UDW2	Q6UDW2 plasmodium
94	43	39.4	1325	2	Q6LFQ7	Q6LFQ7 plasmodium
95	43	39.4	1327	2	Q9NFB4	Q9NFB4 plasmodium
96	43	39.4	1778	2	Q9BPP7	Q9BPP7 antheraea y
97	43	39.4	1778	2	Q9GUX5	Q9GUX5 antheraea p
98	43	39.4	2171	1	CCAC_RABIT	P15381 o voltage-d
99	42	38.5	73	2	Q7QPI9	Q7QPI9 giardia lam
100	42	38.5	127	2	Q7YDJ6	Q7YDJ6 ranunculus
101	42	38.5	130	1	RS8_YERPE	Q8Z198 yersinia pe
102	42	38.5	130	2	O664T5	O664T5 yersinia pe
103	42	38.5	137	2	Q8NAF9	Q8NAF9 homo sapien
104	42	38.5	182	1	YLP3_CAEBL	P34383 caenorhabdi

105	42	38.5	226	2	Q69XV4	Q69xv4 oryza sativ	178	41	37.6	752	1	RRP1_INBP9	O36430 influenza b
106	42	38.5	257	2	Q6GR33	Q6gr33 xenopus lae	179	41	37.6	752	2	Q68IP2	Q68ip2 influenza b
107	42	38.5	265	2	Q6KQ07	Q6kq07 dictyosteli	180	41	37.6	752	2	Q77SM9	Q77sm9 influenza b
108	42	38.5	274	2	Q6GN60	Q6gn60 xenopus lae	181	41	37.6	752	2	Q77SN0	Q77sn0 influenza b
109	42	38.5	305	2	Q9RDP5	Q9rdp5 streptomyce	182	41	37.6	752	2	Q77SN1	Q77sn1 influenza b
110	42	38.5	356	2	Q9N3M8	Q9n3m8 caenorhabdi	183	41	37.6	752	2	Q77SN2	Q77sn2 influenza b
111	42	38.5	362	2	Q8IIE3	Q8iie3 plasmodium	184	41	37.6	752	2	Q80DM8	Q80dm8 influenza b
112	42	38.5	375	2	Q96Y62	Q96y62 sulfolobus	185	41	37.6	752	2	Q80DN5	Q80dn5 influenza b
113	42	38.5	402	1	ISPG_SYNEL	Q8d70 synchococc	186	41	37.6	752	2	Q9IMP8	Q9imp8 influenza b
114	42	38.5	457	2	Q750A7	Q750a7 ashbya goss	187	41	37.6	752	2	Q9PWU1	Q9pwu1 influenza b
115	42	38.5	461	2	Q69XV5	Q69xv5 oryza sativ	188	41	37.6	752	2	Q9QLJ8	Q9qlj8 influenza b
116	42	38.5	513	2	Q9A731	Q9a731 caulobacter	189	41	37.6	752	2	Q9QLJ9	Q9qlj9 influenza b
117	42	38.5	535	2	Q6BUX0	Q6bux0 debaryomyce	190	41	37.6	752	2	Q9QLK0	Q9qlk0 influenza b
118	42	38.5	574	2	Q8QOC1	Q8qoc1 pseudomonas	191	41	37.6	752	2	Q9QLK1	Q9qlk1 influenza b
119	42	38.5	731	2	Q86557	Q86557 streptomyce	192	41	37.6	752	2	Q9QLK2	Q9qlk2 influenza b
120	42	38.5	776	2	Q785X4	Q785x4 neurospora	193	41	37.6	752	2	Q9QLK3	Q9qlk3 influenza b
121	42	38.5	787	2	Q96020	Q96u20 neurospora	194	41	37.6	752	2	Q9QLK4	Q9qlk4 influenza b
122	42	38.5	845	2	Q8WQJ3	Q8wqj3 plasmodium	195	41	37.6	752	2	Q9QLK5	Q9qlk5 influenza b
123	42	38.5	915	2	Q7UV66	Q7uv66 rhodospirell	196	41	37.6	752	2	Q9QLK6	Q9qlk6 influenza b
124	42	38.5	957	2	Q9K760	Q9k760 bacillus ha	197	41	37.6	752	2	Q9QLK7	Q9qlk7 influenza b
125	42	38.5	973	2	Q9NC89	Q9nc89 strongyloce	198	41	37.6	752	2	Q9QLK8	Q9qlk8 influenza b
126	42	38.5	1075	2	Q9NC90	Q9nc90 strongyloce	199	41	37.6	752	2	Q9QLK9	Q9qlk9 influenza b
127	42	38.5	1304	2	Q8WT63	Q8wt63 plasmodium	200	41	37.6	888	2	Q75AE3	Q75ae3 ashbya goss
128	42	38.5	1319	2	Q7SDE1	Q7sde1 neurospora	201	41	37.6	1233	1	RGY2_SULTO	Q975p6 sulfolobus
129	42	38.5	1450	2	Q8I5X9	Q8i5x9 plasmodium	202	41	37.6	1334	2	Q97322	Q97322 plasmodium
130	42	38.5	1919	2	Q8LRK9	Q8lrk9 arabidopsis	203	41	37.6	1969	2	Q69HL6	Q69hl6 ciona intes
131	42	38.5	1994	2	Q9LP19	Q9lp19 arabidopsis	204	40.5	37.2	205	2	Q6FZU4	Q6fzu4 bartonella
132	42	38.5	3115	2	Q9VQV1	Q9vqv1 drosophila	205	40.5	37.2	223	2	Q801A6	Q801a6 latimeria m
133	42	38.5	4280	2	Q9UB29	Q9ub29 caenorhabdi	206	40.5	37.2	247	2	Q7VN89	Q7vnn89 haemophilus
134	42	38.5	4450	2	Q9UB28	Q9ub28 caenorhabdi	207	40.5	37.2	252	2	Q9LIQ7	Q9llq7 streptomyce
135	42	38.5	19066	2	Q801W8	Q801w8 brachydanio	208	40.5	37.2	302	2	Q9HXC1	Q9hxc1 pseudomonas
136	41.5	38.1	108	2	Q6ESN2	Q6esn2 oryza sativ	209	40.5	37.2	431	2	Q56454	Q56454 paracoccus
137	41.5	38.1	325	2	Q9PP25	Q9pp25 campylobact	210	40.5	37.2	503	2	Q6FZW1	Q6fzw1 bartonella
138	41.5	38.1	341	2	Q72KA9	Q72ka9 thermus the	211	40.5	37.2	507	2	Q8YGW3	Q8ygw3 brucella me
139	41.5	38.1	470	2	Q66IF4	Q66if4 xenopus tro	212	40.5	37.2	507	2	Q8G100	Q8g100 brucella su
140	41	37.6	46	2	Q848W4	Q848w4 bacillus me	213	40.5	37.2	946	1	IHB_DROME	Q81643 drosophila
141	41	37.6	76	2	Q8S3A8	Q8s3a8 physcomitre	214	40.5	37.2	1679	2	Q81LA0	Q81la0 plasmodium
142	41	37.6	100	2	Q647D0	Q647d0 thermoprote	215	40.5	37.2	3164	2	Q813E6	Q813e6 plasmodium
143	41	37.6	129	2	Q74NG1	Q74ng1 nanoarchaeu	216	40	36.7	55	2	Q8S2X3	Q8s2x3 zea mays (m
144	41	37.6	129	2	Q6XYX4	Q6xyx4 spiropasma	217	40	36.7	56	2	Q8LNE9	Q8lne9 oryza sativ
145	41	37.6	130	1	RS8_BUCAI	P57577 buchnera ap	218	40	36.7	56	2	Q8RUB4	Q8rub4 zea mays (m
146	41	37.6	137	2	Q7S2B1	Q7s2b1 xenopus lae	219	40	36.7	67	2	Q82548	Q82548 influenza a
147	41	37.6	147	1	Y237_TROWT	P67323 tropheryma	220	40	36.7	78	2	Q82547	Q82547 influenza a
148	41	37.6	147	1	Y533_TROWB	P67324 tropheryma	221	40	36.7	79	2	Q6Z419	Q6z419 oryza sativ
149	41	37.6	154	2	Q8BUS2	Q8bus2 mus musculu	222	40	36.7	84	2	Q8H522	Q8h522 oryza sativ
150	41	37.6	158	2	Q72V51	Q72v51 xenopus lae	223	40	36.7	124	2	Q91TY9	Q91ty9 influenza a
151	41	37.6	160	1	RRAL_VIBPA	Q8rad2 vibrio para	224	40	36.7	129	2	Q91TZ1	Q91tz1 influenza a
152	41	37.6	164	2	Q7TV85	Q7tv85 prochloroco	225	40	36.7	130	1	RS8_BUCAP	P59030 buchnera ap
153	41	37.6	184	2	Q728K5	Q728k5 desulfovibr	226	40	36.7	131	2	Q7NQG6	Q7nqg6 chromobacte
154	41	37.6	191	2	Q9AY18	Q9ay18 funaria apo	227	40	36.7	131	2	Q7V7B7	Q7v7b7 bordetella
155	41	37.6	193	2	Q9AY16	Q9ay16 entosthodon	228	40	36.7	131	2	Q7W2E1	Q7w2e1 bordetella
156	41	37.6	238	2	Q74551	Q74551 schizosacch	229	40	36.7	131	2	Q7WRA9	Q7wra9 bordetella
157	41	37.6	255	2	Q8MI30	Q8mi30 equus cabal	230	40	36.7	131	2	Q7WRA9	Q7wra9 bordetella
158	41	37.6	255	2	Q8DTU7	Q8dtu7 streptococc	231	40	36.7	132	1	RS8_TREPA	Q82333 treponema p
159	41	37.6	281	1	DPHS_MOUSE	Q9cwq0 mus musculu	232	40	36.7	150	2	Q9KCP2	Q9kcp2 bacillus ha
160	41	37.6	281	2	Q6PAC5	Q6pac5 mus musculu	233	40	36.7	162	2	Q8HZN2	Q8hzn2 elephas max
161	41	37.6	288	2	Q81CQ3	Q81cq3 bacillus ce	234	40	36.7	162	2	O48953	O48953 arabidopsis
162	41	37.6	294	2	Q7RPL7	Q7rpl7 plasmodium	235	40	36.7	176	2	Q9HIV8	Q9hiv8 thermoplasma
163	41	37.6	308	2	Q6LRD5	Q6lrds photobacter	236	40	36.7	187	2	Q8HU07	Q8hu07 rhodobryum
164	41	37.6	312	2	Q6HI38	Q6hi38 bacillus th	237	40	36.7	188	2	Q6JKP4	Q6jkp4 influenza a
165	41	37.6	314	2	Q7RJ65	Q7rj65 plasmodium	238	40	36.7	188	2	Q6JKP5	Q6jkp5 influenza a
166	41	37.6	332	2	Q7QB96	Q7qb96 anopheles g	239	40	36.7	188	2	Q6JKP7	Q6jkp7 influenza a
167	41	37.6	373	2	Q6D5A6	Q6d5a6 erwinia car	240	40	36.7	191	2	Q6W760	Q6w760 influenza a
168	41	37.6	437	2	Q871H0	Q871h0 neurospora	241	40	36.7	191	2	Q6W761	Q6w761 influenza a
169	41	37.6	481	2	Q7S7L7	Q7s7l7 neurospora	242	40	36.7	191	2	Q8BCD5	Q8bcd5 influenza a
170	41	37.6	644	2	Q7RCW9	Q7rcw9 plasmodium	243	40	36.7	191	2	Q8BCD6	Q8bcd6 influenza a
171	41	37.6	721	2	Q9PA43	Q9pa43 xyella fas	244	40	36.7	191	2	Q8BCD7	Q8bcd7 influenza a
172	41	37.6	730	2	Q7SHT6	Q7sht6 neurospora	245	40	36.7	191	2	Q8BCD8	Q8bcd8 influenza a
173	41	37.6	739	2	Q9Q0S6	Q9q0s6 influenza a	246	40	36.7	191	2	Q8BCD9	Q8bcd9 influenza a
174	41	37.6	747	2	Q8QPM0	Q8qpm0 influenza b	247	40	36.7	191	2	Q8BCE0	Q8bce0 influenza a
175	41	37.6	752	1	RRP1_INBAC	P13871 influenza b	248	40	36.7	191	2	Q8BCE1	Q8bce1 influenza a
176	41	37.6	752	1	RRP1_INBAD	P13872 influenza b	249	40	36.7	191	2	Q8BCE2	Q8bce2 influenza a
177	41	37.6	752	1	RRP1_INBLE	P07832 influenza b	250	40	36.7	191	2	Q8BCE3	Q8bce3 influenza a

251	40	36.7	191	2	Q8BCE4	Q8bce4 influenza a	324	40	36.7	647	2	Q809M6	Q809m6 influenza a
252	40	36.7	213	2	Q89S17	Q89s17 brachyrihizob	325	40	36.7	647	2	Q809M7	Q809m7 influenza a
253	40	36.7	252	2	Q04455	Q04455 pseudomonas	326	40	36.7	660	2	Q71FW4	Q71fw4 influenza a
254	40	36.7	256	2	Q8BC95	Q8bc95 influenza a	327	40	36.7	683	2	Q6DNU0	Q6dnu0 influenza a
255	40	36.7	280	2	Q98KM9	Q98km9 rhizobium l	328	40	36.7	683	2	Q71FV9	Q71fv9 influenza a
256	40	36.7	283	2	Q7R7D1	Q7r7d1 plasmodium	329	40	36.7	689	2	Q71FW5	Q71fw5 influenza a
257	40	36.7	288	2	Q9DW23	Q9dw23 rat cytomeg	330	40	36.7	690	2	Q6DNS7	Q6dns7 influenza a
258	40	36.7	290	2	Q8X681	Q8x681 escherichia	331	40	36.7	692	2	Q82572	Q82572 influenza a
259	40	36.7	302	2	Q96OH4	Q96oh4 drosophila	332	40	36.7	696	2	Q71FW2	Q71fw2 influenza a
260	40	36.7	304	1	HEM3_XANCP	Q8p536 xanthomonas	333	40	36.7	696	2	Q778V2	Q778v2 influenza a
261	40	36.7	312	1	Q81PV8	Q81pv8 bacillus an	334	40	36.7	703	2	Q71FW0	Q71fw0 influenza a
262	40	36.7	315	1	MHPR_ECOLI	P77569 escherichia	335	40	36.7	704	2	Q67EK9	Q67ek9 influenza a
263	40	36.7	315	2	Q7AH54	Q7ah54 escherichia	336	40	36.7	706	2	Q6DNT6	Q6dnt6 influenza a
264	40	36.7	330	2	Q85ZW5	Q85zw5 mus musculus	337	40	36.7	713	2	Q67EK7	Q67ek7 influenza a
265	40	36.7	338	2	Q7R9R7	Q7r9r7 plasmodium	338	40	36.7	717	2	Q67EK8	Q67ek8 influenza a
266	40	36.7	362	2	Q61L91	Q61l91 drosophila	339	40	36.7	717	2	Q67EL4	Q67el4 influenza a
267	40	36.7	363	2	Q673E6	Q673e6 medicago tr	340	40	36.7	718	2	Q67EL5	Q67el5 influenza a
268	40	36.7	368	2	Q7RSM6	Q7rsw6 plasmodium	341	40	36.7	718	2	Q67EK0	Q67ek0 influenza a
269	40	36.7	381	2	Q8CL19	Q8cl19 rhizobium l	342	40	36.7	718	2	Q6DNS6	Q6dns6 influenza a
270	40	36.7	381	2	Q8QPH7	Q8qph7 influenza a	343	40	36.7	720	2	Q9PZF3	Q9pzf3 influenza a
271	40	36.7	382	2	Q9QOK4	Q9qok4 influenza a	344	40	36.7	721	2	Q6J850	Q6j850 influenza a
272	40	36.7	382	2	Q9QOK5	Q9qok5 influenza a	345	40	36.7	722	2	Q6DNS3	Q6dns3 influenza a
273	40	36.7	382	2	Q9QOK6	Q9qok6 influenza a	346	40	36.7	726	2	Q67EJ9	Q67ej9 influenza a
274	40	36.7	382	2	Q9QJC1	Q9qjc1 influenza a	347	40	36.7	726	2	Q67EK6	Q67ek6 influenza a
275	40	36.7	389	1	PNCB_ECO57	Q8xds8 escherichia	348	40	36.7	726	2	Q67EL3	Q67el3 influenza a
276	40	36.7	399	1	PNCB_ECOLI	P18133 escherichia	349	40	36.7	726	2	Q67EL5	Q67el5 influenza a
277	40	36.7	399	1	PNCB_SALTI	Q8z7y9 salmonella	350	40	36.7	727	2	Q6J848	Q6j848 influenza a
278	40	36.7	399	1	PNCB_SALTY	P22253 salmonella	351	40	36.7	728	2	Q71FW1	Q71fw1 influenza a
279	40	36.7	400	2	Q7UD27	Q7ud27 shigella fl	352	40	36.7	730	1	SMIA_SCHAM	Q26473 schistocerc
280	40	36.7	401	2	Q82N33	Q82n33 streptomyce	353	40	36.7	736	2	Q6J855	Q6j855 influenza a
281	40	36.7	416	2	Q83LN3	Q83ln3 shigella fl	354	40	36.7	736	2	Q9QOS2	Q9qos2 influenza a
282	40	36.7	416	2	Q8FJ98	Q8fj98 escherichia	355	40	36.7	738	2	Q9PY91	Q9py91 influenza a
283	40	36.7	422	1	PGLI_ARATH	P49062 arabidopsis	356	40	36.7	739	2	Q71FW6	Q71fw6 influenza a
284	40	36.7	422	1	Q9K426	Q9k426 streptomyce	357	40	36.7	739	2	Q9QOS5	Q9qos5 influenza a
285	40	36.7	430	2	Q67EK3	Q67ek3 influenza a	358	40	36.7	742	2	Q9PZH8	Q9pzh8 influenza a
286	40	36.7	430	2	Q67EK4	Q67ek4 influenza a	359	40	36.7	742	2	Q9PZH9	Q9pzh9 influenza a
287	40	36.7	430	2	Q67EK5	Q67ek5 influenza a	360	40	36.7	742	2	Q9PZ10	Q9pz10 influenza a
288	40	36.7	435	2	O16968	O16968 caenorhabdi	361	40	36.7	742	2	Q9PZ11	Q9pz11 influenza a
289	40	36.7	445	2	Q9GL39	Q9gl39 bos taurus	362	40	36.7	742	2	Q9PZ12	Q9pz12 influenza a
290	40	36.7	463	1	Q67EK1	Q67ek1 influenza a	363	40	36.7	742	2	Q9PZ13	Q9pz13 influenza a
291	40	36.7	465	1	HMA2_HORVU	Q96563 hordeum vul	364	40	36.7	742	2	Q9PZ15	Q9pz15 influenza a
292	40	36.7	466	2	Q67EK2	Q67ek2 influenza a	365	40	36.7	742	2	Q9PZN9	Q9pzn9 influenza a
293	40	36.7	470	2	Q67EL2	Q67el2 influenza a	366	40	36.7	742	2	Q9QOS7	Q9qos7 influenza a
294	40	36.7	471	1	YIRI_DROME	P16424 drosophila	367	40	36.7	744	2	Q71FW3	Q71fw3 influenza a
295	40	36.7	479	2	Q919V1	Q919v1 influenza a	368	40	36.7	744	2	Q9QOS4	Q9qos4 influenza a
296	40	36.7	479	2	Q919V2	Q919v2 influenza a	369	40	36.7	745	2	Q6W8X6	Q6w8x6 influenza a
297	40	36.7	479	2	Q919V3	Q919v3 influenza a	370	40	36.7	745	2	Q9QOS8	Q9qos8 influenza a
298	40	36.7	488	2	Q8XT25	Q8xt25 ralestonia s	371	40	36.7	745	2	Q9QOS3	Q9qos3 influenza a
299	40	36.7	482	2	Q8QPH6	Q8qph6 influenza a	372	40	36.7	746	2	Q8QPH8	Q8qph8 influenza a
300	40	36.7	496	2	Q8QPH5	Q8qph5 influenza a	373	40	36.7	746	2	Q9QOS9	Q9qos9 influenza a
301	40	36.7	497	2	Q75KY5	Q75ky5 oryza sativ	374	40	36.7	746	2	Q9QOS0	Q9qos0 influenza a
302	40	36.7	498	1	NMT2_BOVIN	Q9n181 bos taurus	375	40	36.7	746	2	Q9QOS1	Q9qos1 influenza a
303	40	36.7	508	2	Q8UV48	Q8uv48 influenza a	376	40	36.7	747	2	Q6DNT7	Q6dnt7 influenza a
304	40	36.7	525	2	Q6FS20	Q6fa20 candida gla	377	40	36.7	748	2	Q9QOS8	Q9qos8 influenza a
305	40	36.7	527	1	HMA1_HORVU	Q42843 hordeum vul	378	40	36.7	749	2	Q9QOS3	Q9qos3 influenza a
306	40	36.7	528	2	Q97379	Q97379 strongyloce	379	40	36.7	750	2	Q8UY47	Q8uy47 influenza a
307	40	36.7	530	1	HMA2_ARATH	P49294 arabidopsis	380	40	36.7	751	2	Q8QM22	Q8qm22 influenza a
308	40	36.7	536	1	HEM1_ORYSA	Q48674 oryza sativ	381	40	36.7	751	2	Q8QPH3	Q8qph3 influenza a
309	40	36.7	536	2	Q9FW00	Q9fw00 oryza sativ	382	40	36.7	751	2	Q8QPH4	Q8qph4 influenza a
310	40	36.7	537	2	Q9V7E0	Q9v7e0 drosophila	383	40	36.7	751	2	Q8QPH9	Q8qph9 influenza a
311	40	36.7	552	2	Q6ASM7	Q6asm7 propionibac	384	40	36.7	751	2	Q91CC5	Q91cc5 influenza a
312	40	36.7	577	1	YQ4B_CAEEL	Q17426 caenorhabdi	385	40	36.7	751	2	Q91CC6	Q91cc6 influenza a
313	40	36.7	586	2	Q62YB1	Q62yb1 bacillus li	386	40	36.7	751	2	Q71FW0	Q71fw0 influenza a
314	40	36.7	586	2	Q71FU9	Q71fu9 influenza a	387	40	36.7	752	2	Q8JN15	Q8jnl5 influenza a
315	40	36.7	587	1	HE_PARLI	P22757 paracentrot	388	40	36.7	752	2	Q71FW6	Q71fw6 influenza a
316	40	36.7	587	2	Q65MW8	Q65mw8 bacillus li	389	40	36.7	752	2	Q71FW8	Q71fw8 influenza a
317	40	36.7	588	2	Q70681	Q70681 sugarcane s	390	40	36.7	752	2	Q71FW3	Q71fw3 influenza a
318	40	36.7	619	2	Q6E1Y9	Q6e1y9 canis famil	391	40	36.7	755	2	Q8JT71	Q8jct71 influenza a
319	40	36.7	628	2	Q6DNS4	Q6dns4 influenza a	392	40	36.7	755	2	Q8QM32	Q8qm32 influenza a
320	40	36.7	628	2	Q6J845	Q6j845 influenza a	393	40	36.7	755	2	Q6DTW6	Q6dtw6 influenza a
321	40	36.7	633	2	Q8MLA8	Q8mla8 drosophila	394	40	36.7	755	2	Q6DXT4	Q6dxt4 influenza a
322	40	36.7	633	2	Q7PIA3	Q7pia3 chromobacte	395	40	36.7	756	2	Q8QM23	Q8qm23 influenza a
323	40	36.7	644	1	SYR_AERPE	Q9yb39 aeropyrum p	396	40	36.7	756	2	Q8QM25	Q8qm25 influenza a

397	Q8QM26	influenza a	470	36.7	757	2	Q6E3N5	Q6e3n5 influenza a			
398	Q8QM28	influenza a	471	40	36.7	757	2	Q6E3N6	Q6e3n6 influenza a		
399	Q91E77	influenza a	472	40	36.7	757	2	Q6E3N7	Q6e3n7 influenza a		
400	Q6DNO8	influenza a	473	40	36.7	757	2	Q6E3N8	Q6e3n8 influenza a		
401	Q6DNO8	influenza a	474	40	36.7	757	2	Q6E3N9	Q6e3n9 influenza a		
402	Q6DNT0	influenza a	475	40	36.7	757	2	Q6E3P1	Q6e3p1 influenza a		
403	Q6DNT1	influenza a	476	40	36.7	757	2	Q6E3P2	Q6e3p2 influenza a		
404	Q6DNT2	influenza a	477	40	36.7	757	2	Q6E3P3	Q6e3p3 influenza a		
405	Q6DNT3	influenza a	478	40	36.7	757	2	Q6E3P4	Q6e3p4 influenza a		
406	Q6DNT4	influenza a	479	40	36.7	757	2	Q6E3P5	Q6e3p5 influenza a		
407	Q6DNT5	influenza a	480	40	36.7	757	2	Q6E3P6	Q6e3p6 influenza a		
408	Q6DNT8	influenza a	481	40	36.7	757	2	Q6E3P7	Q6e3p7 influenza a		
409	Q6DNT9	influenza a	482	40	36.7	757	2	Q6E3P8	Q6e3p8 influenza a		
410	Q6DNU1	influenza a	483	40	36.7	757	2	Q6E3P9	Q6e3p9 influenza a		
411	Q6DNU2	influenza a	484	40	36.7	757	2	Q6E3Q0	Q6e3q0 influenza a		
412	Q6DNU3	influenza a	485	40	36.7	757	2	Q6E3Q2	Q6e3q2 influenza a		
413	Q6DNU9	influenza a	486	40	36.7	757	2	Q6E3Q3	Q6e3q3 influenza a		
414	Q6DNU0	influenza a	487	40	36.7	757	2	Q6E3Q4	Q6e3q4 influenza a		
415	Q6DNUV1	influenza a	488	40	36.7	757	2	Q6E3Q5	Q6e3q5 influenza a		
416	1	RRP1_IABEI	P21426	influenza a	489	40	36.7	757	2	Q61WJ3	Q61wj3 influenza a
417	1	RRP1_IABEI	P16502	influenza a	490	40	36.7	757	2	Q6J0Q4	Q6j0q4 influenza a
418	1	RRP1_IABOM	Q82571	influenza a	491	40	36.7	757	2	Q6J851	Q6j851 influenza a
419	1	RRP1_IAGU2	P16503	influenza a	492	40	36.7	757	2	Q6J856	Q6j856 influenza a
420	1	RRP1_IATHE	P16504	influenza a	493	40	36.7	757	2	Q6PNE2	Q6pne2 influenza a
421	1	RRP1_IATHE	P16505	influenza a	494	40	36.7	757	2	Q6R2G3	Q6r2g3 influenza a
422	1	RRP1_IATHE	P18882	influenza a	495	40	36.7	757	2	Q6VGI1	Q6vgi1 influenza a
423	1	RRP1_IATIT	Q91741	influenza a	496	40	36.7	757	2	Q6VGI2	Q6vgi2 influenza a
424	1	RRP1_IATOK	P16506	influenza a	497	40	36.7	757	2	Q6VGI3	Q6vgi3 influenza a
425	1	RRP1_IATOK	P26119	influenza a	498	40	36.7	757	2	Q6W8X7	Q6w8x7 influenza a
426	1	RRP1_IATOK	P26120	influenza a	499	40	36.7	757	2	Q6XS26	Q6xs26 influenza a
427	1	RRP1_IATOK	P26121	influenza a	500	40	36.7	757	2	Q6XS27	Q6xs27 influenza a
428	1	RRP1_IAMAN	P16508	influenza a							
429	1	RRP1_IAMAN	P16507	influenza a							
430	1	RRP1_IAMN5	P16507	influenza a							
431	1	RRP1_IAPUE	P03431	influenza a							
432	1	RRP1_IASIN	P16511	influenza a							
433	1	RRP1_IATKM	P16513	influenza a							
434	1	RRP1_IAMN5	P03430	influenza a							
435	1	RRP1_IAMN5	P16514	influenza a							
436	1	RRP1_IAMN5	P16509	influenza a							
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468	1	RRP1_IAMN5	P16512	influenza a							
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ALIGNMENTS

RESULT 1
 LPP3_HUMAN
 ID_LPP3_HUMAN STANDARD; PRT; 311 AA.
 AC O14495; O96GWD; Q99782;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DE 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Lipid phosphate phosphohydrolase 3 (EC 3.1.3.4) (Phosphatidic acid
 phosphate 2b) (phosphatidate phosphohydrolase type 2b) (PAP2b) (PAP-
 2b) (PAP2-beta) (Vascular endothelial growth factor and type I
 collagen inducible protein) (VCIP).
 GN Name=PAP2b; Synonyms=LPP3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., CHARACTERIZATION, AND INDUCTION.
 RX MEDLINE=97450990; PubMed=9305923; DOI=10.1074/jbc.272.39.24572;
 RA Kai M., Wada I., Imai S.-I., Sakane F., Kanoh H.;
 RT "Cloning and characterization of two human isozymes of Mg2+-
 independent phosphatidic acid phosphatase.";
 RL J. Biol. Chem. 272:24572-24578(1997).
 RN [2]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE=98371049; PubMed=9705349; DOI=10.1074/jbc.273.34.22059;
 RA Roberts R., Sciorra V.A., Morris A.J.;
 RT "Human type 2 phosphatidic acid phosphohydrolases. Substrate
 specificity of the type 2a, 2b, and 2c enzymes and cell surface
 activity of the 2a isoform.";
 RL J. Biol. Chem. 273:22059-22067(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX PubMed=12660161; DOI=10.1093/emboj/cdg165;
 RA Huntsree J.O., Feng S., Thakker G.D., Yang J., Hong J., Wary K.K.;
 RT "Regulation of cell-cell interactions by phosphatidic acid phosphatase
 2b/VCIP.";

EMBO J. 22:1539-1554(2003).
[4]
SEQUENCE FROM N.A.
Leung D.W., Tompkins C.K.;
"Molecular cloning of and expression of an isoform of human
phosphatidic acid phosphatase cDNA";
Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
[5]
SEQUENCE FROM N.A.
MEDLINE=97264341; PubMed=9110174;
Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Liu W.,
Ricafrante J.Y., Wentland M.A., Lennon G., Gibbs R.A.;
"Large-scale concatenation cDNA sequencing.";
Genome Res. 7:353-358(1997).
[6]
SEQUENCE FROM N.A.
TISSUE=Placenta;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Rosa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kertteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[7]
SUBUNIT.
PubMed=14725715; DOI=10.1186/1471-2091-5-2;
Burnett C., Makridou P., Hewlett L., Howard K.;
"Lipid phosphate phosphatases dimerise, but this interaction is not
required for in vivo activity.";
BMC Biochem. 5:2-2(2004).
CC -!- FUNCTION: Catalyzes the conversion of phosphatidic acid (PA) to
diacylglycerol (DG). In addition it hydrolyzes lysophosphatidic
acid (LPA), ceramide-1-phosphate (C-1-P) and sphingosine-1-
phosphate (S-1-P). The relative catalytic efficiency is LPA = PA >
C-1-P > S-1-P. May be involved in cell adhesion and in cell-cell
interactions.
CC -!- CATALYTIC ACTIVITY: A 3-sn-phosphatidate + H(2O) = a 1,2-diacyl-
sn-glycerol + phosphate.
CC -!- ENZYME REGULATION: Inhibited by sphingosine, zinc ions and
propanolol. Not inhibited by N-ethylmaleimide treatment.
CC -!- SUBUNIT: Homodimer. This complex seems not to be involved in
substrate recognition, it may confer only structural or functional
stability.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Post-Golgi and
plasma membrane localization.
CC -!- TISSUE SPECIFICITY: Ubiquitously expressed. Highly expressed in
heart and placenta.
CC -!- INDUCTION: By epidermal growth factor (EGF), vascular endothelial
growth factor (VEGF), basic fibroblast growth factor (bFGF) and
phorbol myristate acetate (PMA).
CC -!- PTM: N-glycosylated. Contains high-mannose oligosaccharides.
CC -!- SIMILARITY: Belongs to the PA-phosphatase related phosphoesterase
family.
CC -!- CAUTION: Ref.5 sequence differs from that shown due to a
frameshift in position 225.

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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

CC EMBL; AB000889; BAA22594.1; -;
CC EMBL; AF017786; AAC63433.1; -;
CC EMBL; AF480883; AAO84481.1; -;
CC EMBL; AF043329; RAD02271.1; -;
CC EMBL; U79294; AAB50222.1; ALT_FRAME.
CC EMBL; BC003196; AAH03196.1; -;
CC Genew; HGNC:9229; PPA2P28.
CC H-InvDB; HIX0000628; -;
CC Reactome; O14495; -;
CC MIM; 607125; -;
CC GO; GO:0016020; C:membrane; TAS.
CC GO; GO:0004721; F:phosphoprotein phosphatase activity; TAS.
CC GO; GO:0008151; P:cell growth and/or maintenance; TAS.
CC GO; GO:0008354; P:germ-cell migration; TAS.
CC InterPro; IPR008934; ACPase VanPerase.
CC InterPro; IPR000326; Pesterase_PA_PTP.
CC Pfam; PF01569; PAP2; 1.
CC SMART; SM00014; acidppc; 1.
KW Glycoprotein; Hydrolase; Transmembrane.
FT DOMAIN 1 33 Cytoplasmic (Potential).
FT TRANSMEM 34 54 Potential.
FT DOMAIN 55 85 Lumenal (Potential).
FT TRANSMEM 86 106 Potential.
FT DOMAIN 107 122 Cytoplasmic (Potential).
FT TRANSMEM 123 143 Potential.
FT DOMAIN 144 193 Lumenal (Potential).
FT TRANSMEM 194 214 Potential.
FT DOMAIN 215 227 Cytoplasmic (Potential).
FT TRANSMEM 228 248 Potential.
FT DOMAIN 249 257 Lumenal (Potential).
FT TRANSMEM 258 278 Potential.
FT DOMAIN 279 311 Cytoplasmic (Potential).
FT CARBOHYD 170 170 N-linked (GlcNAc...) (Potential).
FT CONFLICT 282 282 T -> M (in Ref. 6).
SQ SEQUENCE 311 AA; 35116 MW; CB3F60189044DA31 CRC64;

Query Match 100.0%; Score 109; DB 1; Length 311;
Best Local Similarity 100.0%; Pred. No. 9.9e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGYIQRRCRGDDSKVQEAR 20
Db 173 EGYIQRRCRGDDSKVQEAR 192

RESULT 2
LPP3 MOUSE
ID LPP3 MOUSE STANDARD; PRT; 312 AA.
AC Q99JF8; Q8BTB7;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Lipid phosphate phosphohydrolase 3 (EC 3.1.3.4) (Phosphatidic acid
phosphatase 2b) (Phosphatidate phosphohydrolase type 2b) (PAP2b) (PAP-
2b) (PAP2-beta).
DE Name=Ppap2b; Synonyms=Lpp3;
GN Mus musculus (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierzki R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lernerhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlee G., Pesole G.,
RA Petrovsky N., Pillai K., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Simple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Buetow K.H., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP FUNCTION, AND DISEASE.
RX PubMed=12925589; DOI=10.1242/dev.00635;
RA Escalante-Alcalde D., Hernandez L., Le Stunff H., Maeda R., Lee H.-S.,
RA Cheng G.-J., Sciorra V.A., Daar I., Spiegel S., Morris A.J.,
RA Stewart C.L.;
RT "The lipid phosphatase LPP3 regulates extra-embryonic vasculogenesis
RT and axis patterning.";
RL Development 130:4623-4637(2003).
CC -!- FUNCTION: Catalyzes the conversion of phosphatidic acid (PA) to
CC diacylglycerol (DG). In addition it hydrolyzes lysophosphatidic
CC acid (LPA), ceramide-1-phosphate (C-1-P) and sphingosine-1-
CC phosphate (S-1-P) (By similarity). Essential to the formation of
CC the chorio-allantoic placenta and extra-embryonic vasculature.
CC Also mediates gastrulation and axis formation, probably by
CC regulating the Wnt signaling pathway.
CC -!- CATALYTIC ACTIVITY: A 3-sn-phosphatidate + H(2)O = a 1,2-diacyl-
CC sn-glycerol + phosphate.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum associated (By similarity).
CC -!- DISEASE: Ppap2b deficient embryos fail to form a chorio-allantoic
CC placenta and yolk sac vasculature. A subset of embryos also show a
CC shortening of the anterior-posterior axis and frequent duplication

CC of axial structures. Loss of Ppap2b results in a marked increase
CC in beta-catenin-mediated T-cell factor (TCF) transcription.
CC -!- SIMILARITY: Belongs to the PA-phosphatase related phosphoesterase
CC family.
CC -!- CAUTION: Ref.1 sequence differs from that shown due to a
CC frameshift in position 226.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AK011276; BAC25327.1; ALT_FRAME.
CC EMBL; BC005558; AAH05558.1; -.
CC MGD; MGI:1915166; Ppap2b.
CC GO; GO:0042577; F:lipid phosphatase activity; IMP.
CC GO; GO:0001569; P:blood vessel development; IMP.
CC GO; GO:0010003; P:gastrulation (sensu Mammalia); IMP.
CC GO; GO:0006644; P:phospholipid metabolism; IMP.
CC GO; GO:0030111; P:regulation of Wnt receptor signaling pathway; IDA.
CC InterPro; IPR008934; AcPase VanPase.
CC InterPro; IPR00326; Pesterase_PA_PTP.
CC Pfam; PF01569; PAP2; 1.
CC SMART; SM00014; acidPPC; 1.
CC Developmental protein; Glycoprotein; Hydrolase; Transmembrane.
KW DOMAIN 1 33 Cytoplasmic (Potential).
FT TRANSMEM 34 54 Potential.
FT DOMAIN 55 85 Luminal (Potential).
FT TRANSMEM 86 106 Potential.
FT DOMAIN 107 123 Cytoplasmic (Potential).
FT TRANSMEM 124 144 Potential.
FT DOMAIN 145 194 Luminal (Potential).
FT TRANSMEM 195 215 Potential.
FT DOMAIN 216 226 Cytoplasmic (Potential).
FT TRANSMEM 227 247 Potential.
FT DOMAIN 248 258 Luminal (Potential).
FT TRANSMEM 259 279 Potential.
FT DOMAIN 280 312 Cytoplasmic (Potential).
FT CARBOHYD 171 171 N-linked (GlcNAc..) (Potential).
SQ SEQUENCE 312 AA; 35216 MW; D78298E04B57D7D CRC64;
Query Match 96.3%; Score 105; DB 1; Length 312;
Best Local Similarity 95.0%; Pred. No. 4.7e-09;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 EGYIQNYRCRGDDSKVQEAR 20
|||||||:|||||||
Db 174 EGYIQNYRCRGEDSKVQEAR 193
RESULT 3
ID LPP3 RAT STANDARD; PRT; 312 AA.
AC P97544;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Lipid phosphate phosphohydrolase 3 (EC 3.1.3.4) (Phosphatidic acid
DE phosphate 2b) (Phosphatidate phosphohydrolase type 2b) (PAP2b) (PAP-
DE 2b) (PAP2-beta) (Differentially expressed in rat intestine 42)
DE (Dri42).
GN Name=Ppap2b; Synonyms=Lpp3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., TOPOLOGY, AND N-GLYCOSYLATION.
RC STRAIN=WiStar; TISSUE=Small intestine;
RX MEDLINE=97094703; PubMed=8939937; DOI=10.1074/jbc.271.47.29928;

RA Barila D., Plateroti M., Nobili F., Muda A.O., Xie Y., Morimoto T.,
RA Perozzi G.;
RT "The Dri 42 gene, whose expression is upregulated during epithelial
RT differentiation, encodes a novel ER resident transmembrane protein.";
RL J. Biol. Chem. 271:29928-29936(1996).
RN [2]
RN TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
RX PubMed=8055940;
RX Barila D., Murgia C., Nobili F., Gaetani S., Perozzi G.;
RT "Subtractive hybridization cloning of novel genes differentially
RT expressed during intestinal development.";
RL Eur. J. Biochem. 223:701-709(1994).
RN [3]
RN TISSUE SPECIFICITY.
RP STRAIN=Sprague-Dawley;
RX MEDLINE=2155999; PubMed=11704545;
RX Nanjundan M., Possmayer F.;
RT "Molecular cloning and expression of pulmonary lipid phosphate
RT phosphohydrolases";
RL Am. J. Physiol. 281:L1484-L1493(2001).
CC -I- FUNCTION: Catalyzes the conversion of phosphatidic acid (PA) to
CC diacylglycerol (DG). In addition it hydrolyzes lysophosphatidic
CC acid (LPA), ceramide-1-phosphate (C-1-P) and sphingosine-1-
CC phosphate (S-1-P) (By similarity). Involved in the regulation of
CC epithelial differentiation.
CC -I- CATALYTIC ACTIVITY: A 3-sn-phosphatidate + H(2)O = a 1,2-diacyl-
CC sn-glycerol + phosphate.
CC -I- SUBUNIT: Homodimer (By similarity).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum associated.
CC -I- TISSUE SPECIFICITY: Detected in epithelial cells of intestinal
CC mucosa, lung, liver and brain.
CC -I- DEVELOPMENTAL STAGE: Expression is increased during epithelial
CC differentiation in intestinal mucosa as well as in kidney, liver
CC and lung.
CC -I- PTM: N-glycosylated.
CC -I- SIMILARITY: Belongs to the PA-phosphatase related phosphoesterase
CC family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: Y07783; CAA69106.1; --
CC InterPro; IPR008934; AcPase_VanPeraase.
CC InterPro; IPR000326; Pesterase_PA_PTP.
CC Pfam; PF01569; PAP2; 1.
CC SMART; SM00014; acidppc; 1.
CC Endoplasmic reticulum; Glycoprotein; Hydrolase; Transmembrane.
CC DOMAIN 1 33 Cytoplasmic (Potential).
CC TRANSMEM 34 54 Luminal (Potential).
CC DOMAIN 55 85 Luminal (Potential).
CC TRANSMEM 86 106 Potential.
CC DOMAIN 107 123 Cytoplasmic (Potential).
CC TRANSMEM 124 144 Potential.
CC DOMAIN 145 194 Luminal (Potential).
CC TRANSMEM 195 215 Potential.
CC DOMAIN 216 226 Cytoplasmic (Potential).
CC TRANSMEM 227 247 Potential.
CC DOMAIN 248 258 Luminal (Potential).
CC TRANSMEM 259 279 Potential.
CC DOMAIN 280 312 Potential.
CC CARBOHYD 171 171 N-linked (GlcNAc...) (Potential).
CC SEQUENCE 312 AA; 35318 MW; 9B47FD321DB0419 CRC64;
Query Match 96.3%; Score 105; DB 1; Length 312;
Best Local Similarity 95.0%; Pred. No. 4.7e-09;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGYIQRRCRGDDSKVQEAR 20
DB 174 EGYIQRRCRGDDSKVQEAR 193
|||||
RESULT 4
Q6IMX4 PRELIMINARY; PRT; 312 AA.
ID Q6IMX4
AC Q6IMX4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ER transmembrane protein Dri 42.
GN Name=Dri42;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Heart;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins E.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Heart;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072544; AAH72544.1; --
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR008934; AcPase_VanPeraase.
DR InterPro; IPR000326; Pesterase_PA_PTP.
DR Pfam; PF01569; PAP2; 1.
DR SMART; SM00014; acidppc; 1.
DR Transmembrane.
RW SEQUENCE 312 AA; 35233 MW; CDA54495C0E7D37D CRC64;
Query Match 96.3%; Score 105; DB 2; Length 312;
Best Local Similarity 95.0%; Pred. No. 4.7e-09;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGYIQRRCRGDDSKVQEAR 20
DB 174 EGYIQRRCRGDDSKVQEAR 193
|||||
RESULT 5
Q68F34 PRELIMINARY; PRT; 307 AA.
ID Q68F34
AC Q68F34;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MGC81884 protein.

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GN Names=MGC81884;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.M., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullany S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Klein S., Gerhard D.S.;
RA Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC080011; AAH80011.1; -.
DR InterPro; IPR008934; AcPase_VanPerase.
DR InterPro; IPR000326; Pesterase_PA_PTP.
DR Pfam; PF01569; PAP2; 1.
DR SMART; SM00014; acidPPC; 1.
SQ SEQUENCE 307 AA; 34498 MW; 09666E6DA6265308 CRC64;

Query Match 67.9%; Score 74; DB 2; Length 307;
Best Local Similarity 68.4%; Pred. No. 0.00073;
Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 GYIYVRCRGDDSKVQEAR 20
Db |||:|||:|||:|||
175 GYIYVRCRGPPNKVWEAR 193

RESULT 6
Q6AX87 PRELIMINARY; PRT; 307 AA.
ID Q6AX87
AC Q6AX87
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MGC81990 protein.
GN Name=MGC81990;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
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OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.M., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullany S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Klein S., Gerhard D.S.;
RA Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC079709; AAH79709.1; -.
DR InterPro; IPR008934; AcPase_VanPerase.
DR InterPro; IPR000326; Pesterase_PA_PTP.
DR Pfam; PF01569; PAP2; 1.
DR SMART; SM00014; acidPPC; 1.
SQ SEQUENCE 307 AA; 34417 MW; 23P956E7B8FFED0D CRC64;

Query Match 65.1%; Score 71; DB 2; Length 307;
Best Local Similarity 68.4%; Pred. No. 0.0023;
Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 GYIYVRCRGDDSKVQEAR 20
Db |||:|||:|||:|||
175 GYIYVRCRGPPNKVWEAR 193

RESULT 7
Q95L84 PRELIMINARY; PRT; 167 AA.
ID Q95L84
AC Q95L84
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phosphatidic acid phosphatase type 2A (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22306422; PubMed=12388084;
RA Wang D.-A., Du H., Jaggar J.H., Brindley D.N., Tigyi G.J.,
RA Watsky M.A.;
RA "Injury-elicited differential transcriptional regulation of
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RT	phospholipid growth factor receptors in the cornea.";	
RL	Am. J. Physiol. Cell Physiol. 283:C1646-C1654 (2002).	
CC	EMBL; AF040277; AAL01884.1; -	
CC	DR InterPro; IPR008934; ACPase_VanPerase.	
CC	DR InterPro; IPR000326; Pesterase_PA_PTP.	
CC	DR Pfam; PF01569; PAP2.1.	
CC	DR SMART; SM00014; acidPPc; 1.	
CC	DR NON_TER 167	
CC	DR NON_TER 167	
CC	FT SEQUENCE 167 AA; 19922 MW; 5185AECB0C8E8FB CRC64;	
CC	Query Match 64.3%; Score 70; DB 2; Length 167;	
CC	Best Local Similarity 60.0%; Pred. No. 0.0018;	
CC	Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;	
QY	1 EGYQNYRCRGDDSKVQEAR 20	
DB	122 DGYIENVCRGNAQVKVEGR 141	
CC	-----	
CC	EMBL; U90556; AAB50246.1; -	
CC	EMBL; AF503609; AAM28631.1; -	
CC	GO; GO:0005624; C:membrane fraction; ISS.	
CC	GO; GO:0008195; P:phosphatidate phosphatase activity; ISS.	
CC	GO; GO:0030521; P:androgen receptor signaling pathway; ISS.	
CC	GO; GO:0008285; P:negative regulation of cell proliferation; ISS.	
CC	GO; GO:0046839; P:phospholipid dephosphorylation; ISS.	
CC	GO; GO:0007205; P:protein kinase C activation; ISS.	
CC	GO; GO:0019216; P:regulation of lipid metabolism; ISS.	
CC	DR InterPro; IPR008934; ACPase_VanPerase.	
CC	DR InterPro; IPR000326; Pesterase_PA_PTP.	
CC	DR Pfam; PF01569; PAP2.1.	
CC	DR SMART; SM00014; acidPPc; 1.	
KW	Alternative splicing; Glycoprotein; Hydrolase; Transmembrane.	
FT	DOMAIN 1 6	
FT	TRANSMEM 7 27	
FT	DOMAIN 28 53	
FT	TRANSMEM 54 74	
FT	DOMAIN 75 88	
FT	TRANSMEM 89 109	
FT	DOMAIN 110 164	
FT	TRANSMEM 165 185	
FT	DOMAIN 186 194	
FT	TRANSMEM 195 215	
FT	DOMAIN 216 229	
FT	TRANSMEM 230 250	
FT	DOMAIN 251 282	
FT	CARBOHYD 142 142	
FT	VARSPLIC 21 70	
CC	-----	
CC	GLPFIILTSRHTPFQFGVCTDESIKYVPREDTIPVALLGG	
CC	IVIPFCIIIV -> SMPMAVNLGQIYFPQRFQFCSDNSVKY	
CC	PYHDSVTSTVLVLVLGLGPIPS (in isoform 2).	
CC	/FTID-VSP 009653.	
CC	FT SEQUENCE 282 AA; 31996 MW; A4ED3DEB33FD7943 CRC64;	
CC	Query Match 60.6%; Score 66; DB 1; Length 282;	
CC	Best Local Similarity 50.0%; Pred. No. 0.015;	
CC	Matches 10; Conservative 7; Mismatches 3; Indels 0; Gaps 0;	
QY	1 EGYQNYRCRGDDSKVQEAR 20	
DB	145 DGYIENVCRGNAQVKVEGR 164	
CC	-----	
CC	EMBL; U90556; AAB50246.1; -	
CC	EMBL; AF503609; AAM28631.1; -	
CC	GO; GO:0005624; C:membrane fraction; ISS.	
CC	GO; GO:0008195; P:phosphatidate phosphatase activity; ISS.	
CC	GO; GO:0030521; P:androgen receptor signaling pathway; ISS.	
CC	GO; GO:0008285; P:negative regulation of cell proliferation; ISS.	
CC	GO; GO:0046839; P:phospholipid dephosphorylation; ISS.	
CC	GO; GO:0007205; P:protein kinase C activation; ISS.	
CC	GO; GO:0019216; P:regulation of lipid metabolism; ISS.	
CC	DR InterPro; IPR008934; ACPase_VanPerase.	
CC	DR InterPro; IPR000326; Pesterase_PA_PTP.	
CC	DR Pfam; PF01569; PAP2.1.	
CC	DR SMART; SM00014; acidPPc; 1.	
KW	Alternative splicing; Glycoprotein; Hydrolase; Transmembrane.	
FT	DOMAIN 1 6	
FT	TRANSMEM 7 27	
FT	DOMAIN 28 53	
FT	TRANSMEM 54 74	
FT	DOMAIN 75 88	
FT	TRANSMEM 89 109	
FT	DOMAIN 110 164	
FT	TRANSMEM 165 185	
FT	DOMAIN 186 194	
FT	TRANSMEM 195 215	
FT	DOMAIN 216 229	
FT	TRANSMEM 230 250	
FT	DOMAIN 251 282	
FT	CARBOHYD 142 142	
FT	VARSPLIC 21 70	
CC	-----	
CC	GLPFIILTSRHTPFQFGVCTDESIKYVPREDTIPVALLGG	
CC	IVIPFCIIIV -> SMPMAVNLGQIYFPQRFQFCSDNSVKY	
CC	PYHDSVTSTVLVLVLGLGPIPS (in isoform 2).	
CC	/FTID-VSP 009653.	
CC	FT SEQUENCE 282 AA; 31996 MW; A4ED3DEB33FD7943 CRC64;	
CC	Query Match 60.6%; Score 66; DB 1; Length 282;	
CC	Best Local Similarity 50.0%; Pred. No. 0.015;	
CC	Matches 10; Conservative 7; Mismatches 3; Indels 0; Gaps 0;	
QY	1 EGYQNYRCRGDDSKVQEAR 20	
DB	145 DGYIENVCRGNAQVKVEGR 164	
CC	-----	
CC	EMBL; U90556; AAB50246.1; -	
CC	EMBL; AF503609; AAM28631.1; -	
CC	GO; GO:0005624; C:membrane fraction; ISS.	
CC	GO; GO:0008195; P:phosphatidate phosphatase activity; ISS.	
CC	GO; GO:0030521; P:androgen receptor signaling pathway; ISS.	
CC	GO; GO:0008285; P:negative regulation of cell proliferation; ISS.	
CC	GO; GO:0046839; P:phospholipid dephosphorylation; ISS.	
CC	GO; GO:0007205; P:protein kinase C activation; ISS.	
CC	GO; GO:0019216; P:regulation of lipid metabolism; ISS.	
CC	DR InterPro; IPR008934; ACPase_VanPerase.	
CC	DR InterPro; IPR000326; Pesterase_PA_PTP.	

RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Prange C.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny N.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywicki M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RA Strausberg R.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; BC061815; AH461815.1; -;
 DR InterPro; IPR008934; AcPase_VanParase.
 DR InterPro; IPR00326; Pesterase_PA_PTP.
 DR Pfam; PF01569; PAP2; 1.
 DR SMART; SM00014; acidPPc; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 282 AA; 32000 MW; 108FDIC5F3FCB8E9 CRC64;
 Query Match 60.6%; Score 66; DB 2; Length 282;
 Best Local Similarity 50.0%; Pred. No. 0.015;
 Matches 10; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EGYIQNYRCRGDDSKVQEAR 20
 DB 145 DGYIENFVCGNEQKVRGR 164
 RESULT 10
 LPPI_MOUSE
 ID LPPI_MOUSE STANDARD; PRT; 283 AA.
 AC Q61469; Q61690; Q8BPB8;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DE 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Lipid phosphate phosphohydrolase 1 (EC 3.1.3.4) (Phosphatidic acid
 DE phosphatase 2a) (PAP2-alpha) (Hydrogen peroxide-inducible protein 53) (Hic53) (35-
 DE kDa PAP) (mpAP).
 GN Name=Pap2a; Synonym=Hpic53, LPP1;
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND INDUCTION.
 RC TISSUE=Calvaria;
 RX MEDLINE=96032549; PubMed=7556647; DOI=10.1016/0014-5793(95)00957-B;
 RA Egawa K., Yoshiwara M., Shibamura M., Nose K.;
 RT "Isolation of a novel ras-reversion gene that is induced by hydrogen
 RT peroxide from a mouse osteoblastic cell line, MC3T3-E1.";
 RL FEBS Lett. 372:74-77 (1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Kidney;
 RX MEDLINE=96324980; PubMed=8702556; DOI=10.1074/jbc.271.31.18931;

RA Kai M., Wada I., Imai S.-I., Sakane F., Kanoh H.;
 RT "Identification and cDNA cloning of 35-kDa phosphatidic acid
 RT phosphatase (type 2) bound to plasma membranes.";
 RL J. Biol. Chem. 271:18931-18938 (1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=FVB/N;
 RA Yokoyama K., Tigyi G.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBSJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC STRAIN=C57BL/6J; TISSUE=Ovary, and Uterus;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nitaiko I., Oeato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sadelain A., Schneider C., Sempile C.A., Setou M., Shimada M.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verdugo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shizaki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 RN [5]
 RP CHARACTERIZATION.
 RC TISSUE=Liver;
 RX PubMed=10359651; DOI=10.1042/0264-6021.3400677;
 RA Jasinska R., Zhang Q.-X., Pilquill C., Singh I., Xu J., Dewald J.,
 RA Dillon D.A., Berthiaume L.G., Carman G.W., Waggoner D.W.,
 RA Brindley D.N.;
 RT "Lipid phosphate phosphohydrolase-1 degrades exogenous glycerolipid
 RT and sphingolipid phosphate esters.";
 RL Biochem. J. 340:677-686 (1999).
 RN [6]
 RP SUBUNIT.
 RX PubMed=14725715; DOI=10.1186/1471-2091-5-2;
 RA Burnett C., Makridou P., Hewlett L., Howard K.;
 RT "Lipid phosphate phosphatases dimerise, but this interaction is not
 RT required for in vivo activity.";
 RL BMC Biochem. 5:2-2 (2004).
 RN [7]
 RP OVEREXPRESSION.
 RX PubMed=14687668; DOI=10.1016/j.cellsig.2003.08.012;
 RA Yue J., Yokoyama K., Balazs L., Baker D.L., Smalley D., Pilquill C.,
 RA Brindley D.N., Tigyi G.;
 RT "Mice with transgenic overexpression of lipid phosphate phosphatase-1
 RT display multiple organotypic deficits without alteration in
 RT circulating lysophosphatidate level.";
 RL Cell. Signal. 16:385-399 (2004).
 CC -!- FUNCTION: Broad-specificity phosphohydrolase that dephosphorylates
 CC exogenous bioactive glycerolipids and sphingolipids. Catalyzes the
 CC conversion of phosphatidic acid (PA) to diacylglycerol (DG). In
 CC addition it hydrolyzes lysophosphatidic acid (lPA), diacyl
 CC glycerol pyrophosphate (DGPP), ceramide-1-phosphate (C-1-P) and

CC sphingosine-1-phosphate (S-1-P). The relative catalytic efficiency
is LPA > PA > C-1-P > S-1-P.
CC -!- CATALYTIC ACTIVITY: A 3-sn-phosphatidate + H(2)O = a 1,2-diacyl-
CC sn-glycerol + phosphate.
CC -!- SUBUNIT: Homodimer. This complex seems not to be involved in
CC substrate recognition, it may confer only structural or functional
CC stability.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Found
CC predominantly in plasma membrane.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q61469-1; Sequence=displayed;
CC Name=2;
CC IsoId=Q61469-2; Sequence=VSP_009652;
CC -!- TISSUE SPECIFICITY: Highly expressed in kidney and lung. Almost
CC undetectable in brain, heart, bone, muscle or spleen.
CC -!- INDUCTION: Moderately, by hydrogen peroxide, calcium ionophore and
CC dexamethasone.
CC -!- PTM: N-glycosylated. Contains high-mannose oligosaccharide.
CC -!- MISCELLANEOUS: Overexpression elicited a number of phenotypic
CC alteration without affecting several aspects of LPA signaling.
CC Phenotypic abnormalities affect primarily three organs: the liver,
CC the skin, and the reproductive organs. There is a reduction on
CC body size, birth weight, abnormalities in fur growth, and a
CC severely impaired spermatogenesis.
CC -!- SIMILARITY: Belongs to the PA-phosphatase related phosphoesterase
CC family.
CC -!- CAUTION: Ref.1 sequence differs from that shown due to numerous
CC frame shifts.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; LA3371; AA085353.1; ALT_SEQ.
DR EMBL; D84376; BA012335.1; -.
DR EMBL; AY247795; AAP04434.1; -.
DR EMBL; AY247796; AAP04435.1; -.
DR EMBL; AK07275; BAC36724.1; -.
DR F01; S66668; S66668.
DR MGD; MGI:104646; Hpic53.
DR MGD; MGI:108412; Ppap2a.
DR GO; GO:0005624; C:membrane fraction; ISS.
DR GO; GO:0008195; P:phosphatidate phosphatase activity; ISS.
DR GO; GO:0030521; P:androgen receptor signaling pathway; ISS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.
DR GO; GO:0046839; P:phospholipid dephosphorylation; ISS.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IDA.
DR GO; GO:0007205; P:protein kinase C activation; ISS.
DR GO; GO:0019216; P:regulation of lipid metabolism; ISS.
DR InterPro; IPR008934; Acpase_vanPerase.
DR InterPro; IPR000326; Pesterase_PA_FTP.
DR Pfam; PF01569; PAP2; 1.
DR SMART; SM00014; acidppc; 1.
KW Alternative splicing; Glycoprotein; Hydrolase; Transmembrane.
FT DOMAIN 1 6 Cytoplasmic (Potential).
FT TRANSMEM 7 27 Potential.
FT DOMAIN 28 53 Extracellular (Potential).
FT TRANSMEM 54 74 Potential.
FT DOMAIN 75 88 Cytoplasmic (Potential).
FT TRANSMEM 89 109 Potential.
FT DOMAIN 110 164 Extracellular (Potential).
FT TRANSMEM 165 185 Potential.
FT DOMAIN 186 199 Cytoplasmic (Potential).
FT TRANSMEM 200 220 Potential.
FT DOMAIN 221 229 Extracellular (Potential).
FT TRANSMEM 230 250 Potential.
FT DOMAIN 251 283 Cytoplasmic (Potential).

FT CARBOHYD 142 142 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 21 70 GUPFAILSRHPPFGRIFCNDSDSKIPFKEDTIPALGG
IVIPFCIIIV -> AMPMTILKLGKVPFGFGFTDNSVKY
PYHDSIPSRILAILGLGLPIFS (in isoform 2).
FT FTID=VSP_009652.
SQ SEQUENCE 283 AA; 31891 MW; 669690568549CC6 CRC64;
Query Match 59.6%; Score 65; DB 1; Length 283;
Best Local Similarity 50.0%; Pred. No. 0.022;
Matches 10; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
QY 1 EGVIONYRCRGDDSKVQEAR 20
DB 145 DGIYIEDYICQGNKVKR 164
RESULT 11
ID LPPI_CAVPO STANDARD; PRT; 285 AA.
AC O88956; O88957;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Lipid phosphate phosphohydrolase 1 (EC 3.1.3.4) (Phosphatidic acid
DE phosphatase 2a) (Phosphatidate phosphohydrolase type 2a) (PAP2a) (PAP-
DE 2a) (PAP2-alpha).
GN Name=PPAP2a; Synonyms=LPP1, PAP2a;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Airway smooth muscle;
RX MEDLINE=99334234; PubMed=10405762; DOI=10.1016/S0898-6568(99)00028-5;
RA Tate R.J., Tolan D., Pyne S.;
RT "Molecular cloning of magnesium-independent type 2 phosphatidic acid
RT phosphatases from airway smooth muscle."
RL Cell. Signal. 11:515-522(1999).
CC -!- FUNCTION: Broad-specificity phosphohydrolase that dephosphorylates
CC exogenous bioactive glycerolipids and sphingolipids. Catalyzes the
CC conversion of phosphatidic acid (PA) to diacylglycerol (DG). In
CC addition it hydrolyzes lysophosphatidic acid (LPA), ceramide-1-
CC phosphate (C-1-P) and sphingosine-1-phosphate (S-1-P) (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: A 3-sn-phosphatidate + H(2)O = a 1,2-diacyl-
CC sn-glycerol + phosphate.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane
CC (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=PAP2a1;
CC IsoId=O88956-1; Sequence=Displayed;
CC Name=2; Synonyms=PAP2a2;
CC IsoId=O88956-2; Sequence=VSP_009650;
CC -!- SIMILARITY: Belongs to the PA-phosphatase related phosphoesterase
CC family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF088283; AAC63333.1; -.
DR EMBL; AF088284; AAC63334.1; -.
DR GO; GO:0005624; C:membrane fraction; ISS.
DR GO; GO:0008195; P:phosphatidate phosphatase activity; ISS.
DR GO; GO:0030521; P:androgen receptor signaling pathway; ISS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.

DR GO: GO:0046839; P:phospholipid dephosphorylation; ISS.
 DR GO: GO:0007205; P:protein kinase C activation; ISS.
 DR GO: GO:0019216; P:regulation of lipid metabolism; ISS.
 DR InterPro: IPR008934; ACPase_VanParase.
 DR InterPro: IPR000326; Pesterase_PA_PTP.
 DR Pfam: PF01569; PAP2; 1.
 DR SMART: SM00014; acidPPC; 1.
 KW Alternative splicing; Glycoprotein; Hydrolase; Transmembrane.
 FT DOMAIN 1 6 Cytoplasmic (Potential).
 FT TRANSMEM 7 27 Potential.
 FT DOMAIN 28 53 Luminal (Potential).
 FT TRANSMEM 54 74 Potential.
 FT DOMAIN 75 94 Cytoplasmic (Potential).
 FT TRANSMEM 95 115 Potential.
 FT DOMAIN 116 165 Luminal (Potential).
 FT TRANSMEM 166 186 Potential.
 FT DOMAIN 187 199 Cytoplasmic (Potential).
 FT TRANSMEM 200 220 Potential.
 FT DOMAIN 221 229 Luminal (Potential).
 FT TRANSMEM 230 250 Potential.
 FT DOMAIN 251 285 N-linked (GlcNAc-) (Potential).
 FT CARBOHYD 142 142 GLPFAILTSRHPFGRGIFCNDESISKYPKENTIPYALLGG
 FT VARSPIC 21 70 IMPFSIV -> SMPMAVNLGQIYPPFGFGFCNDNSIQY
 FT PYHDSVASTILTIIVGLGLPISS (in isoform 2).
 FT /FTid=VSP 009650.
 FT CONFLICT 5 5 A -> T (in Ref. 1; AAC63334).
 FT CONFLICT 218 218 I -> V (in Ref. 1; AAC63334).
 FT SEQUENCE 285 AA; 32133 MW; E6F48E188DE6CF5 CRG64;
 Query Match 56.9%; Score 62; DB 1; Length 285;
 Best Local Similarity 55.0%; Pred. No. 0.069;
 Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 1 EGYIQYRCRGDDSKVQEAR 20
 DB 145 DGYIEYVCRGNAEKVKEGR 164
 RESULT 12
 LPPI_HUMAN
 ID LPPI_HUMAN STANDARD; PRT; 284 AA.
 AC O1494; O60457; O60463;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Lipid phosphate phosphohydrolase 1 (EC 3.1.3.4) (Phosphatidic acid
 DE phosphatase 2a) (Phosphatidate phosphohydrolase type 2a) (PAP2a) (PAP-
 DE 2a) (PAP2-alpha).
 GN Name=PPAP2A; Synonym=LPP1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RN
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
 RX MEDLINE=97450990; PubMed=9305923; DOI=10.1074/jbc.272.39.24572;
 RA Kai M., Wada I., Imai S.-I., Sakane F., Kanoh H.;
 RT "Cloning and characterization of two human isozymes of Mg2+-
 RT independent phosphatidic acid phosphatase.";
 RL J. Biol. Chem. 272:24572-24578 (1997).
 [2]
 RN
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Lung;
 RX MEDLINE=98230079; PubMed=9570154;
 RA Leung D.W., Tompkins C.K., White T.;
 RT "Molecular cloning of two alternatively spliced forms of human
 RT phosphatidic acid phosphatase cDNAs that are differentially expressed
 RT in normal and tumor cells.";
 RL DNA Cell Biol. 17:377-385 (1998).
 [3]
 RN
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Prostate;

RX MEDLINE=98136170; PubMed=9468526; DOI=10.1074/jbc.273.8.4660;
 RA Ulrix W.E.J., Swinnen J., Heyns W., Verhoeven G.;
 RT "Identification of the phosphatidic acid phosphatase type 2a isozyme
 RT as an androgen-regulated gene in the human prostatic Adenocarcinoma
 RT cell line LNCaP.";
 RL J. Biol. Chem. 273:4660-4665 (1998).
 [4]
 RN
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
 RX MEDLINE=98371049; PubMed=9705349; DOI=10.1074/jbc.273.34.22059;
 RA Roberts R., Sciorra V.A., Morris A.J.;
 RT "Human type 2 phosphatidic acid phosphohydrolases. Substrate
 RT specificity of the type 2a, 2b, and 2c enzymes and cell surface
 RT activity of the 2a isoform.";
 RL J. Biol. Chem. 273:22059-22067 (1998).
 [5]
 RN
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy P.H.,
 RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faney J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [6]
 RN
 RP FUNCTION
 RX PubMed=12909631; DOI=10.1074/jbc.M306709200;
 RA Smyth S.S., Sciorra V.A., Sigal Y.J., Pamulkar Z., Wang Z., Xu Y.,
 RA Prestwich G.D., Morris A.J.;
 RT "Lipid phosphate phosphatases regulate lysophosphatidic acid
 RT production and signaling in platelets: studies using chemical
 RT inhibitors of lipid phosphate phosphatase activity.";
 RL J. Biol. Chem. 278:43214-43223 (2003).
 CC
 CC -!- FUNCTION: Broad-specificity phosphohydrolase that dephosphorylates
 CC exogenous bioactive glycerolipids and sphingolipids. Catalyzes the
 CC conversion of phosphatidic acid (PA) to diacylglycerol (DG).
 CC Pivotal regulator of lysophosphatidic acid (LPA) signaling in the
 CC cardiovascular system. Major enzyme responsible of
 CC dephosphorylating LPA in platelets, which terminates signaling
 CC actions of LPA. May control circulating, and possibly also
 CC regulate localized, LPA levels resulting from platelet activation.
 CC It has little activity towards ceramide-1-phosphate (C-1-P) and
 CC sphingosine-1-phosphate (S-1-P). The relative catalytic efficiency
 CC is LPA > PA > S-1-P > C-1-P. It's down-regulation may contribute
 CC to the development of colon adenocarcinoma.
 CC -!- CATALYTIC ACTIVITY: A 3-sn-phosphatidate + H(2)O = a 1,2-diacyl-
 CC sn-glycerol + phosphate.
 CC -!- ENZYME REGULATION: Inhibited by sphingosine, zinc ions and
 CC propanolol. Not inhibited by N-ethylmaleimide treatment.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1; Synonyms=Alpha-1, hLPP1, PAP2-a1;
 CC IsoId=O14494-1; Sequence=Displayed;
 CC Name=2; Synonyms=Alpha-2, hLPP1-a, PAP2-a2;
 CC IsoId=O14494-2; Sequence=VSFP_009651;
 CC -!- TISSUE SPECIFICITY: Ubiquitously expressed with highest expression

CC found in prostate. Isoform 1 is predominant in kidney, lung,
 CC placenta and liver; isoform 2 is predominant in heart and
 CC pancreas. Found to be down-regulated in colon adenocarcinomas.
 CC -I- INDUCTION: By androgens.
 CC -I- PTM: N-glycosylated. Contains high-mannose oligosaccharides.
 CC -I- SIMILARITY: Belongs to the PA-phosphatase related phosphoesterase
 CC family.
 CC -I- CAUTION: Ref.1 states that this phosphatase does not hydrolyze
 CC sphingosine 1-phosphate while Ref.4 states that it does.
 CC -----
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 CC -----
 CC EMBL; AB000888; BAA22593.1; -;
 CC EMBL; AF014402; AAC16032.1; -;
 CC EMBL; AF014403; AAC16033.1; -;
 CC EMBL; Y14436; CAC14588.1; -;
 CC EMBL; AF017116; AAC32041.1; -;
 CC EMBL; BC039847; AAC39847.1; -;
 CC Genew; HGNC:9228; PPAP2A.
 CC Reactome; Q14494; -;
 CC MIM; 607124; -;
 CC GO; GO:0005624; C:membrane fraction; IDA.
 CC GO; GO:0008195; C:phosphatidate phosphatase activity; IDA.
 CC GO; GO:0030521; P:androgen receptor signaling pathway; NAS.
 CC GO; GO:0008285; P:negative regulation of cell proliferation; NAS.
 CC GO; GO:0046839; P:phospholipid dephosphorylation; TAS.
 CC GO; GO:0007205; P:protein kinase C activation; TAS.
 CC GO; GO:0019216; P:regulation of lipid metabolism; NAS.
 CC InterPro; IPR000934; ACPase VanPerase.
 CC InterPro; IPR000326; Pesterase_PA_PTP.
 CC Pfam; PF01569; PAP2; 1.
 CC SMART; SM00014; acidppc; 1.
 CC Alternative splicing; Glycoprotein; Hydrolase; Transmembrane.
 CC DOMAIN 1 6 Cytoplasmic (Potential).
 CC TRANSMEM 7 27 Potential.
 CC DOMAIN 28 53 Extracellular (Potential).
 CC TRANSMEM 54 74 Potential.
 CC DOMAIN 75 94 Cytoplasmic (Potential).
 CC TRANSMEM 95 115 Potential.
 CC DOMAIN 116 164 Extracellular (Potential).
 CC TRANSMEM 165 185 Potential.
 CC DOMAIN 186 199 Cytoplasmic (Potential).
 CC TRANSMEM 200 220 Potential.
 CC DOMAIN 221 229 Extracellular (Potential).
 CC TRANSMEM 230 250 Potential.
 CC DOMAIN 251 284 Cytoplasmic (Potential).
 CC CARBOHYD 142 142 N-linked (GlcNAc...) (Potential).
 CC VARSPIC 21 70 ILIIPFSIIIV -> SMPMAVKLGIIYFQFGFCKDINSINY
 CC PHDSTAASVTLVILGVGLPVSS (in isoform 2).
 CC /FTId-VSP 009651.
 CC L -> FTSRHI (in Ref. 4).
 CC R -> S (in Ref. 2; AAC16033).
 CC SEQUENCE 284 AA; 32156 MW; FC2F00617EE07EB3 CRC64;
 CC -----
 CC Query Match 54.1%; Score 59; DB 1; Length 284;
 CC Best Local Similarity 50.0%; Pred. No. 0.22;
 CC Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 CC -----
 CC QY 1 EGYIYRCRGDSDSKVQEAR 20
 CC DB 145 DGYIYICRGNARVKEGR 164
 CC -----
 CC RESULT 13
 CC Q6GP13 PRELIMINARY; PRT; 284 AA.
 CC ID Q6GP13

AC Q6GP13;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE MGC90748 protein.
 GN Name=MGC80748;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.L., Skalska U., Smallos D.E., Schermer A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Klein S., Gerhard D.S.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; BC073336; AAH73336.1; -;
 DR InterPro; IPR008934; ACPase VanPerase.
 DR InterPro; IPR000326; Pesterase_PA_PTP.
 DR Pfam; PF01569; PAP2; 1.
 DR SMART; SM00014; acidppc; 1.
 DR SEQUENCE 284 AA; 31834 MW; 30D0C7391BB424CB CRC64;
 SQ -----
 CC Query Match 48.6%; Score 53; DB 2; Length 284;
 CC Best Local Similarity 47.4%; Pred. No. 2.2;
 CC Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 CC -----
 CC QY 2 GYIYRCRGDSDSKVQEAR 20
 CC DB 147 GYIETFCVCEGDPKTSSEGR 165
 CC -----
 CC RESULT 14
 CC Y787_METJA STANDARD; PRT; 504 AA.
 CC ID Y787_METJA
 CC AC Q58197;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Hypothetical protein MJ0787.

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OrderedLocusNames=MJ0787;
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii."
RL Science 273:1058-1073(1996).
CC 1- SIMILARITY: Strong, to M.thermoautotrophicum MTH1137.
CC -----
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CC -----
DR EMBL; U67523; AAB98783.1; -.
DR FIC; C64398; C64398.
DR TIGR; MJ0787; -.
DR InterPro; IPR011060; Ribp_bind_barrel.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 504 AA; 56128 MW; 1F6C18C2C655E0C CRC64;
Query Match 47.7%; Score 52; DB 1; Length 504;
Best Local Similarity 57.9%; Pred. No. 6.2;
Matches 11; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 EGYIQNYRCRGDSDSKVQEA 19
Db - 457 EAGINAYPCNGDDKKVLEA 475
RESULT 15
ID Q95ZL6 PRELIMINARY; PRT; 244 AA.
AC Q95ZL6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein M01E11.4.
GN Name=M01E11.4; ORFNames=M01E11.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Pauley A., Gattung S.;
RT "The sequence of C. elegans cosmid M01E11.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RA Pauley A., Gattung S.;
RT "The sequence of C. elegans cosmid M01E11.";
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
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RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; U80450; AAK77613.1; -.
DR WormBase; WBGene00019713; M01E11.4.
DR WormPep; M01E11.4a; CE28610.
KW Hypothetical protein.
SQ SEQUENCE 244 AA; 27837 MW; 9AA335B0442B84C4 CRC64;
Query Match 46.8%; Score 51; DB 2; Length 244;
Best Local Similarity 50.0%; Pred. No. 4.1;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 1 EGYIQNYRCRGDSDSKVQEA 18
Db 34 EGFVTRGGCRGDSQIQE 51
RESULT 16
ID Q95ZL7 PRELIMINARY; PRT; 252 AA.
AC Q95ZL7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein M01E11.4.
GN Name=M01E11.4; ORFNames=M01E11.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Pauley A., Gattung S.;
RT "The sequence of C. elegans cosmid M01E11.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RA Pauley A., Gattung S.;
RT "The sequence of C. elegans cosmid M01E11.";
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
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DR WormBase: WBGene00019713; M01E11.4.
DR WormPep: M01E11.4b; CE28611.
KW Hypothetical protein.
SQ SEQUENCE 252 AA; 28738 MW; FE8556D34587F3E8 CRC64;

Query Match 46.8%; Score 51; DB 2; Length 252;
Best Local Similarity 50.0%; Pred. No. 4.2;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EGYQNYRCRGDDSKVQE 18
||:| | | | | | | |
Db 34 EGPVTRGCGRLDSQJQE 51

RESULT 17
Q7RTC3 PRELIMINARY; PRT; 2736 AA.
AC Q7RTC3;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Names=PY00071;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Anguilo S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Seilengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallow S.J., van Aken S.E., Riedmuller S.B., Feldblum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates P.R., Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL0100019; EAA17884.1; -.
DR InterPro: IPR000357; HEAT.
DR Pfam: PF02985; HEAT; 1.
KW Hypothetical protein.
SQ SEQUENCE 2736 AA; 323770 MW; C219F76G2539AA00 CRC64;

Query Match 46.8%; Score 51; DB 2; Length 2736;
Best Local Similarity 50.0%; Pred. No. 58;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 YIQNYRCRGDDSKVQE 18
||:| | | | | | | |
Db 2533 YIYNVACSTDQKID 2548

RESULT 18
LPP2 MOUSE
ID LPP2 MOUSE STANDARD; PRT; 276 AA.
AC Q9DAX2; Q9WU44;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Lipid phosphate phosphohydrolase 2 (EC 3.1.3.4) (Phosphatidic acid
DE phosphate 2c) (PAP2-gamma) (PAP2-G).
DE 2c) (PAP2-gamma) (PAP2-G).
GN Names=Ppap2c; Synonyms=Lpp2;
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A. (ISOFORM 2).
RP STRAIN=C57BL/6J;
RC MEDLINE=20130123; PubMed=10662554; DOI=10.1006/geno.1999.6055;
RX Zhang N., Copeland N.G., Gilbert D.J., Jenkins N.A., Gridley T.,
RA "Cloning, expression, and chromosomal localization of a mouse gene
RT homologous to the germ cell migration regulator wunen and to type 2
RT phosphatidic acid phosphatases."
RL Genomics 63:142-144(2000).
RN SEQUENCE FROM N.A. (ISOFORM 1).
RP STRAIN=C57BL/6J; TISSUE=Embryo, and Placenta;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Mik H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perteau G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN SEQUENCE FROM N.A. (ISOFORM 1).
RP TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Diaplestein M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Catalyzes the conversion of phosphatidic acid (PA) to
CC diacylglycerol (DG). In addition it hydrolyzes lysophosphatidic
CC acid (LPA), ceramide-1-phosphate (C-1-P) and sphingosine-1-
CC phosphate (S-1-P) (By similarity).

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CC -|- CATALYTIC ACTIVITY: A 3-sn-phosphatidate + H(2)O = a 1,2-diacyl-
CC sn-glycerol + phosphate.
CC -|- SUBUNIT: Homodimer (By similarity).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9DAX2-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9DAX2-2; Sequence=VSP_009654, VSP_009655;
CC -|- TISSUE SPECIFICITY: Expressed at high levels in lung, liver and
CC kidney; at low levels in heart and brain, and was not detected in
CC skeletal muscle.
CC -|- SIMILARITY: Belongs to the PA-phosphatase related phosphoesterase
CC family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF123611; AAD24061.1; -.
CC EMBL; AK005452; BAC24045.1; -.
CC EMBL; AK049581; BAC33824.1; -.
CC EMBL; BC010332; AH10332.1; -.
CC MGD; MGI:1354945; Ppap2c.
CC DR InterPro; IPR008934; AcPase_VanPerase.
CC DR InterPro; IPR000326; Pesterase_PA_PTP.
CC Pfam; PF01569; PAP2; 1.
CC SMART; SM00014; acidppc; 1.
CC Alternative splicing; Glycoprotein; Hydrolase; Transmembrane.
CC KW TRANSMEM 5 25 Potential.
CC FT TRANSMEM 52 72 Potential.
CC FT TRANSMEM 88 108 Potential.
CC FT TRANSMEM 162 182 Potential.
CC FT TRANSMEM 190 210 Potential.
CC FT TRANSMEM 219 239 Potential.
CC FT CARBOHYD 139 139 N-linked (GlcNAc...) (Potential).
CC FT VARSPLIC 240 250 RVSVDFKSRP -> SPTCLTHRLCF (in isoform
CC 2).
CC FT VARSPLIC 251 276 Missing (in isoform 2).
CC FT FTId=VSP_009654.
CC FT FTId=VSP_009655.
CC SQ SEQUENCE 276 AA; 31193 MW; 978A83D468113D2 CRC64;
Query Match 45.9%; Score 50; DB 1; Length 276;
Best Local Similarity 52.6%; Pred. No. 6.9;
Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
QY 2 GYQNYRCRGDSDSKVQEAR 20
||:| |||:| |||
Db 142 GYVQVEVCRGSPANVTAR 160
||:| |||:| |||
RESULT 19
LPP2_RAT STANDARD; PRT; 276 AA.
AC Q8K593;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Lipid phosphate phosphohydrolase 2 (EC 3.1.3.4) (Phosphatidic acid
DE phosphatase 2c) (PAP2-gamma) (PAP2-G).
DE 2c) (PAP2-gamma) (PAP2-G).
GN Name=Ppap2c; Synonyms=Lpp2;
GN Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=lung;
RA Zhao L., Nanjundan M., Possmayer F.;
RT "Expression of lipid phosphate phosphohydrolase isoforms in rat lung
RT development.";
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP TISSUE SPECIFICITY.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=21559999; PubMed=11704545;
RA Nanjundan M., Possmayer F.;
RT "Molecular cloning and expression of pulmonary lipid phosphate
RT phosphohydrolases.";
RL Am. J. Physiol. 281:L1484-L1493 (2001).
CC -|- FUNCTION: Catalyzes the conversion of phosphatidic acid (PA) to
CC diacylglycerol (DG). In addition it hydrolyzes lysophosphatidic
CC acid (LPA), ceramide-1-phosphate (C-1-P) and sphingosine-1-
CC phosphate (S-1-P) (By similarity).
CC -|- CATALYTIC ACTIVITY: A 3-sn-phosphatide + H(2)O = a 1,2-diacyl-
CC sn-glycerol + phosphate.
CC -|- SUBUNIT: Homodimer (By similarity).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- TISSUE SPECIFICITY: Expressed in the brain.
CC -|- SIMILARITY: Belongs to the PA-phosphatase related phosphoesterase
CC family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF503611; AAM28632.1; -.
CC InterPro; IPR008934; AcPase_VanPerase.
CC InterPro; IPR000326; Pesterase_PA_PTP.
CC Pfam; PF01569; PAP2; 1.
CC SMART; SM00014; acidppc; 1.
CC Glycoprotein; Hydrolase; Transmembrane.
CC KW TRANSMEM 5 25 Potential.
CC FT TRANSMEM 52 72 Potential.
CC FT TRANSMEM 88 108 Potential.
CC FT TRANSMEM 162 182 Potential.
CC FT TRANSMEM 190 210 Potential.
CC FT TRANSMEM 226 246 Potential.
CC FT CARBOHYD 139 139 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 155 155 N-linked (GlcNAc...) (Potential).
CC SQ SEQUENCE 276 AA; 31101 MW; 41A0E1243458E24C CRC64;
Query Match 45.9%; Score 50; DB 1; Length 276;
Best Local Similarity 52.6%; Pred. No. 6.9;
Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
QY 2 GYQNYRCRGDSDSKVQEAR 20
||:| |||:| |||
Db 142 GYVQVEVCRGSPANVTAR 160
||:| |||:| |||
RESULT 20
Q83ER2 PRELIMINARY; PRT; 130 AA.
AC Q83ER2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ribosomal protein S8.
DE Name=rpS8; OrderedLocustNames=CBU0252;
OS Coxiella burnetii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Coxiellaceae; Coxiella.
OC NCBI_TaxID=777;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=Nine Mile Phase I / RSA 493;
RX MEDLINE=22608657; PubMed=12704232; DOI=10.1073/pnas.0931379100;
RA Seshadri R., Paulsen I.T., Eissen J.A., Read T.D., Nelson K.E.,
RA Nelson W.C., Ward N.L., Tetelin H., Davidsen T.M., Beanan M.J.,
RA DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.,
RA Khouri H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A.,
RA Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.;
RT "Complete genome sequence of the Q-fever pathogen, Coxiella
burnetii."
RL Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003).
CC -!- SIMILARITY: Belongs to the S8P family of ribosomal proteins.
DR EXBL; AS016960; A089810.1; -.
DR HSP; P56209; ISE1.
DR TIGR; CHU0252; -.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR000630; Ribosomal_S8.
DR Pfam; PF00410; Ribosomal_S8; 1.
DR ProDom; PD001098; Ribosomal_S8; 1.
DR PROSITE; PS00053; RIBOSOMAL_S8; 1.
KW Complete proteome; Ribonucleoprotein; Ribosomal protein.
SQ SEQUENCE 130 AA; 14569 MW; C08C350D7739208D CRC64;

Query Match 44.0%; Score 48; DB 2; Length 130;
Best Local Similarity 58.8%; Pred. No. 6.6;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 EGYIQRRCRGDSDSKVQ 17
DB 42 EGYIVDYREGDUTKAQ 58

RESULT 21
QYR7R7 PRELIMINARY; PRT; 217 AA.
AC QYR7R7;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Putative yirl protein.
GN Names=PY07514;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteza M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; AABL01002781; EAA19991.1; -.
DR InterPro; IPR006477; Yir_bir_cir.
DR Pfam; PF06022; Cir_Bir_Yir; 1.
DR TIGRFAMs; TIGR01590; Yir-bir-cir_Pla; 1.
SQ SEQUENCE 269 AA; 31732 MW; A95E562E05D6119C CRC64;

Query Match 44.0%; Score 48; DB 2; Length 269;
Best Local Similarity 43.8%; Pred. No. 15;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 EGYIQRRCRGDSDSKV 16
DB 33 DSYCNKYKCEGLDKI 48

RESULT 23
QYR8M3 PRELIMINARY; PRT; 283 AA.
AC QYR8M3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Phosphatidic acid phosphatase type 2C isoform 1.
GN Name=MG75849;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RC SEQUENCE FROM N.A.
RP TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

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Best Local Similarity 50.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 GYIQRRCRGDSDSKVQEA 19
DB 43 GYCPNLNCNDDBKVVSA 60

RESULT 22
QYR8M3 PRELIMINARY; PRT; 269 AA.
AC QYR8M3;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Putative yir3 protein.
GN Name=PY07198;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteza M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; AABL01002583; EAA19571.1; -.
DR InterPro; IPR006477; Yir_bir_cir.
DR Pfam; PF06022; Cir_Bir_Yir; 1.
DR TIGRFAMs; TIGR01590; Yir-bir-cir_Pla; 1.
SQ SEQUENCE 269 AA; 31732 MW; A95E562E05D6119C CRC64;

Query Match 44.0%; Score 48; DB 2; Length 269;
Best Local Similarity 43.8%; Pred. No. 15;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 EGYIQRRCRGDSDSKV 16
DB 33 DSYCNKYKCEGLDKI 48

RESULT 23
QYR8M3 PRELIMINARY; PRT; 283 AA.
AC QYR8M3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Phosphatidic acid phosphatase type 2C isoform 1.
GN Name=MG75849;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RC SEQUENCE FROM N.A.
RP TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

```

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC061332; AAH61332.1; -;
DR InterPro; IPR008934; AcPase_VanPerase.
DR InterPro; IPR000326; Pesterase_PA_PTP.
DR Pfam; PF01569; PAP2; 1.
DR SMART; SM00014; acidPPC; 1.
SQ SEQUENCE 283 AA; 3165 MW; 8CAD10984483B453 CRC64;
Query Match 44.0%; Score 48; DB 2; Length 283;
Best Local Similarity 36.8%; Pred. No. 15;
Matches 7; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
QY 2 GYIQNYRCRGGDSKVQEAR 20
Db : 144 GYVDFTCRGYANVTDSR 162
RESULT 24
QYPPD6 PRELIMINARY; PRT; 491 AA.
AC Q7PPD6; (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DE ENSANGP00000021570 (Fragment).
GN Name=ENSANGG00000019081;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OC NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008952; EAA10613.2; -;
DR InterPro; IPR005123; 2OG-Fell_Oxy.
DR InterPro; IPR001440; TPR.
DR InterPro; IPR008941; TPR-like.
DR Pfam; PF03171; 2OG-Fell_Oxy; 1.
DR PROSITE; PS50005; TPR; 1.
DR PROSITE; PS50293; TPR_REGION; 1.
FT NON_TER 1
SQ SEQUENCE 491 AA; 56112 MW; DCB3F52923F03BE6 CRC64;
Query Match 44.0%; Score 48; DB 2; Length 491;

Best Local Similarity 52.9%; Pred. No. 28;
Matches 9; Conservative 3; Mismatches 3; Indels 2; Gaps 1;
QY 1 EGYIQNY--RCRGDSK 15
Db 242 EPYVKNYPSLCRGDDQR 258
RESULT 25
Q6FYZZ PRELIMINARY; PRT; 343 AA.
ID Q6FYZZ;
AC Q6FYZZ;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Aspartate-semialdehyde dehydrogenase.
GN Name=asd; OrderedLocusNames=BQ10170;
OS Bartonella quintana (Rochalimaea quintana).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bartonellaceae; Bartonella.
OC NCBI_TaxID=803;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Toulouse;
RX PubMed=15210978; DOI=10.1073/pnas.0305659101;
RA Almark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardell D.H.,
RA Canbaeck B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvel M.,
RA La Scala B., Holmberg M., Andersson S.G.E.;
RT "The louse-borne human pathogen Bartonella quintana is a genomic
RT derivative of the zoonotic agent Bartonella henselae.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).
DR EMBL; BX97700; CAF26485.1; -;
DR GO; GO:0004073; F:aspartate-semialdehyde dehydrogenase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR GO; GO:0009086; P:methionine biosynthesis; IEA.
DR GO; GO:0009088; P:threonine biosynthesis; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR005986; Asp_ADH_USGL.
DR InterPro; IPR000534; Semiald_dehydrog.
DR Pfam; PF01118; Semialdhyde_dh; 1.
DR Pfam; PF02774; Semialdhyde_dhC; 1.
DR PRINTS; PR01415; ANKYRIN.
DR TIGRFAMs; TIGR01296; asd_B; 1.
KW Complete proteome.
SQ SEQUENCE 343 AA; 37773 MW; CFA3322862A332B0 CRC64;
Query Match 43.1%; Score 47; DB 2; Length 343;
Best Local Similarity 47.6%; Pred. No. 28;
Matches 10; Conservative 3; Mismatches 4; Indels 4; Gaps 1;
QY 2 GYIQNYRCRGGD---SKVOE 18
Db 279 GYITPCTGDDTFISKRE 299
RESULT 26
Q50468 PRELIMINARY; PRT; 705 AA.
ID Q50468
AC Q50468
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Pks002a.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OC NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith D.R.;
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.

RA Robison K.;
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme family.
 CC
 DR EMBL; U00024; AAA50930.1; --
 DR HSSP; P08659; 1LCI.
 DR GO; GO:0003824; P: catalytic activity; IEA.
 DR GO; GO:0048037; F: cofactor binding; IEA.
 DR GO; GO:0008152; P: metabolism; IEA.
 DR InterPro; IPR009081; ACP like.
 DR InterPro; IPR000873; AMP-bind.
 DR InterPro; IPR006163; Phosphateth_bind.
 DR Pfam; PF00501; AMP-binding; 1.
 DR Pfam; PF00550; PP-binding; 1.
 DR PRINTS; PR00154; AMPBINDING.
 DR PROSITE; PS00075; ACP_DOMAIN; 1.
 SQ SEQUENCE 705 AA; 75169 MW; 9f9d4f500690bf5d CRC64;
 Query Match 42.7%; Score 46.5; DB 2; Length 705;
 Best Local Similarity 50.0%; Pred. No. 74;
 Matches 8; Conservative 5; Mismatches 2; Indels 1; Gaps 1;
 QY 1 EGYIONRCRGDDSKV 16
 :|:: ||||| |::|
 Db 378 DGWV-TYRCRADDTTEV 392

RESULT 27
 P96283
 ID P96283 PRELIMINARY; PRT; 705 AA.
 AC P96283; Q7D6D9;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE PROBABLE FATTY-ACID-CoA LIGASE FADD22 (FATTY-ACID-CoA SYNTHETASE)
 DE (FATTY-ACID-CoA SYNTHASE) (PC 6.2.1.-) (Substrate--CoA ligase).
 GN Name-fad22; OrderedLocusNames=WT3021, RV2948c;
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37Rv;
 RX MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
 RA Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,
 RA Tekala F., Badcock K., Basham D., Brown D., Chillingworth T.,
 RA Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
 RA Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
 RA Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
 RA Rogers J., Rutter S., Seeger K., Skelton S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence."
 RL Nature 393:537-544 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RX MEDLINE=22206494; PubMed=12218036;
 RX DOI=10.1126/JB.184.19.5479-5490.2002;
 RA Fieischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J.D., Deboy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,
 RA Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,
 RA Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.,
 RA Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
 RA Fraser C.M.;
 RA "Whole-genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains."
 RL J. Bacteriol. 184:5479-5490 (2002).
 CC -!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme family.
 CC
 DR EMBL; EX842581; CAB06101.1; --

DR EMBL; AB000516; AAK47347.1; --
 DR PIR; A70669; A70669.
 DR HSSP; P08659; 1LCI.
 DR TIGR; MT3021; --
 DR TubercuList; RV2948c; --
 DR GO; GO:0003824; P: catalytic activity; IEA.
 DR GO; GO:0048037; F: cofactor binding; IEA.
 DR GO; GO:0008152; P: metabolism; IEA.
 DR InterPro; IPR009081; ACP like.
 DR InterPro; IPR000873; AMP-bind.
 DR InterPro; IPR006163; Phosphateth_bind.
 DR Pfam; PF00501; AMP-binding; 1.
 DR Pfam; PF00550; PP-binding; 1.
 DR PRINTS; PR00154; AMPBINDING.
 DR PROSITE; PS00075; ACP_DOMAIN; 1.
 KW Ligase.
 SQ SEQUENCE 705 AA; 75197 MW; 600f2d0eabfddf1dc CRC64;
 Query Match 42.7%; Score 46.5; DB 2; Length 705;
 Best Local Similarity 50.0%; Pred. No. 74;
 Matches 8; Conservative 5; Mismatches 2; Indels 1; Gaps 1;
 QY 1 EGYIONRCRGDDSKV 16
 :|:: ||||| |::|
 Db 378 DGWV-TYRCRADDTTEV 392

RESULT 28
 Q7TXK7
 ID Q7TXK7 PRELIMINARY; PRT; 705 AA.
 AC Q7TXK7;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE PROBABLE FATTY-ACID-CoA LIGASE FADD22 (FATTY-ACID-CoA SYNTHETASE)
 DE (FATTY-ACID-CoA SYNTHASE) (EC 6.2.1.-).
 GN Name=fad22; OrderedLocusNames=MB2972c;
 OS Mycobacterium bovis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1765;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AF2122/97;
 RX MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
 RA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
 RA Pryor M., Duthoy S., Grondin S., Lacroix C., Mensepe C., Simon S.,
 RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
 RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
 RT "The complete genome sequence of Mycobacterium bovis."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).
 DR EMBL; BX248344; CAD96659.1; --
 DR GO; GO:0048037; F: cofactor binding; IEA.
 DR GO; GO:0008152; P: metabolism; IEA.
 DR InterPro; IPR009081; ACP like.
 DR InterPro; IPR000873; AMP-bind.
 DR InterPro; IPR006163; Phosphateth_bind.
 DR Pfam; PF00501; AMP-binding; 1.
 DR Pfam; PF00550; PP-binding; 1.
 DR PROSITE; PS00075; ACP_DOMAIN; 1.
 KW Complete proteome; Ligase.
 SQ SEQUENCE 705 AA; 75197 MW; 600f2d0eabfddf1dc CRC64;
 Query Match 42.7%; Score 46.5; DB 2; Length 705;
 Best Local Similarity 50.0%; Pred. No. 74;
 Matches 8; Conservative 5; Mismatches 2; Indels 1; Gaps 1;
 QY 1 EGYIONRCRGDDSKV 16
 :|:: ||||| |::|
 Db 378 DGWV-TYRCRADDTTEV 392

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RESULT 29
Q6CZY4      PRELIMINARY;      PRT;      130 AA.
AC Q6CZY4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 10S ribosomal subunit protein S8.
GN Name=rpsh; OrderedlocusNames=EC4017;
OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SCRI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S., Sebahia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmon G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
RA "Genome sequence of the enterobacterial phytopathogen Erwinia
RT carotovora subsp. atroseptica and characterization of virulence
RT factors."
RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
CC -!- SIMILARITY: Belongs to the S8P family of ribosomal proteins.
DR EMBL; BX950851; CAG76914.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; F:protein biosynthesis; IEA.
DR InterPro; IPR000630; Ribosomal S8.
DR Pfam; PF00410; Ribosomal S8; 1.
DR ProDom; PD001098; Ribosomal S8; 1.
DR PROSITE; PS00053; RIBOSOMAL_S8; 1.
KW Complete proteome; Ribonucleoprotein; Ribosomal protein.
SQ SEQUENCE 130 AA; 14211 MW; 5CBED0F565CD3A3C4 CRC64;

Query Match 42.2%; Score 46; DB 2; Length 130;
Best Local Similarity 44.4%; Pred. No. 14;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 EGYIYNYRCRGDSDSKVQE 18
Db |||:||||:|
43 EGYIEDFKIEGTPKPVLE 60

RESULT 30
Q7YU44      PRELIMINARY;      PRT;      340 AA.
AC Q7YU44;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE RE35739p.
GN ORFNames=CG11426;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dreanek D., Farfan D., Friese E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;

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RL Submitted (AUG-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BT009997; AAQ22466.1; -.
DR FlyBase; FBgn0037166; CG11426.
DR InterPro; IPR008934; AcPase_VanParase.
DR Pfam; PF01569; PAP2; 1.
DR SMART; SM00014; acidPPC; 1.
SQ SEQUENCE 340 AA; 37628 MW; 08FA16CDICE34636 CRC64;

Query Match 42.2%; Score 46; DB 2; Length 340;
Best Local Similarity 38.9%; Pred. No. 41;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 3 YIONVYRCRGDSDSKVQEAR 20
Db |||:||||:|
186 YNENYDCAGEGFTVEDVR 203

RESULT 31
Q9VNT9      PRELIMINARY;      PRT;      340 AA.
AC Q9VNT9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG11426-PA.
GN ORFNames=CG11426;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferriaz C., Ferreira S., Fleischmann W.,
RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
Science 287:2185-2195(2000).

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RN  SEQUENCE FROM N.A.
RP  MEDLINE=22426065; PubMed=12537568;
RA  Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA  Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA  George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.B.,
RA  Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA  Svirekas R., Tabor P.S., Wan K., Scapleton M., Sutton G.G., Venter C.,
RA  Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT  "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT  melanogaster euchromatic genome sequence.";
RL  Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN  [3]
RP  SEQUENCE FROM N.A.
RA  MEDLINE=22426070; PubMed=12537573;
RA  Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirekas R.,
RA  Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA  Ashburner M., Celniker S.E.;
RT  "The transposable elements of the Drosophila melanogaster euchromatin:
RT  a genomics perspective.";
RL  Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN  [4]
RP  SEQUENCE FROM N.A.
RA  MEDLINE=22426069; PubMed=12537572;
RA  Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA  Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA  Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA  Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA  Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
RA  Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA  Lewis S.E.;
RT  "Annotation of the Drosophila melanogaster euchromatic genome: a
RT  systematic review.";
RL  Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN  [5]
RP  SEQUENCE FROM N.A.
RG  FlyBase;
RL  Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN  [6]
RP  SEQUENCE FROM N.A.
RG  FlyBase;
RL  Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR  EMBL; A2003597; AAF51831.1; -.
DR  FlyBase; FBgn0037166; CG11426.
DR  InterPro; IPR008934; AcPase_VanParase.
DR  InterPro; IPR000326; Pesterase_PA_PTP.
DR  Pfam; PF01569; PAP2; 1.
DR  SMART; SM00014; acidppc; 1.
SQ  SEQUENCE 340 AA; 37654 MW; 18E77AA8008F2323 CRC64;

Query Match 42.2%; Score 46; DB 2; Length 340;
Best Local Similarity 38.9%; Pred. NO. 41;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 3 YIYRCRGDDSKVQEAR 20
DB 186 YMENYDCAGEGFTVEDVR 203

RESULT 32
Q73RYO PRELIMINARY; PRT; 776 AA.
AC Q73RYO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=WAP4298c;
OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1770;
RN [1]

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RP  SEQUENCE FROM N.A.
RC  STRAIN=K10;
RA  Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
RL  Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AE017242; AAS06848.1; -.
DR  GO; GO:0008152; P:metabolism; IEA.
DR  InterPro; IPR003673; CAIB_BAIF.
DR  Pfam; PF02515; CoA_transf_3; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 776 AA; 82189 MW; 38A4528FCSB0B4BB CRC64;

Query Match 42.2%; Score 46; DB 2; Length 776;
Best Local Similarity 80.0%; Pred. NO. 18+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 YRCRGDDSKV 16
DB 615 YRCRGDDAW 624

RESULT 33
Q95Z20 PRELIMINARY; PRT; 1325 AA.
ID Q95Z20;
AC Q95Z20;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein C09F9.3.
GN ORFNames=C09F9.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Bristol N2;
RX  MEDLINE=99069613; PubMed=9851916;
RA  none;
RT  "Genome sequence of the nematode C.elegans: A platform for
RT  investigating biology.";
RL  Science 282:2012-2018(1998).
RN [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Bristol N2;
RA  Smye R.;
RL  Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR  EMBL; Z81465; CAC42253.2; -.
DR  HSSP; O31465; 1MKT.
DR  WormBase; WBGene00007480; C09F9.3.
DR  WormPep; C09F9.3; CE36977.
DR  GO; GO:0004359; F:glutaminase activity; IEA.
DR  GO; GO:0006541; P:glutamine metabolism; IEA.
DR  InterPro; IPR002110; ANK.
DR  InterPro; IPR007043; Glutaminase.
DR  Pfam; PF00023; Ank; 4.
DR  Pfam; PF04960; Glutaminase; 2.
DR  SMART; SM00248; ANK; 4.
DR  PROSITE; PS50088; ANK_REPEAT; 2.
DR  PROSITE; PS50297; ANK_REPEAT_REGION; 2.
KW ANK repeat; Hypothetical protein.
SQ SEQUENCE 1325 AA; 150066 MW; D163D1D72D33BAC7 CRC64;

Query Match 42.2%; Score 46; DB 2; Length 1325;
Best Local Similarity 50.0%; Pred. NO. 1.8e+02;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 YIYRCRGDDSKVQES 18
DB 360 YMKYRCFPDSQVYE 375

RESULT 34
Q20683

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ID Q20683 PRELIMINARY; PRT; 179 AA.
AC Q20683;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein F52H3.5.
GN ORFNames=F52H3.5;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
[2]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Gardner A.E.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z66512; CAA91325.1; -.
DR PIR; T22521; T22521.
DR WormBase; WEGene0000947; F52H3.5.
DR WormPep; F52H3.5; CE03401.
DR InterPro; IPR001440; TPR.
DR InterPro; IPR008941; TPR-like.
DR Pfam; PF00515; TPR 1; 1.
DR SMART; SM00028; TPR; 3.
DR PROSITE; PS50005; TPR; 1.
DR PROSITE; PS50293; TPR_REGION; 1.
KW Hypothetical protein; Repeat; TPR repeat.
SQ SEQUENCE 179 AA; 19648 MW; 6FF899837C65A18F CRC64;

Query Match 41.7%; Score 45.5; DB 2; Length 179;
Best Local Similarity 45.0%; Pred. No. 24;
Matches 9; Conservative 3; Mismatches 5; Indels 3; Gaps 1;

QY 1 EGYQYQ---YRCRGDSDSKVQ 17
Db 116 QAYVQRASIYRLRGDDDKAR 135

RESULT 35
Q6XNK7 PRELIMINARY; PRT; 1086 AA.
AC Q6XNK7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE NAD dependent glutamate dehydrogenase (EC 1.4.1.2).
GN Name=gdhB;
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=162425;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=G001;
RA Kawaguchi T., Unkles S., Kinghorn J.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY223544; AAP9491.1; -.
DR GO; GO:0004352; F:glutamate dehydrogenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006096; GLFV dehydrog_C.
DR Pfam; PF0208; GLFV_dehydrog; 1.
KW Oxidoreductase.
SQ SEQUENCE 1086 AA; 122429 MW; AF619A4384CC665E CRC64;
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Query Match 41.7%; Score 45.5; DB 2; Length 1086;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 EGYQYQCRGDSKVDK 18
Db 947 QGFVQN-MCVGDDSDSVE 963

RESULT 36
Q7MYG5 PRELIMINARY; PRT; 130 AA.
AC Q7MYG5;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 30S ribosomal protein S14.
GN Name=rpS14; OrderedLocusNames=plu4712;
OS Photorhabdus luminescens (subsp. laumondii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=TT01;
RX MEDLINE=22957627; PubMed=14528314;
RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
RA Dassa E., Derose R., Derzelle S., Freysinet G., Gaudriault S.,
RA Medigue C., Lanois A., Powell K., Sigulier P., Vincent R., Wingate V.,
RA Zouline M., Glaser P., Boemare N., Danchin A., Kunst F.;
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens.";
RL Nat. Biotechnol. 21:1307-1313(2003).
CC -!- SIMILARITY: Belongs to the S8P family of ribosomal proteins.
DR EMBL; BX571874; CAE17084.1; -.
DR HSSP; P24319; IAN7.
DR PhotoList; plu4712; -.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR000630; Ribosomal_S8.
DR Pfam; PF00410; Ribosomal_S8; 1.
DR ProDom; PD001098; Ribosomal_S8; 1.
DR PROSITE; PS00053; RIBOSOMAL_S8; 1.
KW Complete proteome; Ribonucleoprotein; Ribosomal protein.
SQ SEQUENCE 130 AA; 14215 MW; 37DEE66209DEC1C CRC64;

Query Match 41.3%; Score 45; DB 2; Length 130;
Best Local Similarity 58.3%; Pred. No. 21;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EGYQYQCRGD 12
Db 43 EGYIEDYKIEGD 54

RESULT 37
Q7RA96 PRELIMINARY; PRT; 300 AA.
AC Q7RA96;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative yir4 protein.
GN Name=PY06606;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
```


RA	Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA	Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA	Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA	Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblum T.V.,
RA	Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA	Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA	Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA	van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA	Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA	Carucci D.J.;
RT	"Genome sequence and comparative analysis of the model rodent malaria
RT	parasite Plasmodium yoelii yoelii.";
RL	Nature 419:512-519(2002).
CC	-I- CAUTION: The sequence shown here is derived from an
CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC	preliminary data.
DR	EWEL; AABL01002257; EAA19850.1; --
DR	InterPro; IPR006477; Yir_bir_cir.
DR	Pfam; PF06022; Cir Bir Yir; 1.
DR	TIGRFRAMS; TIGR01590; yir-bir-cir_Pla; 1.
SEQ	SEQUENCE 300 AA; 34952 MW; 4DE5BBE02674502 CRC64;
Query Match	41.3%; Score 45; DB 2; Length 300;
Best Local Similarity	43.8%; Pred.No. 52;
Matches	7; Conservative 3; Mismatches 6; Indels 0; Gaps
Qy	. 1 EGYIQNYRCRGDDSKV 16
Dd	: : : :
Dd	26 DGVCDSYRCDSDFEKI 41
RESULT 38	.
Q7RCS6	PRELIMINARY; PRT; 304 AA.
ID	Q7RCS6
AC	Q7RCS6;
DT	01-MAR-2004 (TrEMBLrel. 26, Created)
DT	01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Putative yir4 protein (Fragment).
GN	Name=PY05701;
OS	Plasmodium yoelii yoelii.
OC	Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX	RNBI_TaxID=73239;
NC	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=17XNL;
RX	PubMed=12368865; DOI=10.1038/nature01099;
RA	Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA	Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA	Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA	Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblum T.V.,
RA	Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA	Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA	Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA	van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA	Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA	Carucci D.J.;
RT	"Genome sequence and comparative analysis of the model rodent malaria
RT	parasite Plasmodium yoelii yoelii.";
RL	Nature 419:512-519(2002).
CC	-I- CAUTION: The sequence shown here is derived from an
CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC	preliminary data.
DR	EWEL; AABL01001843; EAA17762.1; --
DR	InterPro; IPR006477; Yir_bir_cir.
DR	Pfam; PF06022; Cir Bir Yir; 1.
DR	TIGRFRAMS; TIGR01590; yir-bir-cir_Pla; 1.
FT	NON TER
FT	1 1
SEQ	SEQUENCE 304 AA; 35494 MW; 9705246F3263A36F CRC64;
Query Match	41.3%; Score 45; DB 2; Length 304;
Best Local Similarity	43.8%; Pred.No. 53;
Matches	7; Conservative 3; Mismatches 6; Indels 0; Gaps

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DR GO: GO:0006520; P:amino acid metabolism; IEA.
DR GO: GO:0009086; P:methionine biosynthesis; IEA.
DR GO: GO:0009088; P:threonine biosynthesis; IEA.
DR InterPro: IPR005986; Asp_ADH_USG1.
DR InterPro: IPR000534; Semiald dehydrog.
DR Pfam: PF01118; Semialdehyde_dh; 1.
DR Pfam: PF02774; Semialdehyde_dhC; 1.
DR TIGRFAMs: TIGR01296; asd B; 1.
SQ SEQUENCE 344 AA; 37431 MW; EA1FF2BA0F742760 CRC64;

Query Match 41.3%; Score 45; DB 2; Length 344;
Best Local Similarity 38.1%; Pred. No. 61;
Matches 8; Conservative 5; Mismatches 4; Indels 4; Gaps 1;

QY 2 GYIQNYRCRGDD----SKVQE 18
Db 279 GYVTPYECAGDATYISRIRE 299

RESULT 41
Q92KY2 PRELIMINARY; PRT; 344 AA.
AC Q92KY2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PUTATIVE ASPARTATE-SEMIALDEHYDE DEHYDROGENASE PROTEIN (EC
DE 1.2.1.11).
GN CRFNames=Smc04410;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
ON NCBI_TaxID=382;
RX [1] SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398;
RA Capela D., Barloy-Hubler J., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kias E., Lelaure V., Masuy D.,
RA Fohl T., Portetelle D., Puhler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;
RA "Analysis of the chromosome sequence of the legume symbiont
RT - Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882 (2001).
DR EMBL: AL591793; CAC47895.1; -.
DR HSSP: P44801; INWC.
DR GO: GO:0004073; F:aspartate-semialdehyde dehydrogenase activity; IEA.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0006520; P:amino acid metabolism; IEA.
DR GO: GO:0009086; P:methionine biosynthesis; IEA.
DR GO: GO:0009088; P:threonine biosynthesis; IEA.
DR InterPro: IPR005986; Asp_ADH_USG1.
DR InterPro: IPR000534; Semiald dehydrog.
DR Pfam: PF01118; Semialdehyde_dh; 1.
DR Pfam: PF02774; Semialdehyde_dhC; 1.
DR TIGRFAMs: TIGR01296; asd B; 1.
DR Complete proteome; Oxidoreductase.
SQ SEQUENCE 344 AA; 37573 MW; 0C8CF8F08B8D7A84 CRC64;

Query Match 41.3%; Score 45; DB 2; Length 344;
Best Local Similarity 38.1%; Pred. No. 61;
Matches 8; Conservative 5; Mismatches 4; Indels 4; Gaps 1;

QY 2 GYIQNYRCRGDD----SKVQE 18
Db 279 GYVTPYECAGDATYISRIRE 299

RESULT 42
Q96180 PRELIMINARY; PRT; 505 AA.
ID Q96180
AC Q96180;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PRSS12 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RX [1] SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RX [2] SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC007761; AAH07761.1; -.
DR HSSP: O08380; 1BY2.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005507; F:copper ion binding; IEA.
DR GO: GO:0004720; F:protein-lysine 6-oxidase activity; IEA.
DR GO: GO:0005044; F:scavenger receptor activity; IEA.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR001695; Lysyl oxidase.
DR InterPro: IPR001190; Strc_Receptor.
DR Pfam: PF00051; Kringle; 1.
DR Pfam: PF00530; SRCR; 3.
DR PRINTS: PR00018; KRINGLE.
DR PRINTS: PR00258; SPERACTRCPTR.
DR ProDom: PD000395; Kringle; 1.
DR ProDom: PD013887; Lysyl oxidase; 1.
DR SMART: SM00130; KR; 1.
DR SMART: SM00202; SR; 3.
DR PROSITE: PS00021; KRINGLE_1; 1.
DR PROSITE: PS00070; KRINGLE_2; 1.
DR PROSITE: PS00420; SRCR_1; 2.
DR PROSITE: PS00287; SRCR_2; 3.
DR Kringle.
KW Kringle.
SQ SEQUENCE 505 AA; 55658 MW; 7FF863A6246226BD CRC64;

Query Match 41.3%; Score 45; DB 2; Length 505;
Best Local Similarity 50.0%; Pred. No. 92;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 YIQNYRCRGDDSKV 16
Db 233 YWSNVRCRGDEENI 246

RESULT 43
P73606 PRELIMINARY; PRT; 607 AA.
ID P73606

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AC P73606;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE S11855 protein.
GN OrderedLocusNames=slr1855;
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=11148;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC6803;
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugiyura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL; D90908; BAA17650.1; -.
DR PIR; S77092; S77092.
DR InterPro; IPR008928; Glyco_trans_6hp.
KW Complete proteome.
SQ SEQUENCE 607 AA; 70003 MW; 873842F37B6AB0F3 CRC64;

Query Match 41.3%; Score 45; DB 2; Length 607;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 GYIQNYRCRGDSDKVOEA 19
DB 241 GPIQTYRCGTGDRILHDA 258

RESULT 44
NETR HUMAN
ID NETR HUMAN STANDARD; PRT; 875 AA.
AC P56730; Q9UP16;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Neurotysin precursor (SC 3.4.21.-) (Motopsin) (Leydin).
GN Name=PRSS12;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98201705; PubMed=9540828; DOI=10.1016/S0167-4781(97)00205-4;
RA Proba K., Gschwend T.P., Sonderegger P.;
RT "Cloning and sequencing of the cDNA encoding human neurotysin.";
RL Biochim. Biophys. Acta 1396:143-147(1998).
RN [2]
RP SEQUENCE OF 615-875 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=99203523; PubMed=101030556;
RA Poorafshar M., Hellman L.;
RT "Cloning and structural analysis of leydin, a novel human serine
RT protease expressed by the Leydig cells of the testis.";
RL Eur. J. Biochem. 261:244-250(1999).
RN [3]
RP DISEASE.
RX PubMed=12459588; DOI=10.1126/science.1076521;
RA Molinari F., Rio M., Meskenaitė V., Encha-Razavi F., Auge J., Bacq D.,
RA Briault S., Vekemans M., Munnich A., Attie-Bitach T., Sonderegger P.,
RA Colleaux L.;
RT "Truncating neurotysin mutation in autosomal recessive nonsyndromic
RT mental retardation.";
```

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Science 298:1779-1781(2002).
-!- FUNCTION: Plays a role in neuronal plasticity and the proteolytic
CC action may subserve structural reorganizations associated with
CC learning and memory operations (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Brian and Leydig cells of the testis.
CC -!- DISEASE: Defects in PRSS12 are a cause of autosomal recessive
CC nonsyndromic mental retardation [MIM:249500]. Mental retardation
CC is a mental disorder characterized by significantly subaverage
CC general intellectual functioning associated with impairments in
CC adaptive behavior and manifested during the developmental
CC period.
-!- SIMILARITY: Belongs to the peptidase S1 family.
CC -!- SIMILARITY: Contains 1 kringle domain.
CC -!- SIMILARITY: Contains 4 SRCR domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AJ001531; CAA04816.1; -.
DR EMBL; AF077298; AAD25919.1; -.
DR HSP; P00760; IEZX.
DR MEROPS; S01.237; -.
DR Genew; HGNC:9477; PRSS12.
DR MIM; 606709; -.
DR MIM; 249500; -.
DR GO; GO:0008236; F:serine-type peptidase activity; TAS.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001114; Peptidase_S1A.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF00051; Kringle; 1.
DR Pfam; PF00530; SRCR; 4.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00258; SPERACTRCPTR.
DR ProDom; PD000395; Kringle; 1.
DR ProDom; PD013887; Lysyl_oxidase; 2.
DR SMART; SM00130; KR; 1.
DR SMART; SM00202; SR; 4.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00420; SRCR_1; 3.
DR PROSITE; PS0287; SRCR_2; 4.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Glycoprotein; Hydrolase; Kringle; Repeat; Serine protease; Signal.
FT SIGNAL 1 20
FT CHAIN 21 875 Neurotysin.
FT DOMAIN 23 92 Pro-rich.
FT DOMAIN 93 165 Kringle.
FT DOMAIN 170 271 SRCR 1.
FT DOMAIN 280 381 SRCR 2.
FT DOMAIN 387 487 SRCR 3.
FT DOMAIN 500 601 SRCR 4.
FT DOMAIN 619 875 Serine protease.
FT SITE 619 630 Zymogen activation region.
FT ACT_SITE 676 676 Reactive bond (Potential).
FT ACT_SITE 726 726 Charge relay system.
FT ACT_SITE 825 825 Charge relay system.
FT DISULFID 619 750 Potential.
FT CARBOHYD 26 26 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 683 683 N-linked (GlcNAc...) (Potential).
FT CONFLICT 683 683 A -> V (in Ref. 2).
```

FT CONFLICT 701 701 E -> V (in Ref. 2).
 FT CONFLICT 839 841 VVY -> AAL (in Ref. 2).
 SQ SEQUENCE 875 AA; 97011 MW; B66EC946DC208DC8 CRC64;

Query Match 41.3%; Score 45; DB 1; Length 875;
 Best Local Similarity 50.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 YIQNYRCRGDDSKV 16
 | | | | | :
 Db 233 YWSNVRCDDENI 246

RESULT 45

Q9BS83 ID Q9BS83 PRELIMINARY; PRT; 63 AA.
 AC Q9BS83
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE NMT2 protein (Fragment).
 GN Name=NMT2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skaleka U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC005232; AAH05232.1; -.
 DR HSSP; P30418; 11YK.
 DR GO; GO:0004379; F:glycylpeptide N-tetradecanoyltransferase ac. . .; IEA.
 DR GO; GO:0006499; P:N-terminal protein myristoylation; IEA.
 DR InterPro; IPR000903; Myristoyl trans.
 DR Pfam; PF02799; NMT C; 1.
 DR PROSITE; PS00976; NMT 2; UNKNOWN_1.
 FT NON TER 1
 SQ SEQUENCE 63 AA; 7126 MW; FBDG31797497830 CRC64;

Query Match 40.4%; Score 44; DB 2; Length 63;
 Best Local Similarity 53.8%; Pred. No. 14;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 YIQNYRCRGDDSK 15
 | : | | | | :
 Db 29 YLYNRCFGTDSE 41

RESULT 46
 Q8Q0W8 ID Q8Q0W8 PRELIMINARY; PRT; 121 AA.
 AC Q8Q0W8
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE RNA signal recognition particle 4.5S RNA.
 GN OrderedLocusNames=MM0012;
 OS Methanosarcina mazei (Methanosarcina frisia).
 OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
 OC Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2209;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Goei / GoI / ATCC BAA-199 / DSM 3647 / OCM 88;
 RX MEDLINE=22120827; PubMed=12125824;
 RA Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
 RA Martinez-Arias R., Henne A., Wietzer A., Baeumer S., Jacobi C.,
 RA Brueggemann H., Lienard T., Christmann A., Boencke M., Steckel S.,
 RA Bhattacharya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
 RA Fritz H.-J., Gottschalk G.;
 RT "The genome of Methanosarcina mazei: evidence for lateral gene
 transfer between Bacteria and Archaea.";
 RL J. Mol. Microbiol. Biotechnol. 4:453-461 (2002).
 DR EMBL; AE013220; AAM29708.1; -.
 DR InterPro; IPR009874; DUF1428.
 DR Pfam; PF07237; DUF1428; 1.
 KW Complete proteome.
 SQ SEQUENCE 121 AA; 14293 MW; 7895D708A18368EE CRC64;
 Query Match 40.4%; Score 44; DB 2; Length 121;
 Best Local Similarity 41.2%; Pred. No. 28;
 Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 GYIQNYRCRGDDSKVQE 18
 | : | | | | :
 Db 35 GALEYYECIGDDLDIEE 51

RESULT 47

Q897T4 ID Q897T4 PRELIMINARY; PRT; 172 AA.
 AC Q897T4
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative acetyltransferase.
 GN OrderedLocusNames=CTC00643;
 OS Clostridium tetani.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Massachusetts / E88;
 RX MEDLINE=22457253; PubMed=1255129; DOI=10.1073/pnas.0335853100;
 RA Brueggemann H., Baeumer S., Fricke W.F., Wietzer A., Liesegang H.,
 RA Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
 RA Gottschalk G.;
 RT "The genome sequence of Clostridium tetani, the causative agent of
 tetanus disease.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321 (2003).
 DR EMBL; AE015938; AA035252.1; -.
 DR GO; GO:0008080; F:N-acetyltransferase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR InterPro; IPR000182; GCN5acetyl trans.
 DR Pfam; PF00583; Acetyltransf 1; 1.
 KW Complete proteome; Transferase.
 SQ SEQUENCE 172 AA; 20351 MW; B645F6A57C0F1BF9 CRC64;
 Query Match 40.4%; Score 44; DB 2; Length 172;

```
Best Local Similarity 37.9%; Pred. No. 42;
Matches 11; Conservative 4; Mismatches 2; Indels 12; Gaps 2;

Qy 1 EGYI-----QNYRCRG-----DDSKVQ 17
Db 97 DGYIAGIFVDSNYRCQGIGLALDEAKQ 125

RESULT 48
Q8SSM8 PRELIMINARY; PRT; 338 AA.
AC Q8SSM8
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2004 (TrEMBLrel. 21, Last sequence update)
DE FRUCTOSE-BISPHOSPHATE ALDOLASE B.
GN Name=ECU01.0240;
OS Encephalitozoon cuniculi GB-M1.
OC Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
OX NCBI_TaxID=284813;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RC MEDLINE=21576510; PubMed=11719806; DOI=10.1038/35106579;
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thonarat F.,
RA Prentier G., Barbe V., Peyrecaillade E., Brottier P., Wincker P.,
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA Weissenbach J., Vivares C.P.;
RT "Genome sequence and gene compaction of the eukaryote parasite
RT Encephalitozoon cuniculi.";
RL Nature 414:450-453(2001).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RC Genoscope;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL391737; CAP24894.1; -.
DR HSSP; P05062; 1005.
DR GO; GO:0004332; P:fructose-bisphosphate aldolase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR000741; Aldolase I.
DR Pfam; PF00274; Glycolytic; 1.
SQ SEQUENCE 338 AA; 37916 MW; 2158A1DAE05A7AF9 CRC64;

Query Match 40.4%; Score 44; DB 2; Length 338;
Best Local Similarity 40.0%; Pred. No. 87;
Matches 8; Conservative 7; Mismatches 3; Indels 2; Gaps 1;

Qy 1 EGYIQNYRCRGDDSKVQEAR 20
Db 299 DGVLETW--RGDDSNIEEAQ 316

RESULT 49
DIAC_HUMAN STANDARD; PRT; 385 AA.
AC Q01459;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Di-N-acetylchitinobiase precursor (EC 3.2.1.-).
GN Name=CTBS; Synonyms=CTB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RC MEDLINE=92406917; PubMed=1527079;
RA Fisher K.J., Aronson N.N. Jr.;
RT "cloning and expression of the cDNA sequence encoding the lysosomal
RT glycosidase di-N-acetylchitinobiase.";
```

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=mx FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Adds a myristoyl group to the N-terminal glycine residue
CC of certain cellular proteins (By similarity).
CC -I- CATALYTIC ACTIVITY: Tetradecanoyl-CoA + glycyl-peptide = CoA + N-
CC tetradecanoylglycyl-peptide.
CC -I- SIMILARITY: Belongs to the NMT family.
DR EMBL; BC037647; AAH37647.1; -.
DR HSSP; P30418; 1NMT.
DR MGD; MGI:1202298; Nmt2.
DR GO; GO:0005737; C:cytoplasm; TAS.
DR GO; GO:0004379; F:glycylpeptide N-tetradecanoyltransferase ac. . .; TAS.
DR GO; GO:0006499; P:N-terminal protein myristoylation; TAS.
DR InterPro; IPR000903; Myristoyl_trans.
DR Pfam; PF01233; NMT; 1.
DR Pfam; PF02799; NMT_C; 1.
DR PROSITE; PS00975; NMT_1; 1.
DR PROSITE; PS00976; NMT_2; UNKNOWN_1.
KW Acyltransferase; Transferase.
SQ * SEQUENCE 485 AA; 56537 MW; E4081964FCB3E56E CRC64;

Query Match 40.4%; Score 44; DB 2; Length 485;
Best Local Similarity 53.8%; Pred. NO. 1.3e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 YIQNYRCRGDQSK 15
|: ||| |:
Db 466 YLYNWRCPGTDE 478

Search completed: September 7, 2005, 19:57:12
Job time : 86.2326 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 7, 2005, 19:49:10 ; Search time 15.3488 Seconds
(without alignments)
125.373 Million cell updates/sec

Title: US-10-812-238B-2

Perfect score: 109

Sequence: 1 EGYIQNYRCRGDDSKVQEAR 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

1: PIR 79:*

2: Pirl:*

3: Pirl:*

4: Pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	59.6	325	2 S66668	hydrogen peroxide-
2	52	47.7	504	2 C64398	hypothetical prote
3	51	46.8	303	2 T29321	hypothetical prote
4	46.5	42.7	705	2 A70669	probable acid-CoA
5	46	42.2	518	2 T19133	hypothetical prote
6	46	42.2	564	2 T19132	hypothetical prote
7	46	42.2	873	2 T19131	hypothetical prote
8	45.5	41.7	179	2 T22521	hypothetical prote
9	45	41.3	607	2 S77092	hypothetical prote
10	44	40.4	395	2 A44102	di-N-acetylchitobi
11	43	39.4	274	2 T32736	hypothetical prote
12	43	39.4	319	2 AE2823	conserved hypothet
13	43	39.4	341	2 T16951	hypothetical prote
14	43	39.4	369	2 D97601	hypothetical prote
15	43	39.4	505	2 A55923	KOR4 protein - yea
16	43	39.4	542	2 T10245	glutamyl-tRNA redu
17	43	39.4	565	2 G89813	DNA polymerase III
18	43	39.4	1150	2 T18303	DNA binding regula
19	43	39.4	1331	2 S05011	calcium channel al
20	43	39.4	2166	2 S11339	calcium channel pr
21	43	39.4	2171	2 S05054	calcium channel al
22	42	38.5	130	2 AH0027	30S ribosomal prot
23	42	38.5	182	2 S28311	hypothetical prote
24	42	38.5	513	2 B87484	anthranilate synth
25	42	38.5	731	2 T29129	probable ATP/GTP b
26	42	38.5	957	2 A84089	hypothetical prote
27	42	38.5	1825	2 C88400	protein H19M22.1 [
28	42	38.5	1825	2 T32828	hypothetical prote
29	42	38.5	1994	2 D86452	protein F6N18.13 [

30	41.5	38.1	325	2 B81364	probable periplasm
31	41	37.6	130	2 C84989	30S ribosomal prot
32	41	37.6	238	2 T11718	hypothetical prote
33	41	37.6	721	2 H82528	L-ascorbate oxidase
34	41	37.6	752	1 P1IVBC	RNA-directed RNA p
35	41	37.6	752	1 P1IVBL	RNA-directed RNA p
36	41	37.6	752	1 P1IVBM	RNA-directed RNA p
37	40.5	37.2	302	2 H83159	conserved hypothet
38	40.5	37.2	373	2 FW0042	activin - fruit fl
39	40.5	37.2	507	2 AD3382	ABC transporter-as
40	40	36.7	132	2 E71356	probable ribosomal
41	40	36.7	150	2 G83840	ferric uptake regu
42	40	36.7	252	2 A48904	aminoglycoside ade
43	40	36.7	290	2 E85529	transcription regu
44	40	36.7	315	2 A90679	mhp operon transcr
45	40	36.7	315	2 B64762	nicotinate phospho
46	40	36.7	400	1 A39130	nicotinate phospho
47	40	36.7	400	1 JU0756	nicotinate phospho
48	40	36.7	400	1 A06617	nicotinate phospho
49	40	36.7	400	2 F90755	nicotinate phospho
50	40	36.7	400	2 D85619	nicotinate phospho
51	40	36.7	422	2 S34199	polysaccharuronase
52	40	36.7	435	2 T32195	hypothetical prote
53	40	36.7	465	2 T05734	glutamyl-tRNA redu
54	40	36.7	471	2 S03110	hypothetical prote
55	40	36.7	528	2 T05732	probable glutamyl-
56	40	36.7	530	2 S65773	glutamyl-tRNA redu
57	40	36.7	530	2 G86233	hypothetical prote
58	40	36.7	577	2 T18646	hypothetical prote
59	40	36.7	587	2 S12805	envelysin (EC 3.4.
60	40	36.7	587	2 S41409	envelysin (EC 3.4.
61	40	36.7	644	2 B72559	probable arginyl-t
62	40	36.7	730	2 JH0798	fasciclin IV precu
63	40	36.7	757	1 A60008	RNA-directed RNA p
64	40	36.7	757	1 B60011	RNA-directed RNA p
65	40	36.7	757	1 P1IV61	RNA-directed RNA p
66	40	36.7	757	1 P1IV33	RNA-directed RNA p
67	40	36.7	757	1 P1IV34	RNA-directed RNA p
68	40	36.7	757	1 P1IV68	RNA-directed RNA p
69	40	36.7	757	2 S06212	RNA-directed RNA p
70	40	36.7	924	2 S34926	hypothetical prote
71	40	36.7	2212	2 T28157	erythrocyte membra
72	40	36.7	2238	1 RRVUBY	genome polyprotein
73	40	36.7	2847	2 T28161	hypothetical prote
74	39.5	36.2	348	2 T16794	hypothetical prote
75	39	35.8	168	2 C83505	probable outer mem
76	39	35.8	185	2 H87107	ribosome recycling
77	39	35.8	191	2 AG2916	conserved hypothet
78	39	35.8	235	2 B97691	phbF protein (AF02
79	39	35.8	240	2 S65218	hypothetical prote
80	39	35.8	253	2 H87134	3-oxoacyl-[ACP] re
81	39	35.8	280	2 T43011	suppressor protein
82	39	35.8	288	2 E97864	hypothetical prote
83	39	35.8	297	2 C97192	uncharacterized pr
84	39	35.8	301	2 B64189	glycine cleavage s
85	39	35.8	344	2 T05437	hypothetical prote
86	39	35.8	348	2 H85256	hypothetical prote
87	39	35.8	376	2 T32837	hypothetical prote
88	39	35.8	393	2 A75079	hypothetical prote
89	39	35.8	394	2 S77272	hypothetical prote
90	39	35.8	430	2 S75313	serine-tRNA ligase
91	39	35.8	462	2 AH1130	glutamate decarbox
92	39	35.8	470	2 E72376	hypothetical prote
93	39	35.8	521	2 T18896	glypican 1 precurs
94	39	35.8	543	2 E96616	hypothetical prote
95	39	35.8	552	2 T10186	glutamyl-tRNA redu
96	39	35.8	653	2 G96675	hypothetical prote
97	39	35.8	654	2 T24168	hypothetical prote
98	39	35.8	662	2 T41442	omnipotent nonsense
99	39	35.8	662	2 T51948	omnipotent nonsense
100	39	35.8	662	2 I37892	IL12 receptor comp
101	39	35.8	776	2 T09938	hypothetical prote
102	39	35.8	801	2 A99862	Na+/H+ antiporter

103	39	35.8	917	2	I48950	telencephalin prec	176	37	33.9	92	2	G90850	hypothetical prote
104	39	35.8	1162	2	T18199	reverse transcript	177	37	33.9	130	1	R3EC8	ribosomal protein
105	39	35.8	1267	1	MXR31	lambda 3 protein -	178	37	33.9	130	2	AG1007	30S ribosomal chai
106	39	35.8	1267	1	MXR32	lambda 3 protein -	179	37	33.9	130	2	C91150	30S ribosomal subu
107	39	35.8	1267	1	MXR33	lambda 3 protein -	180	37	33.9	130	2	C91150	30S ribosomal subu
108	39	35.8	1268	2	T31420	C-terminal domain-	181	37	33.9	153	2	B83595	transcription regu
109	39	35.8	1403	2	S64142	hypothetical prote	182	37	33.9	158	2	B83365	transcription elon
110	39	35.8	1603	2	T24098	hypothetical prote	183	37	33.9	158	2	A80426	transcription regu
111	39	35.8	2204	1	RRZNV	genome polyprotein	184	37	33.9	159	2	A82219	c-8 sterol isomera
112	39	35.8	2493	2	S45734	probable membrane	185	37	33.9	219	2	T38129	reverse transcript
113	39	35.8	3228	2	T21381	hypothetical prote	186	37	33.9	246	2	I50209	probable membrane
114	39	35.8	9376	2	T14593	syngomycin synth	187	37	33.9	249	2	AB0537	periplasmic fibrin
115	38.5	35.3	448	2	S39348	26S ATP/ubiquitin	188	37	33.9	257	2	AH0859	structural protein
116	38.5	35.3	489	2	C87480	conserved hypotet	189	37	33.9	281	2	S44052	lyophospholipase
117	38.5	35.3	662	2	T18233	probable transcript	190	37	33.9	324	2	H86244	transcription regu
118	38.5	35.3	707	2	F89255	probable acyl-CoA	191	37	33.9	329	2	AH2127	probable pectinest
119	38.5	35.3	1287	2	T42658	hypothetical prote	192	37	33.9	352	2	C84603	probable pectinest
120	38	34.9	97	2	A82158	hypothetical prote	193	37	33.9	359	2	AH3465	oxidoreductase (BC
121	38	34.9	129	2	A89002	hypothetical prote	194	37	33.9	400	2	S46358	protein kinase (BC
122	38	34.9	160	2	A89809	hypothetical prote	195	37	33.9	402	1	F48552	protein kinase (BC
123	38	34.9	162	2	F82084	hypothetical prote	196	37	33.9	434	2	F69081	sensory transducti
124	38	34.9	172	2	F81439	probable 2-demethy	197	37	33.9	435	2	A46206	voltage-gated sodi
125	38	34.9	203	2	S64863	translation initia	198	37	33.9	443	2	H87911	protein B0205.4 [i
126	38	34.9	250	2	AC0630	probable membrane	199	37	33.9	450	2	H81338	probable sugar tra
127	38	34.9	248	2	AC0630	response regulator	200	37	33.9	452	2	G90072	hypothetical prote
128	38	34.9	258	2	T21959	vacJ lipoprotein h	201	37	33.9	486	2	F71825	replicative DNA he
129	38	34.9	303	2	G95169	hypothetical prote	202	37	33.9	488	2	B64690	replicative DNA he
130	38	34.9	303	2	G98035	thioredoxin reduct	203	37	33.9	497	2	B97555	hypothetical prote
131	38	34.9	326	2	A97259	thioredoxin-disulf	204	37	33.9	497	2	A02775	funarate hydratase
132	38	34.9	336	2	T31249	mannose-6 phosphate	205	37	33.9	502	2	S38139	lasi protein - yea
133	38	34.9	345	2	B83260	hypothetical prote	206	37	33.9	509	2	S18872	legumin-like stora
134	38	34.9	346	2	T49085	probable transcript	207	37	33.9	514	2	T00934	probable cytochrom
135	38	34.9	389	2	T27085	hypothetical prote	208	37	33.9	559	2	T48041	hypothetical prote
136	38	34.9	405	2	S42371	hypothetical prote	209	37	33.9	562	2	AF0852	secretory protein
137	38	34.9	408	2	AF2118	hypothetical prote	210	37	33.9	563	2	S54420	invasion protein i
138	38	34.9	420	2	T21960	hypothetical prote	211	37	33.9	712	2	A47718	reverse transcript
139	38	34.9	423	2	E69052	hypothetical prote	212	37	33.9	723	2	B82353	DNA helicase II VC
140	38	34.9	432	2	C85087	conserved hypotet	213	37	33.9	757	2	T51428	hypothetical prote
141	38	34.9	449	2	F83627	hypothetical prote	214	37	33.9	796	2	B88029	protein F46F5.11 [
142	38	34.9	455	2	E83332	hypothetical prote	215	37	33.9	824	2	T10615	hypothetical prote
143	38	34.9	482	2	H71400	toluate 1,2-dioxyg	216	37	33.9	918	2	E82486	hypothetical prote
144	38	34.9	508	2	T47484	hypothetical prote	217	37	33.9	985	2	B84489	proteinase VCA0223
145	38	34.9	511	2	G90455	neopullulanase - S	218	37	33.9	988	2	F86316	hypothetical prote
146	38	34.9	516	2	S14694	acid phosphatase,	219	37	33.9	1030	2	JC6027	protein T10022.13
147	38	34.9	533	2	T13607	hypothetical prote	220	37	33.9	1038	2	F96763	115K outer membran
148	38	34.9	544	2	C86405	hypothetical prote	221	37	33.9	1237	2	T14633	hypothetical prote
149	38	34.9	563	2	AG2923	probable sphingos	222	37	33.9	1263	2	T15496	hypothetical prote
150	38	34.9	563	2	G97697	conserved hypotet	223	37	33.9	1341	2	T18301	latrophilin-2, spl
151	38	34.9	572	1	VGNZBA	hypothetical prote	224	37	33.9	1354	2	T18375	latrophilin-2 (spl
152	38	34.9	671	2	AC1407	cell fusion glycop	225	37	33.9	1356	2	T18367	latrophilin-2, spl
153	38	34.9	671	2	AC1407	transketolase homo	226	37	33.9	1369	2	T18379	latrophilin-2 (spl
154	38	34.9	698	2	AC1783	transketolase homo	227	37	33.9	1384	2	T18366	latrophilin-2, spl
155	38	34.9	718	1	A54796	regulatory protein	228	37	33.9	1397	2	T18377	latrophilin-2 (spl
156	38	34.9	837	2	A42112	DNA topoisomerase	229	37	33.9	1420	2	T17158	latrophilin-2 (spl
157	38	34.9	883	2	T49781	mucin-like peptide	230	37	33.9	1435	2	T18381	latrophilin-2 (spl
158	38	34.9	1071	2	E85343	related to mutanas	231	37	33.9	1450	2	T18380	latrophilin-2 (spl
159	38	34.9	1071	2	T51224	hypothetical prote	232	37	33.9	1452	2	T18385	latrophilin-2 (spl
160	38	34.9	1289	2	AB2217	related to small s	233	37	33.9	1463	2	T17158	CL2AB protein - ra
161	38	34.9	1494	2	T13798	hypothetical prote	234	37	33.9	1463	2	T18387	latrophilin-2 (spl
162	38	34.9	1520	2	A81731	hypothetical prote	235	37	33.9	1465	2	T18383	latrophilin-2 (spl
163	38	34.9	1763	2	T19183	polymorphic membra	236	37	33.9	1478	2	T18388	CL2AB protein - ra
164	38	34.9	1769	2	T19184	hypothetical prote	237	37	33.9	1478	2	T17157	latrophilin-2 (spl
165	38	34.9	1812	2	I49350	hypothetical prote	238	37	33.9	1487	2	T18386	CL2AA protein - ra
166	38	34.9	4957	2	T03455	breast/ovarian can	239	37	33.9	1463	2	T17159	latrophilin-2 (spl
167	38	34.9	5262	2	T03454	ALR protein - huma	240	37	33.9	1465	2	T17159	CL2AC protein - ra
168	37.5	34.4	255	2	D86752	ALR protein - huma	241	37	33.9	1465	2	T17160	latrophilin-2 (spl
169	37.5	34.4	269	2	AC0727	prophage p12 prote	242	37	33.9	1478	2	T18388	CL2BA protein - ra
170	37.5	34.4	277	1	MN1H32	32K nonstructural	243	37	33.9	1478	2	T17185	CL2BC protein - ra
171	37.5	34.4	421	2	C95880	probable protein [244	37	33.9	1552	2	T14324	alpha-latrototoxin r
172	37.5	34.4	421	2	A83139	hypothetical prote	245	37	33.9	1658	2	T05408	hypothetical prote
173	37.5	34.4	503	2	T46852	anthranilate synth	246	37	33.9	1658	2	T42642	phosphoinoside 3
174	37.5	34.4	888	2	H88085	protein T11f1.8 [i	247	37	33.9	1694	2	JQ1896	hypothetical 191.1
175	37.5	34.4	2153	2	T14893	scavenger receptor	248	37	33.9	1984	2	A44396	p-type cation tran

249	37	33.9	2523	2	T18477	hypothetical prote	322	36	33.0	484	2	E84254	hypothetical prote
250	36.5	33.5	174	2	A10618	conserved S-adenosyl	323	36	33.0	487	2	AD3643	adhesin aidA-1 [lm
251	36.5	33.0	269	2	S49049	probable S-adenosyl	324	36	33.0	488	1	EXHU	coagulation factor
252	36.5	33.5	269	2	D90945	probable enzyme [i	325	36	33.0	491	2	E87452	ankyrin-related pr
253	36.5	33.5	269	2	G85793	probable enzyme ye	326	36	33.0	527	2	T22867	hypothetical prote
254	36.5	33.5	351	1	SAVZVV	surface antigen pr	327	36	33.0	535	2	T04402	probable glutamyl-
255	36.5	33.5	351	1	SAVZWR	surface antigen pr	328	36	33.0	540	2	S76869	hypothetical prote
256	36.5	33.5	353	1	SAVZVC	surface antigen pr	329	36	33.0	554	2	B85072	hypothetical prote
257	36.5	33.5	354	2	T46877	B20R protein - var	330	36	33.0	574	1	VGNZAR	cell fusion glycop
258	36.5	33.5	354	2	T28616	hypothetical prote	331	36	33.0	574	1	VGNZAR	cell fusion glycop
259	36.5	33.5	355	2	D72174	D9R protein - vari	332	36	33.0	574	1	VGNZHB	cell fusion glycop
260	36.5	33.5	375	2	S62606	semenciotin - mous	333	36	33.0	574	1	VGNZL	cell fusion glycop
261	36.5	33.5	427	2	T14237	hypothetical prote	334	36	33.0	574	2	B28929	cell fusion glycop
262	36.5	33.5	489	2	S66564	acetyl CoA carboxy	335	36	33.0	574	2	S37254	cell fusion protei
263	36.5	33.5	613	2	T24662	hypothetical prote	336	36	33.0	587	2	C71433	probable membrane
264	36.5	33.5	638	2	T24661	hypothetical prote	337	36	33.0	601	2	T21329	hypothetical prote
265	36.5	33.5	878	2	F64425	valine-tRNA ligase	338	36	33.0	602	1	S46676	probable phosphoe
266	36.5	33.5	1022	2	T24663	hypothetical prote	339	36	33.0	660	2	T20569	hypothetical prote
267	36.5	33.5	1143	2	S46122	SNF2 protein homol	340	36	33.0	683	2	S65002	acetate-CoA ligase
268	36.5	33.5	1339	2	JCS508	DNA-directed DNA p	341	36	33.0	705	1	I39759	serine/threonine-s
269	36	33.0	36	2	A81164	hypothetical prote	342	36	33.0	710	1	S70965	serine/threonine-s
270	36	33.0	84	1	WMBPWB	gene p protein - p	343	36	33.0	733	2	T04070	hypothetical prote
271	36	33.0	87	2	JQ1683	UL49A protein - hu	344	36	33.0	740	2	AC0119	hypothetical prote
272	36	33.0	98	2	F70769	hypothetical prote	345	36	33.0	742	2	E84285	hypothetical prote
273	36	33.0	111	2	C71401	hypothetical prote	346	36	33.0	789	2	T51310	RNA helicase RH28
274	36	33.0	115	2	F86666	hypothetical prote	347	36	33.0	805	2	S68441	leptin receptor, s
275	36	33.0	132	2	F82916	ribosomal protein	348	36	33.0	808	2	H64474	hypothetical prote
276	36	33.0	138	2	C90460	hypothetical prote	349	36	33.0	819	2	AC2029	hypothetical prote
277	36	33.0	141	2	C64218	ribosomal protein	350	36	33.0	822	2	S77112	DNA mismatch repai
278	36	33.0	142	2	JH0586	ribosomal protein	351	36	33.0	880	2	D69427	conserved hypotet
279	36	33.0	160	2	G95271	hypothetical prote	352	36	33.0	881	1	W2B855	gene 55 protein -
280	36	33.0	161	2	I48158	coagulation factor	353	36	33.0	892	2	S68439	leptin receptor, s
281	36	33.0	168	2	S51484	hypothetical prote	354	36	33.0	894	2	S68437	leptin receptor, s
282	36	33.0	175	2	S61599	probable membrane	355	36	33.0	895	2	S74225	leptin receptor, i
283	36	33.0	180	2	AC3270	hypothetical expor	356	36	33.0	900	2	S68440	leptin receptor, s
284	36	33.0	200	2	D90133	26S proteasome SU	357	36	33.0	1035	2	T42093	phospholipase D (E
285	36	33.0	200	2	T02826	ribosomal protein	358	36	33.0	1036	2	T13732	phospholipase D (E
286	36	33.0	221	2	T04238	hypothetical prote	359	36	33.0	1037	2	T13943	phospholipase D (E
287	36	33.0	236	2	T02314	hypothetical prote	360	36	33.0	1074	2	T17203	phospholipase (EC
288	36	33.0	240	2	E86418	probable eukaryoti	361	36	33.0	1074	2	T13725	phospholipase D (E
289	36	33.0	248	2	F64908	probable dehydroge	362	36	33.0	1075	2	T46635	phospholipase D (E
290	36	33.0	248	2	D90897	probable oxidoredu	363	36	33.0	1131	2	T09701	phytochrome - Scot
291	36	33.0	248	2	C85720	probable oxidoredu	364	36	33.0	1162	2	PC4184	leptin receptor, O
292	36	33.0	259	2	T22862	hypothetical prote	365	36	33.0	1162	2	S68438	leptin receptor, s
293	36	33.0	264	2	F90051	hypothetical prote	366	36	33.0	1191	2	B97116	chromosome segrega
294	36	33.0	282	2	H71823	biotin synthetase	367	36	33.0	1341	2	S09579	tail fiber protein
295	36	33.0	282	2	F64695	biotin synthetase	368	36	33.0	1436	2	A46496	antigen WC1.1 prec
296	36	33.0	286	2	G98209	3-oxoadipate enoi-	369	36	33.0	2042	2	T18399	variant-specific s
297	36	33.0	286	2	AB3077	hydrolase [impor-	370	36	33.0	3020	2	A43932	mucin 2 precursor,
298	36	33.0	287	2	D81295	cytochrome-c oxida	371	35.5	32.6	80	2	T14387	metallothionein-I
299	36	33.0	295	2	G81785	hypothetical prote	372	35.5	32.6	162	2	F83407	probable phenazine
300	36	33.0	296	2	A48496	transcription regu	373	35.5	32.6	191	2	F86357	Subunit 6b of cyto
301	36	33.0	312	2	E83624	probable transcrip	374	35.5	32.6	242	1	WJMSX3	homeotic protein H
302	36	33.0	329	2	T20546	hypothetical prote	375	35.5	32.6	258	2	G64992	hypothetical prote
303	36	33.0	336	2	T01977	hypothetical prote	376	35.5	32.6	258	2	D91017	hypothetical prote
304	36	33.0	339	2	G90760	probable integrase	377	35.5	32.6	258	2	F85861	hypothetical prote
305	36	33.0	339	2	E85624	probable integrase	378	35.5	32.6	269	2	A46506	leukocyte activati
306	36	33.0	347	2	T35013	probable membrane	379	35.5	32.6	320	2	S58734	probable membrane
307	36	33.0	350	2	D83102	xenobiotic reducta	380	35.5	32.6	363	2	T51341	RNA helicase RH9 (
308	36	33.0	361	2	AF3560	aspartate-semialde	381	35.5	32.6	392	2	H71520	probable hth trans
309	36	33.0	362	2	I40304	outer membrane lip	382	35.5	32.6	411	2	I51285	hepatocyte growth
310	36	33.0	373	2	T35452	probable solute bi	383	35.5	32.6	469	2	T21672	hypothetical prote
311	36	33.0	392	2	D91188	probable regulator	384	35.5	32.6	505	1	TVHUHC	protein-tyrosine k
312	36	33.0	392	2	E86799	prophage pi3 prote	385	35.5	32.6	579	2	AH3225	amidohydrolase [m
313	36	33.0	392	2	D84130	hypothetical prote	386	35.5	32.6	598	2	T40676	hypothetical prote
314	36	33.0	392	2	B86032	probable regulator	387	35	32.1	52	2	S19316	chlorophyll a/b-bi
315	36	33.0	392	2	S47790	xylose operon regu	388	35	32.1	93	2	AF0480	hypothetical prote
316	36	33.0	411	2	H72494	hypothetical prote	389	35	32.1	93	2	S49825	hypothetical prote
317	36	33.0	420	2	T02363	hypothetical prote	390	35	32.1	110	2	T46071	hypothetical prote
318	36	33.0	453	2	T24127	probable chitinase	391	35	32.1	122	2	T04118	mitochondrial proc
319	36	33.0	458	2	S53936	hypothetical prote	392	35	32.1	130	2	JC2280	ribosomal protein
320	36	33.0	461	1	E69360	4-hydroxyphenylac	393	35	32.1	132	2	T45380	ribosomal protein
321	36	33.0	482	1	EXRT	coagulation factor	394	35	32.1	132	2	B85092	hypothetical prote

395	35	32.1	133	2	S29885	ribosomal protein	468	35	32.1	505	2	F95345	FixL Oxygen regula
396	35	32.1	137	2	T33210	hypothetical prote	469	35	32.1	505	2	S39984	nitrogen fixation
397	35	32.1	154	2	F87526	apaG protein [impo	470	35	32.1	509	2	T02864	probable Zn finger
398	35	32.1	160	2	E82382	transcription regu	471	35	32.1	509	2	T37587	hypothetical trp-a
399	35	32.1	185	2	T35471	Ribosome recycling	472	35	32.1	518	2	T09354	hypothetical prote
400	35	32.1	187	2	A10520	AmpD protein (anhy	473	35	32.1	524	2	A32617	phytoene dehydroge
401	35	32.1	188	2	H95211	anthranilate synth	474	35	32.1	525	1	X2AD10	penton protein (II
402	35	32.1	188	2	B98076	anthranilate synth	475	35	32.1	525	2	T25900	hypothetical prote
403	35	32.1	189	2	S41410	insecticynanin prec	476	35	32.1	525	2	B26446	vif2 protein - Ag
404	35	32.1	195	2	S38667	ribonuclease (EC 3	477	35	32.1	533	2	B26446	cell division cont
405	35	32.1	205	2	S34833	stylar protein (al	478	35	32.1	539	2	A54294	hypothetical prote
406	35	32.1	218	2	T08737	hypothetical prote	479	35	32.1	548	2	T22137	extracellular matr
407	35	32.1	231	2	AD2892	conserved hypotet	480	35	32.1	559	2	A57474	cysteine proteinas
408	35	32.1	239	1	R3223	ribosomal protein	481	35	32.1	583	2	S46265	probable membrane
409	35	32.1	240	2	T50831	superoxide dismuta	482	35	32.1	598	2	S51456	hypothetical prote
410	35	32.1	240	2	C83702	transcription regu	483	35	32.1	608	1	S28313	hydrogenase (EC 1.
411	35	32.1	250	2	C84637	probable replicati	484	35	32.1	617	2	S08317	hydrogenase (EC 1.
412	35	32.1	252	2	T46247	hypothetical prote	485	35	32.1	618	1	B43255	hydrogenase (EC 1.
413	35	32.1	264	2	T31238	trak protein homol	486	35	32.1	618	2	S09251	hydrogenase (EC 1.
414	35	32.1	272	2	T15351	hypothetical prote	487	35	32.1	619	1	JH0776	hydrogenase (EC 1.
415	35	32.1	281	1	B47629	cell surface glyco	488	35	32.1	619	2	A45625	phosphoenolpyruvat
416	35	32.1	285	2	A86419	probable eukaryoti	489	35	32.1	627	2	E96190	hypothetical prote
417	35	32.1	287	2	T25064	hypothetical prote	490	35	32.1	651	2	T32875	hypothetical prote
418	35	32.1	287	2	B82806	integral membrane	491	35	32.1	655	2	T34219	hypothetical prote
419	35	32.1	289	2	A95158	homoserine kinase	492	35	32.1	656	2	T10664	serine/threonine-s
420	35	32.1	289	2	A98024	homoserine kinase	493	35	32.1	670	2	T09205	hypothetical prote
421	35	32.1	289	2	T16530	hypothetical prote	494	35	32.1	670	2	T09274	hypothetical prote
422	35	32.1	291	2	T28846	hypothetical prote	495	35	32.1	678	2	T04832	probable serine/th
423	35	32.1	291	2	AE2000	hypothetical prote	496	35	32.1	729	2	T23972	hypothetical prote
424	35	32.1	295	2	C81200	glutamyl-tRNA synt	497	35	32.1	754	2	C96807	hypothetical prote
425	35	32.1	312	2	T35940	probable transport	498	35	32.1	759	2	T43031	DNA topoisomerase
426	35	32.1	320	2	B44059	36K protein - appl	499	35	32.1	762	2	G88436	protein T04A8.13 [
427	35	32.1	327	2	G97667	hypothetical prote	500	35	32.1	773	2	I59351	carnitine O-palmit
428	35	32.1	333	2	A88504	protein B0361.5 [i				787	2	H86707	formate C-acetyltr
429	35	32.1	337	2	S55932	NCA3 protein precu							
430	35	32.1	338	2	E71195	hypothetical prote							
431	35	32.1	342	2	T45577	protein kinase-lik							
432	35	32.1	347	2	B72596	hypothetical prote							
433	35	32.1	348	2	C97633	probable ATP-bindi							
434	35	32.1	348	2	AF2856	hypothetical prote							
435	35	32.1	356	2	H72395	probable aldose 1-							
436	35	32.1	361	2	I05005	gene wnt8 protein							
437	35	32.1	361	2	A86841	hypothetical prote							
438	35	32.1	362	2	F64070	h18 bifunctional							
439	35	32.1	365	2	S46357	casein kinase-1 ho							
440	35	32.1	377	2	T33765	hypothetical prote							
441	35	32.1	377	2	T47439	hypothetical prote							
442	35	32.1	379	2	S27383	elastase inhibitor							
443	35	32.1	380	2	T32163	hypothetical prote							
444	35	32.1	384	1	S41584	histidinol-phospha							
445	35	32.1	388	2	A39756	circumsporozoite p							
446	35	32.1	389	1	A48329	histidinol-phospha							
447	35	32.1	392	2	A86252	hypothetical prote							
448	35	32.1	395	2	E86152	chalcone synthase							
449	35	32.1	402	2	E69107	hypothetical prote							
450	35	32.1	404	2	S13648	SCU1 protein - yea							
451	35	32.1	405	2	S05428	circumsporozoite p							
452	35	32.1	405	2	OZZQAP	circumsporozoite p							
453	35	32.1	412	1	C81376	hypothetical prote							
454	35	32.1	417	2	T33376	hypothetical prote							
455	35	32.1	424	2	A54533	circumsporozoite p							
456	35	32.1	428	2	S36856	glycolipid 2-alpha							
457	35	32.1	442	2	A54529	circumsporozoite p							
458	35	32.1	442	2	JC5594	jerky gene protein							
459	35	32.1	444	2	S57989	probable membrane							
460	35	32.1	448	2	A43304	phosphomannomutase							
461	35	32.1	454	2	AH1025	DNA helicase [impo							
462	35	32.1	462	2	S53084	gamma-tubulin - Eu							
463	35	32.1	462	2	H95914	hypothetical membr							
464	35	32.1	465	2	F75524	hypothetical prote							
465	35	32.1	476	2	T23083	3-isopropylmalate							
466	35	32.1	503	2	S38005	hypothetical prote							
467	35	32.1	504	2	A81922	probable cell-surf							

ALIGNMENTS

RESULT 1

hydrogen peroxide-inducible protein - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C:Accession: S66668

R: Egawa, K.; Yoshiwara, M.; Shibamura, M.; Nose, K.

FEBS Lett. 372, 74-77, 1995

A:Title: Isolation of a novel ras-recision gene that is induced by hydrogen peroxide from

A:Reference number: S66668; MUID:96032549; PMID:7556647

A:Accession: S66668

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-325 <EGL>

A:Cross-references: UNIPROT:Q61469; EMBL:L43371; NID:gl161099; PIDN:AAA5353.1; PID:gl161

A>Note: in the authors' translation residues 241-260 do not match the nucleotide sequence

Query Match 59.6%; Score 65; DB 2; Length 325;

Best Local Similarity 50.0%; Pred No. 0.0061;

Matches 10; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 EGYQNYRCRGDSKVQEAR 20

:||||:|:|:|:|

Db 256 DGYIEDYICQNEEKVKEGR 275

RESULT 2

hypothetical protein homolog MJ0787 - Methanococcus jannaschii

C:Species: Methanococcus jannaschii

C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C:Accession: C64398

R: Buit, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, C.

; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodex, A.;

rean, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.

A;Experimental source: strain Bristol N2; clone F54D7

C;Genetics:

A;Gene: CESP:F54D7.4

A;Map position: 1

A;Introns: 10/1; 54/2; 78/3; 124/1; 203/1; 258/2

Query Match 39.4%; Score 43; DB 2; Length 274;

Best Local Similarity 57.1%; Pred. No. 23;

Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EGYQNYRCRGDDSK 14

||:| ||||| |||

Db 222 EDHIGTRICGDNSS 235

RESULT 12

AE2823

conserved hypothetical protein Atu2011 [imported] - Agrobacterium tumefaciens (strain C58)

C;Species: Agrobacterium tumefaciens

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C;Accession: AE2823

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClellan

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AE2823

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-319 <KUR>

A;Cross-references: UNIPROT:Q8UDV8; GB:AE008688; PIDN:AA43003.1; PID:g17740465; GSPDB:C

A;Experimental source: strain C58 (Dupont)

C;Genetics:

A;Gene: Atu2011

A;Map position: circular chromosome

Query Match 39.4%; Score 43; DB 2; Length 319;

Best Local Similarity 50.0%; Pred. No. 27;

Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 GYQNYRCRGDDSK 15

||:| ||||| |||

Db 50 GYLQKYLVEGNDNR 63

RESULT 13

T16951

hypothetical protein T28D9.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C;Accession: T16951

R;Fulton, L.

submitted to the EMBL Data Library, June 1995

A;Description: The sequence of C. elegans cosmid T28D9.

A;Reference number: Z18614

A;Accession: T16951

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-341 <FUL>

A;Cross-references: UNIPROT:Q10022; EMBL:U28738; NID:g861262; PID:g861267; PIDN:AAA68312

A;Experimental source: strain Bristol N2

C;Genetics:

A;Gene: CESP:T28D9.3

A;Introns: 87/3; 127/1; 172/2; 209/3; 269/3; 303/1

Query Match 39.4%; Score 43; DB 2; Length 341;

Best Local Similarity 50.0%; Pred. No. 28;

Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 3 YIQNYRCRGDDSKVQEAR 20

||:| ||||| |||

Db 173 YITDYTCGPPELVLEAR 190

RESULT 14

D97601

hypothetical protein AGR_C_3649 [imported] - Agrobacterium tumefaciens (strain C58, Cerec

C;Species: Agrobacterium tumefaciens

C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004

C;Accession: D97601

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,

A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A;Reference number: A97359; MUID:21608551; PMID:11743194

A;Accession: D97601

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-369 <KUR>

A;Cross-references: UNIPROT:Q8UDV8; GB:AE007869; PIDN:AAK87765.1; PID:g15157135; GSPDB:G

C;Genetics:

A;Gene: AGR_C_3649

A;Map position: circular chromosome

Query Match 39.4%; Score 43; DB 2; Length 369;

Best Local Similarity 50.0%; Pred. No. 31;

Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 GYQNYRCRGDDSK 15

||:| ||||| |||

Db 100 GYLQKYLVEGNDNR 113

RESULT 15

AS5923

KNR4 protein - yeast (Saccharomyces cerevisiae)

N;Alternate names: protein 505; protein G8553; protein YGR229c; SM11 protein

C;Species: Saccharomyces cerevisiae

C;Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004

C;Accession: AS5923; S57693; S64553; S63909

R;Hong, Z.; Mann, P.; Brown, N.H.; Tran, L.E.; Shaw, K.J.; Hare, R.S.; DiDomenico, B.

Mol. Cell. Biol. 14, 1017-1025, 1994

A;Title: Cloning and characterization of KNR4, a yeast gene involved in (1,3)-beta-glucar

A;Reference number: AS5923; MUID:94119053; PMID:8289782

A;Accession: AS5923

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-505 <HON>

A;Cross-references: UNIPROT:P32566; GB:I13164; NID:g311112; PIDN:AAA67469.1; PID:g311113

A;Note: authors translated the codon AAC for residue 388 as Ala, and GCA for residue 389

R;van der Aart, Q.J.M.; Kleine, K.; Steensma, H.Y.

submitted to the EMBL Data Library, June 1995

A;Description: Sequence analysis of the 43 kb CRM1-YLM9-PET54-SM11-PHO81-YHB4-PFK1 region

A;Reference number: S57680

A;Accession: S57693

A;Molecule type: DNA

A;Residues: 1-505 <VAN>

A;Cross-references: EMBL:X87941; NID:g886908; PID:g886922

A;Experimental source: strain S288C

R;van der Aart, Q.J.M.; Steensma, H.Y.

submitted to the Protein Sequence Database, May 1996

A;Reference number: S64553

A;Accession: S64553

A;Molecule type: DNA

A;Residues: 1-505 <VAN>

A;Cross-references: EMBL:Z73013; NID:g1323411; PID:e243665; PID:g1323413; MIPPS:YGR229C

A;Experimental source: strain S288C

R;van der Aart, Q.J.M.; Kleine, K.; Steensma, H.Y.

Yeast 12, 385-390, 1996

A;Title: Sequence analysis of the 43 kb CRM1-YLM9-PET54-DIE2-SM11-PHO81-YHB4-PFK1 region

A;Reference number: S63896; MUID:96267763; PMID:8701610

A;Accession: S63909

A;Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-505 <VAF>
A:Cross-references: EMBL:X87941; NID:g886908; PIDN:CRA61178.1; PID:g886922
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995
C:Genetics:
A:Gene: SGD:SM11; KNR4
A:Cross-references: SGD:S0003461; MIPS:YGR229C
A:Map position: 7R
C:Superfamily: cell wall assembly and cell proliferation coordinating protein, KNR4 type

Query Match 39.4%; Score 43; DB 2; Length 505;
Best Local Similarity 72.7%; Pred. No. 42;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 RGDGSKVQEAR 20
| | | | | | | | | |
Db 487 RSDDAKVEAR 497

RESULT 16
T10245
glutamyl-tRNA reduglutamyl-tRNA reductase (EC 1.2.1.-) 2 - cucumber
C:Species: Cucumis sativus (cucumber)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10245
R:Tanaka, R.; Yoshida, K.; Nakayashiki, T.; Masuda, T.; Tsuji, H.; Inokuchi, H.; Tanaka, R.
Plant Physiol. 110, 1223-1230, 1996
A:Title: Differential expression of two hema mRNAs encoding glutamyl-tRNA reductase prot
A:Reference number: Z16983; MUID:97088717; PMID:8934625
A:Accession: T10245
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-542 <TAN>
A:Cross-references: UNIPROT:P49295; EMBL:D67088; NID:g1015318; PIDN:BA11091.1; PID:g101
A:Experimental source: cv. Aonagajibai; greening cotyledons
C:Genetics:
A:Gene: hemA2
A:Genome: nuclear
C:Function:
A:Description: catalyzes the reduction of glutamyl-tRNA(Glu) by NADPH to glutamic acid 1
A:Pathway: aminolevulinate biosynthesis; porphyrin biosynthesis
C:Superfamily: glutamyl-tRNA reductase
C:Keywords: aminolevulinate biosynthesis; chloroplast; NADP; oxidoreductase; porphyrin b

Query Match 39.4%; Score 43; DB 2; Length 542;
Best Local Similarity 57.1%; Pred. No. 45;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 GYQNYRCRGDPSK 15
| | | | | | | | | |
Db 491 GPIQLHRCGDNSR 504

RESULT 17
G89813
DNA polymerase III gamma and tau subunits [imported] - Staphylococcus aureus (strain N31
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G89813
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G89813
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-565 <KUR>
A:Cross-references: UNIPROT:Q99WC5; GB:BA000018; PID:g13700368; PIDN:BAB41666.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: dnaX

C:Superfamily: DNA-directed DNA polymerase III gamma chain

Query Match 39.4%; Score 43; DB 2; Length 565;
Best Local Similarity 44.4%; Pred. No. 47;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 3 YIQNYRCRGDSDSKVQEAR 20
| | | | | | | | | |
Db 525 YIQNRKNEGDDMPKQQAQ 542

RESULT 18
T18303
DNA binding regulatory protein - Emericella nidulans
C:Species: Emericella nidulans, Aspergillus nidulans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18303
R:Murphy, R.L.; Andrianopoulos, A.; Davis, M.A.; Hynes, M.J.
Mol. Microbiol. 23, 591-602, 1997
A:Title: Identification of amdX, a new Cys-2-His-2 (C2H2) zinc-finger gene involved in th
A:Reference number: Z18871; MUID:97197203; PMID:9044292
A:Accession: T18303
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1150 <MUR>
A:Cross-references: UNIPROT:P79045; EMBL:U56100; NID:g1877524; PID:g1877525; PIDN:AAB530(
C:Genetics:
A:Gene: amdX
A:Introns: 32/1

Query Match 39.4%; Score 43; DB 2; Length 1150;
Best Local Similarity 52.6%; Pred. No. 96;
Matches 10; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 4 IQNYRCR--GDDSKVQEAR 20
: | | | | | | | | | |
Db 802 VQNSRCRLSPDDSKSSDLR 820

RESULT 19
S05011
calcium channel alpha-1 chain, dihydropyridine sensitive, cardiac (clone HTDP 2.0) - rat
N:Alternate names: dihydropyridine receptor, cardiac; voltage-dependent calcium channel t
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jan-2000
C:Accession: S05011
R:Sligh, D.F.; Engle, D.B.; Varadi, G.; Lotan, I.; Singer, D.; Dascal, N.; Schwartz, A.
FEBS Lett. 250, 509-514, 1989
A:Title: Evidence for the existence of a cardiac specific isoform of the alpha(1) subunit
A:Reference number: S05011; MUID:89325623; PMID:2546809
A:Accession: S05011
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1331 <SUI>
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C:Keywords: cardiac muscle; heart

Query Match 39.4%; Score 43; DB 2; Length 1331;
Best Local Similarity 50.0%; Pred. No. 11e+02;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 QNYRCRGDSDSKVQEAR 20
: | | | | | | | | | |
Db 1288 ENSPCRGDSSAARRAR 1303

RESULT 20
S11339
calcium channel protein - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S11339
R:Biel, M.; Ruth, P.; Bosse, E.; Hüllin, R.; Stuehmer, W.; Flockerzi, V.; Hofmann, F.

FEBS Lett. 269, 409-412, 1990
A:Title: Primary structure and functional expression of a high voltage activated calcium
A:Reference number: S11339; MUID:90382589; PMID:2169433
A:Accession: S11339
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2166 <BIE>
A:Cross-references: UNIPROT:P15381; GB:X55763; NID:g1507; PIDN:CAA39289.1; PID:g1508
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 39.4%; Score 43; DB 2; Length 2166;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 QNYRCRGDDSKVQEAR 20
: ||||| :
Db 2023 ENSPCRGDSSAARRAR 2038

RESULT 21
S05054
calcium channel alpha-1 chain, dihydropyridine sensitive, cardiac (clone lambda-CCAR34)
N:Alternate names: dihydropyridine receptor, cardiac
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: S05054
R:Mikami, A.; Imoto, K.; Tanabe, T.; Niidome, T.; Mori, Y.; Takeshima, H.; Narumiya, S.;
Nature 340, 230-233, 1989
A:Title: Primary structure and functional expression of the cardiac dihydropyridine-sens
A:Reference number: S05054; MUID:89330539; PMID:2474130
A:Accession: S05054
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-2171 <MIK>
A:Cross-references: UNIPROT:P15381; EMBL:X15539; NID:g1509; PIDN:CAA33546.1; PID:g1510
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C:Keywords: cardiac muscle; heart; transmembrane protein

Query Match 39.4%; Score 43; DB 2; Length 2171;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 QNYRCRGDDSKVQEAR 20
: ||||| :
Db 2028 ENSPCRGDSSAARRAR 2043

RESULT 22
AH0027
30S ribosomal protein S8 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AH0027
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AH0027
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-130 <KUR>
A:Cross-references: UNIPROT:Q8ZJ98; GB:AL590842; PIDN:CAC89083.1; PID:g15978323; GSPDB:G
C:Genetics:
A:Gene: rpsH
C:Superfamily: Escherichia coli ribosomal protein S8

Query Match 38.5%; Score 42; DB 2; Length 130;
Best Local Similarity 38.9%; Pred. No. 16;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 EGYIQNYRCRGDDSKVQE 18

Db 43 EGFIEDFKIEGDTKPVLE 60
||:|::: || | |
RESULT 23
S28311
hypothetical protein F02A9.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
C:Accession: S28311
R:Barks, M.
submitted to the EMBL Data Library, December 1992
A:Reference number: S28296
A:Accession: S28311
A:Molecule type: DNA
A:Residues: 1-182 <BER>
A:Cross-references: UNIPROT:P34383; EMBL:Z19555; NID:g6705; PID:g6709
C:Genetics:
A:Introns: 170/1
C:Superfamily: Caenorhabditis elegans hypothetical protein F02A9.3

Query Match 38.5%; Score 42; DB 2; Length 182;
Best Local Similarity 46.7%; Pred. No. 22;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 EGYIQNYRCRGDDSK 15
: ||||| :
Db 140 KGYIAEYKALSDDAK 154

RESULT 24
B87484
anthranilate synthase component I [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: B87484
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.;
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Emdolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: AB7249; MUID:21173698; PMID:11259647
A:Accession: B87484
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-513 <STO>
A:Cross-references: UNIPROT:Q9A731; GB:AE005673; NID:g13423344; PIDN:AAK23870.1; GSPDB:G
C:Genetics:
A:Gene: CC1895
C:Superfamily: anthranilate synthase component I

Query Match 38.5%; Score 42; DB 2; Length 513;
Best Local Similarity 50.0%; Pred. No. 63;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 YRCRGDDSKVQE 18
: ||||| :
Db 73 WRCRGDQAEIAE 84

RESULT 25
T29129
probable ATP/GTP binding protein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T29129
R:Parkhill, J.; Barrrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1998
A:Reference number: Z17215
A:Accession: T29129
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-731 <PAR>


```
RESULT 30  
B81364  
C:probable periplasmic protein Cj0906c [imported] - Campylobacter jejuni (strain NCTC 11637)  
C:Species: Campylobacter jejuni  
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004  
R:#Accession: B81364  
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillingworth,  
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrell,  
Nature 403, 665-668, 2000  
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
```


A;Reference number: A81250; MUID:20150912; PMID:10688204

A;Accession: B81364

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-325 <PAR>

A;Cross-references: UNIPROT:Q9PP25; GB:AL1139076; GB:AL111168; NID:g968128; PIDN:CAB7316

A;Experimental source: serotype O2, strain NCTC 11168

C;Genetics:

A;Gene: Cj0906c

C;Superfamily: Helicobacter pylori hypothetical protein jhp0467

Query Match

Best Local Similarity 38.1%; Score 41.5; DB 2; Length 325;

Matches 10; Conservative 1; Mismatches 2; Indels 7; Gaps 1;

QY 3 YIQNYRCRGD-----DSK 15

|||||

297 YTKNYRFGDKILVVKIDSK 316

RESULT 31

C84989

30S ribosomal protein S8 [imported] - Buchnera sp. (strain APS)

C;Species: Buchnera sp.

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C;Accession: C84989

R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.

Nature 407, 81-86, 2000

A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.

A;Reference number: A84930; MUID:20445173; PMID:10993077

A;Accession: C84989

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-130 <STO>

A;Cross-references: GB:AP000398; GSPDB:GN00144

A;Experimental source: strain APS

C;Genetics:

A;Gene: rpsH; BUS10

C;Superfamily: Escherichia coli ribosomal protein S8

Query Match

Best Local Similarity 37.6%; Score 41; DB 2; Length 130;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EGYIQNYRCRGD 12

|||||

43 EGYIKDYNVTGD 54

RESULT 32

T11718

hypothetical protein SPCC777.12c - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C;Accession: T11718

R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, August 1998

A;Reference number: Z17318

A;Accession: T11718

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-238 <SEE>

A;Cross-references: UNIPROT:O74551; EMBL:AL031532

A;Experimental source: strain 972h(-)

C;Genetics:

A;Map position: IIIR

A;Introns: 93/3

A;Note: SPCC777.12c

C;Superfamily: Schizosaccharomyces hypothetical protein SPCC777.12c

Query Match

Best Local Similarity 37.6%; Score 41; DB 2; Length 238;

Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 3 YIQNYRCRGDSSKVOBAR 19

|||||

16 FVAAYSCEGDESAATEA 32

RESULT 33

H82528

L-ascorbate oxidase XP2677 [imported] - Xylella fastidiosa (strain 9a5c)

C;Species: Xylella fastidiosa

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: H82528

R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A82515; MUID:20365717; PMID:10910347

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: H82528

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-721 <SIM>

A;Cross-references: UNIPROT:Q9PA43; GB:AE004073; GB:AE003849; NID:g9107904; PIDN:AAF85474

A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.

; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Miyaki, C.Y.;

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki

A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira

M.; Teuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A;Reference number: A59328

A;Contents: annotation

C;Genetics:

A;Gene: XP2677

Query Match

Best Local Similarity 37.6%; Score 41; DB 2; Length 721;

Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 7 YRCRGDSSKVOBAR 20

|||||

282 YACRGNDGKLRKK 295

RESULT 34

PIIVBC

RNA-directed RNA polymerase (EC 2.7.7.48) 1 - influenza B virus (strain B/Ann Arbor/1/66

N;Alternate names: P1 protein; PB1 protein

C;Species: Influenza B virus

C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004

C;Accession: C28604

R;DeBorde, D.C.; Donabedian, A.M.; Herlocher, M.L.; Naeye, C.W.; Maassab, H.P.

Virology 163, 429-443, 1988

A;Title: Sequence comparison of wild-type and cold-adapted B/Ann Arbor/1/66 influenza vi

A;Reference number: A28604; MUID:88179548; PMID:3354202

A;Accession: C28604

A;Molecule type: genomic RNA

A;Residues: 1-752 <DEB>

A;Cross-references: UNIPROT:PI3871

C;Genetics:

A;Map position: segment 2

C;Superfamily: influenza virus RNA-directed RNA polymerase 1

C;Keywords: nucleotidyltransferase

Query Match

Best Local Similarity 37.6%; Score 41; DB 1; Length 752;

Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY	3	YIQNYRCRGDDSKVQEAR 20		
Db	554	YRYTYKCHRGDSKVEGKR 571		
RESULT 35				
PIVBL				
RNA-directed RNA polymerase (BC 2.7.7.48) 1 - influenza B virus (strain B/Lee/40)				
N/Alternate names: P1 protein; PB1 protein				
C:Species: Influenza B virus				
C>Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004				
C:Accession: A24287				
R:Kemdirim, S.; Palefsky, J.; Briedis, D.J.				
Virology 152, 126-135, 1986				
A:Title: Influenza B virus PB1 protein: nucleotide sequence of the genome RNA segment p1				
A:Reference number: A24287; MUID:86237097; PMID:3754992				
A:Accession: A24287				
A:Molecule type: mRNA				
A:Residues: 1-752 <KEM>				
A:Cross-references: UNIPROT:P07832; GB:M14880; NID:G325275; PIDN:AAA43767.1; PID:G325276				
C:Genetics:				
A:Map position: segment 2				
C:Superfamily: influenza virus RNA-directed RNA polymerase 1				
C:Keywords: nucleotidyltransferase				
Query Match 37.6%; Score 41; DB 1; Length 752;				
Best Local Similarity 44.4%; Pred. NO. 1.3e+02;				
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;				
QY	3	YIQNYRCRGDDSKVQEAR 20		
Db	554	YRYTYKCHRGDSKVEGKR 571		
RESULT 36				
PIVWB				
RNA-directed RNA polymerase (BC 2.7.7.48) 1 - influenza B virus (strain B/Ann Arbor/1/66)				
N/Alternate names: P1 protein; PB1 protein				
C:Species: Influenza B virus				
C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004				
C:Accession: D28604				
R:DeBorde, D.C.; Donabedian, A.M.; Herlocher, M.L.; Naeve, C.W.; Maassab, H.F.				
Virology 163, 429-443, 1988				
A:Title: Sequence comparison of wild-type and cold-adapted B/Ann Arbor/1/66 influenza vi				
A:Reference number: A28604; MUID:88179548; PMID:3354202				
A:Accession: D28604				
A:Molecule type: Genomic RNA				
A:Residues: 1-752 <DEB>				
A:Cross-references: UNIPROT:P13872; GB:M20170; NID:G325281; PIDN:AAA43770.1; PID:G325282				
C:Genetics:				
A:Map position: segment 2				
C:Superfamily: influenza virus RNA-directed RNA polymerase 1				
C:Keywords: nucleotidyltransferase				
Query Match 37.6%; Score 41; DB 1; Length 752;				
Best Local Similarity 44.4%; Pred. NO. 1.3e+02;				
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;				
QY	3	YIQNYRCRGDDSKVQEAR 20		
Db	554	YRYTYKCHRGDSKVEGKR 571		
RESULT 37				
HB3159				
conserved hypothetical protein PA3892 [imported] - Pseudomonas aeruginosa (strain PAO1)				
C:Species: Pseudomonas aeruginosa				
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004				
C:Accession: HB3159				
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B				
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,				
; Lory, S.; Olson, M.V.				
Nature 406, 959-964, 2000				

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoc												
A:Reference number: A82950; MUID:20437337; PMID:10984043												
A:Accession: H83159												
A>Status: preliminary												
A:Molecule type: DNA												
A:Residues: 1-302 <STO>												
A:Cross-references: UNIPROT:Q9HXC1; GB:AE004806; GB:AE004091; NID:g9950067; PIDN:AAG0727;												
A:Experimental source: strain PAO1												
C:Genetics:												
A:Gene: PA3892												
C:Superfamily: Escherichia coli hypothetical protein b1644												
Query Match 37.2%; Score 40.5; DB 2; Length 302;												
Best Local Similarity 42.9%; Pred. No. 65;												
Matches 9; Conservative 5; Mismatches 6; Indels 1; Gaps 1;												
QY	Db	1	EGYQNYRC-RGDDSKVQEAR 20 : : : : : 160 DGYVTNLNVRHGDYARVGEAK 180									
RESULT 38												
PM0042												
activin - fruit fly (Drosophila sp.) (fragment)												
C:Species: Drosophila sp.												
C>Date: 18-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 17-Nov-2000												
C:Accession: PM0042												
R:Kutty, G.; Kutty, R.K.; Samuel, W.; Duncan, T.; Jaworski, C.; Wiggert, B.												
Biochem. Biophys. Res. Commun. 246, 644-649, 1998												
A:Title: Identification of a new member of transforming growth factor-beta superfamily ir												
A:Reference number: PM0042; MUID:98289585; PMID:9618266												
A:Accession: PM0042												
A:Molecule type: mRNA												
A:Residues: 1-373 <KUT>												
A:Cross-references: GB:AF054822												
C:Genetics:												
A:Cross-references: FlyBase:FBgn0024913												
A:Start codon: GGT												
A:Introns: 86/3												
C:Superfamily: inhibin												
Query Match 37.2%; Score 40.5; DB 2; Length 373;												
Best Local Similarity 72.7%; Pred. No. 81;												
Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;												
QY	Db	2	GYIQNYRCRGD 12 295 GYFANY-CRGD 304									
RESULT 39												
AD3382												
ABC transporter-associated protein BMEI1042 [imported] - Brucella melitensis (strain 16M)												
C:Species: Brucella melitensis												
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004												
C:Accession: AD3382												
R:DeIvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, I												
; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc												
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002												
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensi												
A:Reference number: AD3252; PMID:11756688												
A:Accession: AD3382												
A>Status: preliminary												
A:Molecule type: DNA												
A:Residues: 1-507 <KUR>												
A:Cross-references: UNIPROT:Q8YGH3; GB:AE008917; PIDN:AAL52223.1; PID:gl7983006; GSPDB:G												
A:Experimental source: strain 16M												
C:Genetics:												
A:Gene: BMEI1042												
A:Map position: I												
C:Superfamily: conserved hypothetical protein b1683												
Query Match 37.2%; Score 40.5; DB 2; Length 507;												

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Best Local Similarity 42.9%; Pred. No. 1.1e+02;
Matches 9; Conservative 4; Mismatches 3; Indels 5; Gaps 1;

QY 1 EGYIQNY-----RCRGDSDKV 16
    :|||:
    :|||:
Db 306 KGGIYNFVTKRGDCRGDSKI 326
    :|||:
    :|||:

RESULT 40
E71356
A:Accession: E71356
A:Title: probable ribosomal protein S8 (rpsH) - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: E71356
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
reese, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McD
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876
A:Accession: E71356
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-132 <COL>
A:Cross-references: UNIPROT:O83233; GB:AE001202; GB:AE000520; NID:g3322446; PIDN:AAC6518
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0203
C:Superfamily: Escherichia coli ribosomal protein S8

Query Match 36.7%; Score 40; DB 2; Length 132;
Best Local Similarity 50.0%; Pred. No. 34;
Matches 9; Conservative 3; Mismatches 0; Indels 6; Gaps 1;

QY 1 EGYIQNYRCRGDSDKVQE 18
    :|||:
    :|||:
Db 43 EGYIRNFR-----KVEE 54
    :|||:
    :|||:

RESULT 41
G83840
A:Title: ferric uptake regulation protein BHI527 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: G83840
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: G83840
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-150 <STO>
A:Cross-references: UNIPROT:Q9KCP2; GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BA0502
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BHI527
C:Superfamily: ferric uptake regulator

Query Match 36.7%; Score 40; DB 2; Length 150;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 YRCRGDSDK 15
    :|||:
    :|||:
Db 141 HRCQGDESK 149
    :|||:
    :|||:

RESULT 42
A48904
A:Title: aminoglycoside adenyltransferase, ANT(4')-IIa - Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

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C:Accession: A48904
R:Shaw, K.J.; Munayyer, H.; Rather, P.N.; Hare, R.S.; Miller, G.H.
Antimicrob. Agents Chemother. 37, 708-714, 1993
A:Title: Nucleotide sequence analysis and DNA hybridization studies of the ant(4')-IIa ge
A:Reference number: A48904; MUID:93263637; PMID:8494365
A:Accession: A48904
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-252 <SHA>
A:Cross-references: UNIPROT:Q04455; GB:M98270; NID:g151026; PIDN:AAA25717.1; PID:g151028
A:Experimental source: pmg77
A>Note: sequence extracted from NCBI backbone (NCBIN:132199, NCBIP:132200)

Query Match 36.7%; Score 40; DB 2; Length 252;
Best Local Similarity 50.0%; Pred. No. 66;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 GYIQNYRCRGDSDKVQEA 19
    :|||:
    :|||:
Db 133 GKIRNMRGDDDLAVYQA 150
    :|||:
    :|||:

RESULT 43
E85529
A:Title: transcription regulator for mhp operon [imported] - Escherichia coli (strain O157:H7, su
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: E85529
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: E85529
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-230 <STO>
A:Cross-references: UNIPROT:Q8X681; GB:AE005174; NID:g12513182; PIDN:AAG54697.1; GSPDB:GN
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: mhpR

Query Match 36.7%; Score 40; DB 2; Length 290;
Best Local Similarity 50.0%; Pred. No. 76;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 EGYIQNYRCRGDSDKV 16
    :|||:
    :|||:
Db 208 EGYIQNYRGWDQEEKI 223
    :|||:
    :|||:

RESULT 44
A90679
A:Title: transcription regulator for mhp operon [imported] - Escherichia coli (strain O157:H7, su
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: A90679
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: A90679
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-315 <HAY>
A:Cross-references: UNIPROT:Q8X681; GB:BA000007; PIDN:BA833824.1; PID:g13359858; GSPDB:GP
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECs0401

Query Match 36.7%; Score 40; DB 2; Length 315;
Best Local Similarity 50.0%; Pred. No. 82;

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Matches      8;  Conservative      2;  Mismatches      6;  Indels      0;  Gaps      0;

QY      1  EGYQNYRCRGDDSKV 16
      ||| ||||| :|
Db      233 EGYQNYRGWDQEEKI 248

RESULT 45
B64762
mhp operon transcription regulator mhpR - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: B64762
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: B64762
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-315 <BLAT>
A:Cross-references: UNIPROT:P77569; GB:AE0000141; GB:U00096; NID:g1786532; PIDN:AACT73449.
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: mhpR
C:Keywords: transcription regulation

Query Match      36.7%; Score 40; DB 2; Length 315;
Best Local Similarity 50.0%; Pred. No. 82;
Matches      8;  Conservative      2;  Mismatches      6;  Indels      0;  Gaps      0;

QY      1  EGYQNYRCRGDDSKV 16
      ||| ||||| :|
Db      233 EGYQNYRGWDQEEKI 248

RESULT 46
A39130
nicotinate phosphoribosyltransferase (EC 2.4.2.11) - Salmonella typhimurium
C:Species: Salmonella typhimurium
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A39130
R:Vinitsky, A.; Teng, H.; Grubmeyer, C.T.
J. Bacteriol. 173, 536-540, 1991
A:Title: Cloning and nucleic acid sequence of the Salmonella typhimurium pncB gene and
A:Reference number: A39130; MUID:91100340; PMID:1987148
A:Accession: A39130
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-400 <VIN>
A:Cross-references: UNIPROT:P22253; GB:M55986; NID:g154268; PIDN:AAA27190.1; PID:g154269
C:Genetics:
A:Gene: pncB
C:Function:
A:Pathway: nicotinate and nicotinamide metabolism
C:Superfamily: nicotinate phosphoribosyltransferase
C:Keywords: glycosyltransferase; pentosyltransferase

Query Match      36.7%; Score 40; DB 1; Length 400;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches      6;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

QY      7  YRCRGDD 13
      :|||||
Db      39  FRCRGDD 45

RESULT 47
J00756
nicotinate phosphoribosyltransferase (EC 2.4.2.11) - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

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C:Accession: JQ0756; B64833
R:Wubbolds, M.G.; Terpstra, P.; van Beilen, J.B.; Kingma, J.; Meesters, H.A.R.; Witholt,
J. Biol. Chem. 265, 17665-17672, 1990
A:Title: Variation of cofactor levels in Escherichia coli; sequence analysis and expressi
A:Reference number: JQ0756; MUID:91009224; PMID:2211655
A:Accession: JQ0756
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-400 <WUB>
A:Cross-references: UNIPROT:P18133; GB:J05568; NID:g147306; PIDN:AAA24400.1; PID:g147307
A:Experimental source: strain GEC70
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: B64833
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-400 <BLAT>
A:Cross-references: GB:AE000195; GB:U00096; NID:g1787156; PIDN:AACT4017.1; PID:g1787162;
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: pncB
C:Function:
A:Pathway: nicotinate and nicotinamide metabolism
C:Superfamily: nicotinate phosphoribosyltransferase
C:Keywords: glycosyltransferase; pentosyltransferase

Query Match      36.7%; Score 40; DB 1; Length 400;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches      6;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

QY      7  YRCRGDD 13
      :|||||
Db      39  FRCRGDD 45

RESULT 48
AB0617
nicotinate phosphoribosyltransferase [imported] - Salmonella enterica subsp. enterica ser
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AB0617
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AB0617
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-400 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD05404.1; PID:g16502165; GSPDB:GN00176
C:Genetics:
A:Gene: STY1010
C:Superfamily: nicotinate phosphoribosyltransferase

Query Match      36.7%; Score 40; DB 2; Length 400;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches      6;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

QY      7  YRCRGDD 13
      :|||||
Db      39  FRCRGDD 45

RESULT 49
F90735
nicotinate phosphoribosyltransferase [imported] - Escherichia coli (strain O157:H7, subst

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C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: F90755
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
  Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
  DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F90755
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-400 <HAY>
A;Cross-references: UNIPROT:Q8XDE8; GB:BA000007; PIDN:BA834437.1; PID:gl3360473; GSPDB:C
A;Experimental source: strain O157:H7, substrain RMD 0509952
C;Genetics:
A;Gene: ECs1014
C;Superfamily: nicotinate phosphoribosyltransferase

  Query Match          36.7%; Score 40; DB 2; Length 400;
  Best Local Similarity 85.7%; Pred. No. 1e+02;
  Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      7 YRCRGDD 13
Db      39 FRCRGDD 45

RESULT 50
D85619
nicotinate phosphoribosyltransferase [imported] - Escherichia coli (strain O157:H7, subse
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: D85619
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
  Miller, L.; Grothbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
  Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: D85619
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-400 <STO>
A;Cross-references: UNIPROT:Q8XDE8; GB:AE005174; NID:gl2514106; PIDN:AAG55416.1; GSPDB:C
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: pncB
C;Superfamily: nicotinate phosphoribosyltransferase

  Query Match          36.7%; Score 40; DB 2; Length 400;
  Best Local Similarity 85.7%; Pred. No. 1e+02;
  Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      7 YRCRGDD 13
Db      39 FRCRGDD 45

Search completed: September 7, 2005, 20:03:45
Job time : 33.3488 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 7, 2005, 19:37:54 ; Search time 144.186 Seconds
(without alignments)
53.647 Million cell updates/sec

Title: US-10-812-238B-2

Perfect score: 109

Sequence: 1 EGYIQNYRCRGDDSKVQEAR 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	109	100.0	311	2 AAW79286	Aaw79286 Human pro
2	109	100.0	311	7 ADE60703	Ade60703 Human pro
3	109	100.0	311	8 ADM72103	Adm72103 Human tau
4	109	100.0	311	8 ADN04415	Adn04415 Antipsori
5	109	100.0	311	8 ADP24274	Adp24274 PRO polyp
6	105	96.3	312	5 ABB99112	Abb99112 Rat phosp
7	105	96.3	312	7 ADE60701	Ade60701 Rat Prote
8	66	60.6	282	5 ABB99111	Abb99111 Rat phosp
9	66	60.6	282	7 ADE58904	Ade58904 Rat Prote
10	66	60.6	282	7 ADE58900	Ade58900 Rat Prote
11	66	60.6	282	7 ADD45532	Add45532 Rat Prote
12	65	59.6	283	7 ADE61256	Ade61256 Rat Prote
13	59	54.1	221	7 ADJ95120	Adj95120 Novel NOV
14	59	54.1	221	7 ADJ95118	Adj95118 Novel NOV
15	59	54.1	284	2 AAW79284	Aaw79284 Human pro
16	59	54.1	285	2 AAW79285	Aaw79285 Human pro
17	59	54.1	285	2 AAY24916	Aay24916 Human pho
18	59	54.1	285	8 ADM72102	Adm72102 Human tau
19	59	54.1	289	7 ADN95452	Adn95452 Human BEC
20	59	54.1	289	8 ADL06556	Adl06556 Human BEC
21	59	54.1	369	8 ADR66929	Adr66929 Human pro
22	59	54.1	369	8 ADR66031	Adr66031 Human pro
23	59	54.1	371	8 ADR66930	Adr66930 Human pro
24	59	54.1	371	8 ADR66032	Adr66032 Human pro
25	49	45.0	847	8 ADS24124	Ads24124 Bacterial

26	49	45.0	1327	8	ADS24139	Ads24139 Bacterial
27	46.5	42.7	705	7	ADB74255	Adb74255 Mycobacte
28	46	42.2	340	4	ABB62735	Abb62735 Drosophi
29	45	41.3	84	4	AAU60236	Aau60236 Propionib
30	45	41.3	84	6	ABM56755	Abm56755 Propionib
31	45	41.3	135	8	ADL92508	Adl92508 Inabill v
32	45	41.3	135	8	ADR41823	Adr41823 versatille
33	45	41.3	822	2	AAW99087	Aaw99087 Human ser
34	45	41.3	875	2	AAW83361	Aaw83361 Human neu
35	45	41.3	875	8	ADQ21226	Adq21226 Human sof
36	45	41.3	875	6	ADQ89082	Adq89082 Human uro
37	44	40.4	191	6	ABU54593	Abu54593 Human NOV
38	44	40.4	385	7	ADE58277	Ade58277 Human pro
39	44	40.4	485	3	ADM04173	Adm04173 Human pro
40	44	40.4	498	3	AAW79209	Aaw79209 Human tra
41	44	40.4	498	7	ADN95772	Adn95772 Human BEC
42	44	40.4	498	8	ADP23807	Adp23807 PRO polyp
43	44	40.4	1100	8	ADS24143	Ads24143 Bacterial
44	44	40.4	1907	6	ABU62071	Abu62071 Human ske
45	43	39.4	152	4	ABG23434	Abg23434 Novel hum
46	43	39.4	237	4	AAU28253	Aau28253 Novel hum
47	43	39.4	237	8	ADS12199	Ads12199 Human the
48	43	39.4	371	8	ADN72921	Adn72921 Thale cre
49	43	39.4	421	8	ADJ50947	Adj50947 Human nov
50	43	39.4	424	8	ADJ50945	Adj50945 Human nov
51	43	39.4	428	8	ADA83857	Ada83857 Human POM
52	43	39.4	481	8	ADR09234	Adr09234 Human pro
53	43	39.4	481	8	ADS10966	Ads10966 Human the
54	43	39.4	489	7	ADM04303	Adm04303 Human pro
55	43	39.4	505	8	ADS43566	Ads43566 Bacterial
56	43	39.4	557	4	AAU37211	Aau37211 Staphyloc
57	43	39.4	565	6	ADA89639	Ada89639 Staphyloc
58	43	39.4	565	6	ABU15947	Abu15947 Protein e
59	43	39.4	565	6	ABM71598	Abm71598 Staphyloc
60	43	39.4	566	2	AAV49068	Aav49068 Amino aci
61	43	39.4	566	4	AAE31132	Aae31132 Amino aci
62	43	39.4	566	7	ABW01645	Abw01645 Staphyloc
63	43	39.4	840	4	ABG08798	Abg08798 Novel hum
64	42	38.5	92	4	AAU61299	Aau61299 Novel hum
65	42	38.5	92	6	ABM57818	Abm57818 Propionib
66	42	38.5	130	6	ABU50347	Abu50347 Protein e
67	42	38.5	137	7	ADB65039	Adb65039 Human pro
68	42	38.5	157	4	ABE62938	Abe62938 Drosophi
69	42	38.5	167	7	ABO80468	Ab080468 Pseudomon
70	42	38.5	305	8	ADR41635	Adr41635 Lipid acy
71	42	38.5	305	8	ADR41585	Adr41585 Lipid acy
72	42	38.5	393	8	ADN48160	Adn48160 Thermococ
73	42	38.5	554	6	ABU39968	Abu39968 Protein e
74	42	38.5	1166	5	ABP73801	Abp73801 Candida a
75	42	38.5	1304	6	ABP72189	Abp72189 Plasmodiu
76	42	38.5	3115	4	ABB59485	Abb59485 Drosophi
77	41	37.6	64	4	ABB17072	Abb17072 Human ner
78	41	37.6	129	8	ADK16589	Adk16589 Nanoarcha
79	41	37.6	130	6	ABU40522	Abu40522 Protein e
80	41	37.6	132	7	ADF06937	Adf06937 Bacterial
81	41	37.6	190	5	AAE18631	Aae18631 Equine hi
82	41	37.6	201	2	AAV27061	Aav27061 Recombina
83	41	37.6	236	2	AAV27060	Aav27060 Equine Pc
84	41	37.6	255	2	AAV27058	Aav27058 Equine Pc
85	41	37.6	272	7	ABO67231	Ab067231 Klebsiell
86	41	37.6	290	8	ABO84992	Ab084992 Murine ca
87	41	37.6	396	4	AAE09035	Aae09035 Equine in
88	41	37.6	396	4	AAE09034	Aae09034 Equine in
89	41	37.6	451	4	ABB67864	Abb67864 Drosophi
90	41	37.6	752	5	AAE23119	Aae23119 Influenza
91	41	37.6	757	4	AAE09037	Aae09037 Equine in
92	40.5	37.2	314	7	ABO71590	Ab071590 Pseudomon
93	40.5	37.2	371	4	ABB65431	Abb65431 Drosophi
94	40.5	37.2	373	5	ABG79651	Abg79651 Invertebr
95	40	36.7	20	5	ABP56183	Abp56183 Chimeric
96	40	36.7	94	2	AAV35872	Aav35872 Chlamydia
97	40	36.7	131	6	ABU23041	Abu23041 Protein e
98	40	36.7	132	6	ABU48505	Abu48505 Protein e

99	40	36.7	135	8	ADP29987	Adp29987 Human sec	172	39.5	36.2	211	7	ADB70322	Adb70322 Claudin-7
100	40	36.7	140	4	ABBI1487	Abbi1487 Human sec	173	39.5	36.2	211	7	ADD45212	Add45212 Human Pro
101	40	36.7	246	3	AAAG1453	Aag1453 Arabidops	174	39.5	36.2	211	8	AGG32539	Agg32539 Human Cla
102	40	36.7	256	5	ABPA0433	Abp0433 Staphyloc	175	39.5	36.2	211	8	Adj37101	Adj37101 Human mal
103	40	36.7	256	8	ADSO5965	Ads5965 Staphyloc	176	39.5	36.2	211	8	Adi47185	Adi47185 Human cla
104	40	36.7	301	8	ADS26705	Ads26705 Bacterial	177	39.5	36.2	211	8	Adi26768	Adi26768 Human cla
105	40	36.7	301	8	ADS27091	Ads27091 Bacterial	178	39.5	36.2	212	3	AAb52059	Aab52059 Human sec
106	40	36.7	302	8	ADS26338	Ads26338 Bacterial	179	39.5	36.2	225	2	AAy60154	Aay60154 Human end
107	40	36.7	387	4	ABGI4658	Abgi4658 Novel hum	180	39.5	36.2	247	5	AAg75499	Aag75499 Human col
108	40	36.7	396	4	AAE09033	Aae09033 Equine in	181	39.5	36.2	247	5	ABp41921	Abp41921 Human ova
109	40	36.7	396	4	AAE09032	Aae09032 Equine in	182	39.5	36.2	286	6	ABu41431	Abu41431 Protein e
110	40	36.7	400	6	ABU31582	Abu31582 Protein e	183	39.5	36.2	385	8	ADS17418	Ads17418 Amino aci
111	40	36.7	400	6	ABU45262	Abu45262 Protein e	184	39.5	36.2	439	4	ABR70300	Abbr70300 Drosophil
112	40	36.7	400	6	ABU48051	Abu48051 Protein e	185	39.5	36.2	453	8	ADN21519	Adn21519 Bacterial
113	40	36.7	400	6	ABU15369	Abu15369 Protein e	186	39.5	36.2	456	5	ABP38814	Abp38814 Staphyloc
114	40	36.7	401	3	AAAG1452	Aag1452 Arabidops	187	39.5	36.2	1238	7	ABO77617	Abot77617 Pseudomon
115	40	36.7	418	4	AAU43594	Aau43594 Propionib	188	39	35.8	35	5	ADE01639	Ade01639 Hybrid po
116	40	36.7	418	6	ABW40113	Abw40113 Propionib	189	39	35.8	74	4	ABO40096	Abbo40096 Human mus
117	40	36.7	422	3	AAAG1451	Aag1451 Arabidops	190	39	35.8	74	6	ABU13390	Abu13390 Novel hum
118	40	36.7	422	5	ABR90818	Abbr90818 Herbicida	191	39	35.8	74	8	ADJ29416	Adj29416 Human mus
119	40	36.7	424	7	ABO65513	Abot65513 Klebsiell	192	39	35.8	104	4	AAm86759	Aam86759 Human imm
120	40	36.7	434	6	ABR33569	Abrr33569 IL-IRI-CF	193	39	35.8	106	2	AAy60063	Aay60063 Human end
121	40	36.7	440	8	ADN20923	Adn20923 Bacterial	194	39	35.8	122	5	ABP35331	Abpp35331 Human ORF
122	40	36.7	454	4	AAAB31968	Aaab31968 Amino aci	195	39	35.8	127	5	ABG70741	Abg70741 Variable
123	40	36.7	480	4	AAAB31962	Aaab31962 Amino aci	196	39	35.8	131	6	ABU22134	Abu22134 Protein e
124	40	36.7	530	5	ABR90929	Abbr90929 Herbicida	197	39	35.8	132	4	AAAG90344	Aag90344 C Glutami
125	40	36.7	531	8	ABR31960	Abbr31960 Amino aci	198	39	35.8	132	7	ADJ87359	Adj87359 DNA repli
126	40	36.7	531	8	ADJ45219	Adi45219 Rice isop	199	39	35.8	169	7	ABO70827	Abot70827 Pseudomon
127	40	36.7	536	4	AAAB31964	Aaab31964 Amino aci	200	39	35.8	173	3	AAAB13232	Aaab13232 Caenorhab
128	40	36.7	557	4	ABR62937	Abrr62937 Drosophil	201	39	35.8	180	4	AAU43388	Aau43388 Propionib
129	40	36.7	710	7	ABO70541	Abot70541 Pseudomon	202	39	35.8	180	6	ABM39907	Abm39907 Propionib
130	40	36.7	730	2	AAr71379	Aar71379 Grasshopp	203	39	35.8	185	6	ABU35961	Abu35961 Protein e
131	40	36.7	757	4	AAE09036	Aae09036 Equine in	204	39	35.8	253	6	ABU36013	Abu36013 Protein e
132	40	36.7	757	5	AAE23109	Aae23109 Influenza	205	39	35.8	288	4	AAU66266	Aau66266 Propionib
133	40	36.7	757	5	ABP53062	Abpp53062 Plasmid p	206	39	35.8	288	4	AAU66266	Aau66266 Propionib
134	40	36.7	757	5	ABP53069	Abpp53069 Plasmid p	207	39	35.8	297	6	ABU24009	Abu24009 Protein e
135	40	36.7	757	5	ABP53059	Abpp53059 FPV-Brati	208	39	35.8	299	8	ADH72218	Adh72218 Human pro
136	40	36.7	757	5	ABP53070	Abpp53070 Plasmid p	209	39	35.8	301	4	AAU35607	Aau35607 Haemophil
137	40	36.7	757	5	ABP53067	Abpp53067 Plasmid p	210	39	35.8	325	7	ADB65344	Adb65344 Human pro
138	40	36.7	757	5	ABP53060	Abpp53060 WSN-PB1 p	211	39	35.8	402	7	ADB65483	Adb65483 Human pro
139	40	36.7	757	5	ABP53064	Abpp53064 Plasmid p	212	39	35.8	446	5	AAE18103	Aae18103 Human Cyt
140	40	36.7	757	5	ABP53066	Abpp53066 Plasmid p	213	39	35.8	447	5	ABM09643	Abm09643 MutP prot
141	40	36.7	757	5	ABP53068	Abpp53068 Plasmid p	214	39	35.8	447	6	ABG72541	Abg72541 Streptoco
142	40	36.7	757	5	ABP53061	Abpp53061 Plasmid p	215	39	35.8	461	7	ADG33762	Adg33762 Actinomyc
143	40	36.7	757	5	ABP53065	Abpp53065 Plasmid p	216	39	35.8	462	5	ABB47826	Abb47826 Listeria
144	40	36.7	757	5	ABP53063	Abpp53063 Plasmid p	217	39	35.8	466	8	ADN20343	Adn20343 Bacterial
145	40	36.7	757	5	ABP53071	Abpp53071 Plasmid p	218	39	35.8	470	8	ADN20289	Adn20289 Bacterial
146	40	36.7	757	5	ABO05765	Abot05765 Influenza	219	39	35.8	474	6	ABU11478	Abu11478 Human MDD
147	40	36.7	823	6	AAE33571	Aae33571 IL-IRI-CF	220	39	35.8	488	6	ABU11731	Abu11731 Human MDD
148	40	36.7	980	7	ABO82092	Abot82092 Pseudomon	221	39	35.8	509	6	AAU62933	Aau62933 Propionib
149	40	36.7	1235	4	ABG25570	Abg25570 Novel hum	222	39	35.8	509	6	ABM59452	Abm59452 Propionib
150	40	36.7	1299	6	ABP72191	Abp72191 Plasmidiu	223	39	35.8	543	5	ABB91383	Abb91383 Herbicida
151	40	36.7	2847	8	ADP25446	Adp25446 Plasmodi	224	39	35.8	550	7	ADM05649	Adm05649 Human pro
152	40	36.7	5533	4	ABR65772	Abrr65772 Drosophil	225	39	35.8	557	4	AAU36572	Aau36572 Staphyloc
153	40	36.7	5560	8	ABR71160	Abrr71160 Drosophil	226	39	35.8	563	7	AAU33968	Aau33968 Staphyloc
154	40	36.7	5560	8	ADOO1004	Adoo1004 Fruit fly	227	39	35.8	565	4	ADJ769920	Adj769920 Human hea
155	39.5	36.2	84	3	AAAG32835	Aag32835 Zea mays	228	39	35.8	594	4	ABG06747	Abg06747 Novel hum
156	39.5	36.2	106	3	AAAG43871	Aag43871 Zea mays	229	39	35.8	602	6	ADN55582	Adn55582 Human pro
157	39.5	36.2	125	3	AAAG32834	Aag32834 Zea mays	230	39	35.8	614	8	ADR99920	Adr99920 Immune Re
158	39.5	36.2	137	3	AAAY75996	Aay75996 Human ski	231	39	35.8	615	8	ADQ39859	Adq39859 Human myo
159	39.5	36.2	137	4	AAAB55935	Aaab55935 Skin cell	232	39	35.8	616	8	ADR99921	Adr99921 Immune Re
160	39.5	36.2	137	5	ABR72135	Abrr72135 Human pro	233	39	35.8	652	6	ADB08542	Adb08542 Alloiooc
161	39.5	36.2	191	7	ADP45210	Adp45210 Rat Prote	234	39	35.8	654	8	ADN2472	Adn2472 Bacterial
162	39.5	36.2	194	3	AAAB43554	Aaab43554 Human can	235	39	35.8	659	6	ADB08544	Adb08544 Alloiooc
163	39.5	36.2	205	3	AAAB52101	Aaab52101 Human sec	236	39	35.8	660	2	AAE69633	Aae69633 Human int
164	39.5	36.2	210	2	AAAB63697	Aaab63697 Human sec	237	39	35.8	662	2	AAE69632	Aae69632 Human int
165	39.5	36.2	210	2	ADN95565	Adn95565 Human BEC	238	39	35.8	662	2	AAW12772	Aaw12772 Human int
166	39.5	36.2	211	3	AAAY57609	Aay57609 Human apo	239	39	35.8	662	3	AAy83950	Aay83950 Human int
167	39.5	36.2	211	5	AAAB69999	Aaab69999 Human Cla	240	39	35.8	662	7	ADE39706	Ad39706 Human int
168	39.5	36.2	211	5	AAO20544	Aao20544 Human Cla	241	39	35.8	662	8	ADK90610	Adk90610 Human IL-
169	39.5	36.2	211	5	ADJ16800	Adj16800 Human NOV	242	39	35.8	662	8	ADM33833	Adm33833 Human IL-
170	39.5	36.2	211	5	ADJ16799	Adj16799 Human NOV	243	39	35.8	662	8	ADQ39861	Adq39861 Human myo
171	39.5	36.2	211	6	ABJ37066	Abj37066 Human bre	244	39	35.8	662	8	ADQ39860	Adq39860 Human myo

245	39	35.8	675	8	ADS11029	Adsl1029 Human the	318	38	34.9	22	4	AAM67400	Aam67400 Human bon
246	39	35.8	690	8	ADS44300	Ads44300 Bacterial	319	38	34.9	22	4	AAM55015	Aam55015 Human bra
247	39	35.8	692	8	ADS11028	Adsl1028 Human the	320	38	34.9	22	4	ABG49059	Abg49059 Human liv
248	39	35.8	694	8	ADO26838	Ado26838 Human rec	321	38	34.9	22	4	AAM02974	Aam02974 Peptide #
249	39	35.8	702	8	ADO39863	Ado39863 Human myo	322	38	34.9	22	5	ABG37027	Abg37027 Human pep
250	39	35.8	707	6	ABM65866	Abm65866 Proptonib	323	38	34.9	35	3	AAY88793	Aay88793 Core poly
251	39	35.8	709	6	ADR08965	Adr08965 Human pro	324	38	34.9	59	4	AUA49621	Aua49621 Proptonib
252	39	35.8	748	8	ADQ89640	Adq89640 Antagonis	325	38	34.9	59	4	ABM46140	Abm46140 Proptonib
253	39	35.8	754	8	ADQ39862	Adq39862 Human myo	326	38	34.9	77	5	ABP42738	Abp42738 Human ova
254	39	35.8	784	4	ABBG6206	Abbg6206 Drosophil	327	38	34.9	108	7	ADM05267	Adm05267 Human pro
255	39	35.8	790	4	ABBS8707	Abbs8707 Drosophil	328	38	34.9	115	4	ABB70282	Abb70282 Drosophil
256	39	35.8	801	4	AABU34022	Aabu34022 Staphyloc	329	38	34.9	116	4	ABU23431	Abu23431 Protein e
257	39	35.8	801	6	AUAU36926	Aua36926 Staphyloc	330	38	34.9	120	3	AG02326	Ag02326 Human sec
258	39	35.8	801	6	ABM16301	Abm16301 Protein e	331	38	34.9	129	5	AG93128	Ag93128 S. cerevi
259	39	35.8	801	6	ABM70889	Abm70889 Staphyloc	332	38	34.9	132	4	ABG22111	Abg22111 Novel hum
260	39	35.8	809	6	ABU33713	Abu33713 Protein e	333	38	34.9	136	2	AAM73460	Aam73460 Human sec
261	39	35.8	810	6	ADH72220	Adh72220 Human pro	334	38	34.9	164	5	AAE14398	Aae14398 Human thr
262	39	35.8	898	5	AAU09878	Aau09878 Novel hum	335	38	34.9	172	6	ABU26330	Abu26330 Protein e
263	39	35.8	912	2	AAU75206	Aau75206 Rabbit te	336	38	34.9	172	8	ADQ66177	Adq66177 Novel hum
264	39	35.8	912	7	ADE97397	Ade97397 Rabbit te	337	38	34.9	182	6	ABU94238	Abu94238 Trifolium
265	39	35.8	917	2	AAW00930	Aaw00930 Rat ICAM-	338	38	34.9	206	7	ABM85711	Abm85711 Human pro
266	39	35.8	917	2	AAW60160	Aaw60160 Rat inter	339	38	34.9	213	7	ABO73854	Ab073854 Pseudomon
267	39	35.8	917	2	AAW44836	Aaw44836 Rat ICAM-	340	38	34.9	240	6	ABR43219	AbR43219 Human IRA
268	39	35.8	917	2	AAW59003	Aaw59003 Rat ICAM-	341	38	34.9	242	8	ADK65878	Adk65878 Tobacco N
269	39	35.8	917	2	AAU05465	Aau05465 Rat ICAM-	342	38	34.9	250	6	ABU30346	Abu30346 Protein e
270	39	35.8	917	2	AAW73512	Aaw73512 Rat ICAM-	343	38	34.9	265	8	ADK46930	Adk46930 Streptoco
271	39	35.8	917	7	ADE97409	Ade97409 Norway ra	344	38	34.9	266	4	AAE03975	Aae03975 Human gen
272	39	35.8	917	7	ADE97398	Ade97398 Murine in	345	38	34.9	284	7	ADH85709	Adh85709 Enterococ
273	39	35.8	924	2	AAW00931	Aaw00931 Human ICA	346	38	34.9	285	4	ABR73497	AbR73497 Human tra
274	39	35.8	924	2	AAW60161	Aaw60161 Human int	347	38	34.9	303	5	ABP60919	Abp60919 Streptoco
275	39	35.8	924	2	AAW59006	Aaw59006 Human ICA	348	38	34.9	303	6	ABU01907	Abu01907 S. pneumo
276	39	35.8	924	2	AAU05467	Aau05467 Human ICA	349	38	34.9	307	8	ABO84993	Ab084993 Human can
277	39	35.8	924	7	AAW73511	Aaw73511 Human neu	350	38	34.9	322	8	ADS21720	AdS21720 Bacterial
278	39	35.8	924	7	ADE97389	Ade97389 Human int	351	38	34.9	326	6	ABU24002	Abu24002 Protein e
279	39	35.8	924	8	ADQ19157	Adq19157 Human sof	352	38	34.9	335	3	AG17233	Ag17233 Arabidops
280	39	35.8	924	8	ADP45605	Adp45605 Human int	353	38	34.9	341	4	ABG22110	Abg22110 Novel hum
281	39	35.8	1004	6	ABU54557	Abu54557 Human NOV	354	38	34.9	347	2	ABW64537	Abw64537 Human liv
282	39	35.8	1004	8	ADH72222	Adh72222 Human pro	355	38	34.9	347	2	AAW68200	Aaw68200 Human sca
283	39	35.8	1004	8	ADH72214	Adh72214 Human pro	356	38	34.9	347	2	AAU13369	Aau13369 Amino aci
284	39	35.8	1004	8	ADH72224	Adh72224 Human pro	357	38	34.9	347	3	ADC78468	Adc78468 Human PRO
285	39	35.8	1137	4	ABB64738	Abb64738 Drosophil	358	38	34.9	347	4	AAB80237	Aab80237 Human PRO
286	39	35.8	1137	7	ADC52077	Adc52077 Rice line	359	38	34.9	347	5	AAU83648	Aau83648 Human PRO
287	39	35.8	1269	7	ADD46237	Add46237 Rat Prote	360	38	34.9	347	5	ABB84828	Abb84828 Human PRO
288	39	35.8	1272	7	ADD46239	Add46239 Human Pro	361	38	34.9	347	5	ABB95434	Abb95434 Human ang
289	39	35.8	1403	6	ABR52876	AbR52876 Protein s	362	38	34.9	347	6	ABU71615	Abu71615 Human PRO
290	39	35.8	1403	7	ADK62358	Adk62358 Disease t	363	38	34.9	347	6	ABU71470	Abu71470 Human PRO
291	39	35.8	2204	3	AAU51233	Aau51233 Newcastle	364	38	34.9	347	6	ABU80795	Abu80795 Human PRO
292	39	35.8	3069	5	AAE20787	Aae20787 Human C3b	365	38	34.9	347	6	ABO33761	Ab033761 Novel hum
293	39	35.8	3069	5	AAE20900	Aae20900 Human C3b	366	38	34.9	347	6	ABU71316	Abu71316 Human sec
294	39	35.8	3100	5	AAE20789	Aae20789 Human C3b	367	38	34.9	347	6	ABO01799	Ab001799 Novel hum
295	39	35.8	3100	5	AAE20901	Aae20901 Human C3b	368	38	34.9	347	6	ABU54372	Abu54372 Human sec
296	39	35.8	3389	7	ADJ70480	Adj70480 Human hea	369	38	34.9	347	6	ABO47387	Ab047387 Human sec
297	39	35.8	3567	8	ADH72216	Adh72216 Human pro	370	38	34.9	347	6	ABU64524	Abu64524 Human sec
298	38.5	35.3	89	4	ABO55811	Ab055811 Human Gen	371	38	34.9	347	6	ABU67370	Abu67370 Human sec
299	38.5	35.3	114	4	AAU52938	Aau52938 C glutami	372	38	34.9	347	6	ABU89766	Abu89766 Protein d
300	38.5	35.3	149	3	AAU69476	Aau69476 Amino aci	373	38	34.9	347	6	ABO14890	Ab014890 Human sec
301	38.5	35.3	159	7	ADC72626	Adc72626 Human col	374	38	34.9	347	6	ABU82104	Abu82104 Novel hum
302	38.5	35.3	159	7	ADM05361	Adm05361 Human pro	375	38	34.9	347	6	ABU69647	Abu69647 Novel hum
303	38.5	35.3	274	7	ADC99096	Adc99096 Human Kpp	376	38	34.9	347	6	ABO14829	Ab014829 Human sec
304	38.5	35.3	276	2	AAU79287	Aau79287 Human pro	377	38	34.9	347	6	ABU29353	Abu29353 Human sec
305	38.5	35.3	288	8	ABM61975	Abm61975 Tumour-as	378	38	34.9	347	6	ABJ72284	Abj72284 Human PRO
306	38.5	35.3	725	4	AAU67809	Aau67809 Human ret	379	38	34.9	347	6	ADA18209	Ada18209 Human sec
307	38.5	35.3	897	8	ADI45373	Adi45373 Rice isop	380	38	34.9	347	6	ABO32781	Ab032781 Human sec
308	38.5	35.3	902	4	AAU93269	Aau93269 Human pro	381	38	34.9	347	6	ABO34841	Ab034841 Human PRO
309	38.5	35.3	943	4	AAU94457	Aau94457 Human pro	382	38	34.9	347	6	ADA16184	Ada16184 Human sec
310	38.5	35.3	1275	6	AAU25348	Aau25348 Protein e	383	38	34.9	347	6	ADA42329	Ada42329 Human sec
311	38.5	35.3	1316	4	AAU31854	Aau31854 Novel hum	384	38	34.9	347	6	ABJ7519	Abj7519 Human PRO
312	38.5	35.3	1893	6	AAU33681	Aau33681 Human str	385	38	34.9	347	6	ABJ72412	Abj72412 Human PRO
313	38	34.9	22	4	AAU15231	Aau15231 Peptide #	386	38	34.9	347	6	ABO34307	Ab034307 Human sec
314	38	34.9	22	4	ABU34221	Abu34221 Peptide #	387	38	34.9	347	7	ADA16608	Ada16608 Human sec
315	38	34.9	22	4	ABU27692	Abu27692 Peptide #	388	38	34.9	347	7	ADA13037	Ada13037 Human sec
316	38	34.9	22	4	ABU29060	Abu29060 Peptide #	389	38	34.9	347	7	ADA11905	Ada11905 Human sec
317	38	34.9	22	4	ABU19657	Abu19657 Protein #	390	38	34.9	347	7	ADA17252	Ada17252 Human sec

391	38	34.9	347	7	ADA42755	Human sec	464	38	34.9	347	8	ADD74323	Human PRO
392	38	34.9	347	7	ABJ72114	Human mem	465	38	34.9	347	8	ADD76053	Novel hum
393	38	34.9	347	7	ABO17580	Human PRO	466	38	34.9	347	8	ADD85545	Novel hum
394	38	34.9	347	7	ADB83604	Novel hum	467	38	34.9	347	8	ADe05094	Human PRO
395	38	34.9	347	7	ADB80710	Novel hum	468	38	34.9	347	8	ADD75307	Human PRO
396	38	34.9	347	7	ADB73251	Novel hum	469	38	34.9	347	8	ADD76851	Novel hum
397	38	34.9	347	7	ADB78333	Novel hum	470	38	34.9	347	8	ADD86619	Novel hum
398	38	34.9	347	7	ADB84981	Human PRO	471	38	34.9	347	8	ADe73861	Human sec
399	38	34.9	347	7	ADB77674	Human sec	472	38	34.9	347	8	ADD78087	Novel hum
400	38	34.9	347	7	ADB78087	Novel hum	473	38	34.9	347	8	ADD77595	Novel hum
401	38	34.9	347	7	ADB74810	Human sec	474	38	34.9	347	8	ADD77841	Novel hum
402	38	34.9	347	7	ADB87153	Human PRO	475	38	34.9	347	8	ADD85299	Novel hum
403	38	34.9	347	7	ADB84735	Human PRO	476	38	34.9	347	8	ADD73831	Human PRO
404	38	34.9	347	7	ADB83850	Novel hum	477	38	34.9	347	8	ADD74569	Human PRO
405	38	34.9	347	7	ADB73005	Novel hum	478	38	34.9	347	8	ADD77097	Novel hum
406	38	34.9	347	7	ADc28456	Human sec	479	38	34.9	347	8	ADD85791	Novel hum
407	38	34.9	347	7	ADc39656	Human sec	480	38	34.9	347	8	ADe05340	Human PRO
408	38	34.9	347	7	ADc40170	Human sec	481	38	34.9	347	8	ADD74815	Human PRO
409	38	34.9	347	7	ADc18998	Human sec	482	38	34.9	347	8	ADe99415	Human sec
410	38	34.9	347	7	ADc34294	Human sec	483	38	34.9	347	8	ADe98534	Human sec
411	38	34.9	347	7	ADc29349	Human sec	484	38	34.9	347	8	ADe98961	Human sec
412	38	34.9	347	7	ADc28880	Human sec	485	38	34.9	347	8	ADG05627	Novel hum
413	38	34.9	347	7	ADc40765	Human sec	486	38	34.9	347	8	ADG40431	Human sec
414	38	34.9	347	7	ADc19422	Human sec	487	38	34.9	347	8	ADf73825	Human sec
415	38	34.9	347	7	ADc33870	Human sec	488	38	34.9	347	8	ADG27181	Human PRO
416	38	34.9	347	7	ADc132940	Human sec	489	38	34.9	347	8	ADf73401	Human sec
417	38	34.9	347	7	ADc36843	Human PRO	490	38	34.9	347	8	ADG11244	Novel hum
418	38	34.9	347	7	ADc21833	Human PRO	491	38	34.9	347	8	ADG12023	Novel hum
419	38	34.9	347	7	ADc49864	Novel hum	492	38	34.9	347	8	ADf94580	Novel hum
420	38	34.9	347	7	ADc49063	Novel hum	493	38	34.9	347	8	ADG06676	Human PRO
421	38	34.9	347	7	ADc49580	Novel hum	494	38	34.9	347	8	ADG92244	Human sec
422	38	34.9	347	7	ADc47441	Novel hum	495	38	34.9	347	8	ADG92671	Human sec
423	38	34.9	347	7	ADc12392	Human sec	496	38	34.9	347	8	ADH39020	Novel hum
424	38	34.9	347	7	ADc47186	Novel hum	497	38	34.9	347	8	ADH20460	Human sec
425	38	34.9	347	7	ADc78061	Novel hum	498	38	34.9	347	8	ADH43457	Human PRO
426	38	34.9	347	7	ADd06296	Novel hum	499	38	34.9	347	8	ADH07315	Human sec
427	38	34.9	347	7	ADd10313	Human sec	500	38	34.9	347	8	ADH59860	Human sec
428	38	34.9	347	7	ADd077815	Novel hum							
429	38	34.9	347	7	ADd04947	Human sec							
430	38	34.9	347	7	ADd11273	Human sec							
431	38	34.9	347	7	ADd03953	Human sec							
432	38	34.9	347	7	ADd03529	Human sec							
433	38	34.9	347	7	ADd50778	Novel hum							
434	38	34.9	347	7	ADd51024	Novel hum							
435	38	34.9	347	7	ADd37066	Human sec							
436	38	34.9	347	7	ADd50505	Human PRO							
437	38	34.9	347	7	ADd50259	Human PRO							
438	38	34.9	347	7	ADd51270	Novel hum							
439	38	34.9	347	7	ADe34781	Human sec							
440	38	34.9	347	7	ADh59264	Human sec							
441	38	34.9	347	7	ADi38043	Human sec							
442	38	34.9	347	7	ADj26311	Human sec							
443	38	34.9	347	8	ADc48817	Novel hum							
444	38	34.9	347	8	ADe79226	Human sec							
445	38	34.9	347	8	ADe20988	Novel hum							
446	38	34.9	347	8	ADe05832	Human PRO							
447	38	34.9	347	8	ADd75061	Human PRO							
448	38	34.9	347	8	ADd75807	Novel hum							
449	38	34.9	347	8	ADd85039	Novel hum							
450	38	34.9	347	8	ADd86865	Novel hum							
451	38	34.9	347	8	ADe20742	Novel hum							
452	38	34.9	347	8	ADe39039	Novel hum							
453	38	34.9	347	8	ADe79650	Human sec							
454	38	34.9	347	8	ADe05586	Human PRO							
455	38	34.9	347	8	ADd73571	Human PRO							
456	38	34.9	347	8	ADe73326	Human sec							
457	38	34.9	347	8	ADd78411	Novel hum							
458	38	34.9	347	8	ADe41274	Human sec							
459	38	34.9	347	8	ADe21234	Novel hum							
460	38	34.9	347	8	ADd77349	Novel hum							
461	38	34.9	347	8	ADe20496	Novel hum							
462	38	34.9	347	8	ADd75561	Human PRO							
463	38	34.9	347	8	ADd74077	Human PRO							

ALIGNMENTS

RESULT 1

AAW79286

ID AAW79286 standard; protein; 311 AA.

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AC AAW79286;

XX

DT 15-FEB-1999 (first entry)

Human phosphatidic acid phosphatase beta.

XX Phosphatidic acid phosphatase beta; PAP-beta; human; dephosphorylation;
tumour suppressor; cancer; gene therapy.

OS Homo sapiens.

XX WO9846730-A1.

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PD 22-OCT-1998.

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PF 16-APR-1998; 98WO-US007928.

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PR 17-APR-1997; 97US-00842827.

XX

PA (CELL-) CELL THERAPEUTICS INC.

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PI Leung DW, Tompkins CK;

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DR WPI; 1998-594568/50.

DR N-PSDB; AAV69088.

XX

PT New nucleic acid encoding human phosphatidic acid phosphatases - used to

PT regulate levels of lipid cellular mediators and in gene therapy of e.g.
 XX cancer.
 PS Claim 8; Fig 3A-B; 62pp; English.
 XX This is the amino acid sequence of human mature phosphatidic acid
 CC phosphatase-beta (PAP-beta), an enzyme that catalyses the conversion of
 CC phosphatidic acid into diacylglycerol. 3 variants of human PAP, i.e. PAP-
 CC alpha 1 and 2 (see AAW79284-85), PAP-beta (see AAW79286) and PAP-gamma
 CC (see AAW79287) have been identified. The invention provides PAP
 CC polynucleotides (see AAV69086-89) and polypeptides, a method of preparing
 CC PAP in a transformed host cell, and a method of using PAP to
 CC dephosphorylate a substrate, especially lysophosphatidic acid, ceramide 1
 CC -phosphate or sphingosine 1-phosphate, particularly for production of
 CC diacylglycerol, but also monoacylglycerol, ceramide and sphingosine. PAP
 CC is able to control the balance of lipid mediators of cellular activation
 CC and signal transduction. Sequences that encode PAP are potentially
 CC useful, in gene therapy, for treatment of cancer (PAP may be tumour
 CC suppressors, PAP-alpha is expressed at lower levels in cancer cells than
 CC in normal cells of same tissue type), inflammatory disease and diabetes-
 CC associated obesity
 XX
 SQ Sequence 311 AA;
 Query Match 100.0%; Score 109; DB 2; Length 311;
 Best Local Similarity 100.0%; Pred. No. 1.3e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EGYIQNYRCRGDDSKVQEAR 20
 DB 173 EGYIQNYRCRGDDSKVQEAR 192
 RESULT 2
 ADS60703
 ID ADE60703 standard; protein; 311 AA.
 XX ADE60703;
 XX
 XX 29-JAN-2004 (first entry)
 XX Human Protein NP_003704, SEQ ID NO 6615.
 XX
 XX Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; Chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX
 XX Homo sapiens.
 XX
 XX WO2003016475-A2.
 XX
 XX 27-FEB-2003.
 XX
 XX 14-AUG-2002; 2002WO-US025765.
 XX
 XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 XX (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 XX Woolf C, D'urso D, Befort K, Costigan M;
 XX
 XX WPI; 2003-268312/26.
 DR GENBANK; NP_003704.
 XX
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 XX Claim 1; Page; 1017pp; English.
 XX
 XX The invention discloses a composition comprising two or more isolated rat

CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 311 AA;
 Query Match 100.0%; Score 109; DB 7; Length 311;
 Best Local Similarity 100.0%; Pred. No. 1.3e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EGYIQNYRCRGDDSKVQEAR 20
 DB 173 EGYIQNYRCRGDDSKVQEAR 192
 RESULT 3
 ADM72103
 ID ADM72103 standard; protein; 311 AA.
 XX ADM72103;
 XX
 XX 03-JUN-2004 (first entry)
 XX Human tau-related polypeptide PPAP2B.
 XX
 XX Tau; PPAP2A; PPAP2B; IHPK1; IHPK3; IHPK2; FLJ20530; DJ434014.5; EZF1;
 KW Loc127424; Loc113179; KIAA0826; neuroprotective; neurotropic;
 KW antiparkinsonian; tau-protein kinase; human.
 XX
 XX Homo sapiens.
 XX
 XX WO2004022708-A2.
 XX
 XX 18-MAR-2004.
 XX
 XX 04-SEP-2003; 2003WO-US027590.
 XX
 XX 09-SEP-2002; 2002US-0408877P.
 XX
 XX (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 PA Feany MB, Shulman JW;
 XX
 XX WPI; 2004-248456/23.
 XX
 XX New substantially pure Tau-related polypeptides and polynucleotides,
 PT useful for diagnosing and/or treating neurological conditions with
 PT aberrant expression of the Tau-related polypeptide, such as Alzheimer's
 PT disease.
 XX

PS Claim 1; SEQ ID NO 2; 62pp; English.

XX The invention relates to tau-related polypeptide consisting essentially
 CC of an amino acid sequence selected from PPAP2A, PPAP2B, IHPK1, IHPK3,
 CC IHPK2, FLJ20530, D434014.5, EF1, LOC127424, LOC131179 and KIAA0826
 CC (ADM72102-ADM72112 respectively). The methods and compositions of the
 CC present invention are useful for the diagnosis and/or treatment of
 CC neurological diseases or conditions associated with aberrant expression
 CC or activity of the Tau-related polypeptide, such as Alzheimer's disease
 CC and Parkinson's disease. The present sequence represents a human tau-
 CC related polypeptide homologue PPAP2B.

XX Sequence 311 AA;

Query Match 100.0%; Score 109; DB 8; Length 311;

Best Local Similarity 100.0%; Pred. No. 1.3e-08; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGYIYNYRCRGDDSKVQEAR 20

|||||
 DB 173 EGYIYNYRCRGDDSKVQEAR 192

RESULT 4

ADN04415

ID ADN04415 standard; protein; 311 AA.

XX

AC ADN04415;

XX

DT 01-JUL-2004 (first entry)

XX

DE Antipsoriatic protein sequence #401.

XX

KW antipsoriatic; gene therapy; psoriasis; diagnosis.

XX

OS Homo sapiens.

XX

PN WO2004028479-A2.

XX

PD 08-APR-2004.

XX

PF 25-SEP-2003; 2003WO-US030907.

XX

PR 25-SEP-2002; 2002US-0414006P.

XX

PA (GETH) GENENTECH INC.

XX

PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;

XX

DR WPI; 2004-305105/28.

XX

DR N-PSDB; ADN04414.

XX

PT New PRO nucleic acid or polypeptide, useful for preparing a
 PT pharmaceutical composition for diagnosing or treating psoriasis in a
 PT mammal.

XX

PS Claim 9; SEQ ID NO 809; 3069pp; English.

XX

CC The invention relates to novel polynucleotide and polypeptides for
 CC treating psoriasis or a sequence having at least 80% identity to the
 CC above sequences. The nucleic acid is useful for preparing a composition
 CC for diagnosing or treating psoriasis in a mammal. This sequence
 CC corresponds to one of the polypeptides of the invention.

XX Sequence 311 AA;

Query Match

Best Local Similarity 100.0%; Score 109; DB 8; Length 311;

Mismatches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGYIYNYRCRGDDSKVQEAR 20

|||||

DB 173 EGYIYNYRCRGDDSKVQEAR 192

RESULT 5

ADP24274

ID ADP24274 standard; protein; 311 AA.

XX

AC ADP24274;

XX

DT 18-NOV-2004 (first entry)

XX

DE PRO polypeptide SEQ ID NO:1452.

XX

KW PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
 KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
 KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.

OS Unidentified.

XX

PN WO2004041170-A2.

XX

PD 21-MAY-2004.

XX

PF 30-OCT-2003; 2003WO-US034312.

XX

PR 01-NOV-2002; 2002US-0423394P.

XX

PA (GETH) GENENTECH INC.

XX

PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;

XX

PI Wu TD;

XX

DR WPI; 2004-419628/39.

XX

DR N-PSDB; ADP24273.

XX

PT New PRO polypeptides and polynucleotides, useful for treating e.g.
 PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
 PT renal disease, or demyelinating diseases of the central or peripheral
 PT nervous system.

XX

Claim 7; SEQ ID NO 1452; 2940pp; English.

XX

CC The invention relates to a novel isolated nucleic acid and the PRO
 CC polypeptide encoded by it. A protein of the invention has

CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
 CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
 CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its
 CC agonist, antagonist, or antibody that specifically binds to the

CC polypeptide is useful for treating an immune related disorder such as
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic

CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary

CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food

CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein
 CC of the invention.

XX

SQ Sequence 311 AA;

Query Match

100.0%; Score 109; DB 8; Length 311;

Best Local Similarity 100.0%; Pred. No. 1.3e-08; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGYIQNYRCRGDDSKVQEAR 20
|||||
Db 173 EGYIQNYRCRGDDSKVQEAR 192

RESULT 6
ABB99112
ID ABB99112 standard; protein; 312 AA.
XX
AC ABB99112;
XX
DT 29-OCT-2002 (first entry)
XX
DE Rat phosphatase #2.
XX
KW Phosphatase; prenlyphosphoric acid; prenyl alcohol; rat.
XX
OS Rattus norvegicus.
XX
PN WO200253751-A1.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-JP011223.
XX
PR 28-DEC-2000; 2000JP-00401515.
PR 28-DEC-2000; 2000JP-00401806.
XX
PA (TOYW) TOYOTA CHUO KENKYUSHO KK.
(TOYT) TOYOTA JIDOSHA KK.
XX
PI Tokuhiko K, Muramoto N, Yamada Y, Asami O, Hirai M, Ohto C;
PI Obata S, Muramatsu M;
XX
DR WPI; 2002-643303/69.
DR N-PSDB; ABQ78948.
XX
PT Phosphatase polypeptides and encoded polynucleotides with substrate-specificity for prenlyphosphoric acid, applicable in mass-production of all-trans-prenyl alcohols by culturing transformants.
XX
PS Claim 1; Page 67-68; 93pp; Japanese.
XX
CC The invention relates to a novel phosphatase polypeptide, exhibiting substrate-specificity for not less than 15C prenlyphosphoric acid. The polynucleotides and encoded polypeptides are applicable in mass-production of all-trans-prenyl alcohols. The sequence represents a rat phosphatase polypeptide of the invention
XX
SQ Sequence 312 AA;

Query Match 96.3%; Score 105; DB 5; Length 312;
Best Local Similarity 95.0%; Pred. No. 5.4e-08; Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGYIQNYRCRGDDSKVQEAR 20
|||||
Db 174 EGYIQNYRCRGDDSKVQEAR 193

RESULT 7
ADE60701
ID ADE60701 standard; protein; 312 AA.
XX
AC ADE60701;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein CAA69106, SEQ ID NO 6613.
XX

KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
(FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENEANK; CAA69106.
XX
PT New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 312 AA;

Query Match 96.3%; Score 105; DB 7; Length 312;
Best Local Similarity 95.0%; Pred. No. 5.4e-08; Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGYIQNYRCRGDDSKVQEAR 20
|||||
Db 174 EGYIQNYRCRGDDSKVQEAR 193

RESULT 8
ABB99111
ID ABB99111 standard; protein; 282 AA.
XX
AC ABB99111;
XX

XX OS Rattus norvegicus.
 XX PN WO2003016475-A2.
 XX PD 27-FEB-2003.
 XX PF 14-AUG-2002; 2002WO-US025765.
 XX PR 14-AUG-2001; 2001US-0312147P.
 XX PR 01-NOV-2001; 2001US-0346382P.
 XX PR 26-NOV-2001; 2001US-0333347P.
 XX (GEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 XX PI Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 DR GENBANK; BAA12335.
 DR
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 XX Claim 1; Page; 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 283 AA;
 Query Match 59.6%; Score 65; DB 7; Length 283;
 Best Local Similarity 50.0%; Pred. No. 0.095;
 Matches 10; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EGYIQNYRCRGDSKVKQEAR 20
 Db 145 DGYIEDYICQGNKVKQEAR 164
 RESULT 13
 ID ADJ95120
 ID ADJ95120 standard; protein; 221 AA.
 XX
 AC ADJ95120;
 XX
 DT 06-MAY-2004 (first entry)
 XX

DE Novel NOVX protein sequence #174.
 XX
 KW antidiabetic; anorectic; cardiant; hypotensive; antiarteriosclerotic;
 KW anorectic; virucide; antibacterial; fungicide; protozoacide; nootropic;
 KW neuroprotective; antiparkinsonian; anticonvulsant; osteopathic;
 KW antiarthritic; antiinflammatory; dermatological; antiasthmatic;
 KW antileptic; gene therapy; metabolic disorder; diabetes; obesity;
 KW infectious disease; anorexia; cancer; cardiovascular disease;
 KW hypertension; atherosclerosis; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder;
 KW osteoarthritis; hematopoietic disorder; inflammatory skin disorder;
 KW asthma; dyslipidemia; hematogenesis; cell differentiation;
 KW cell proliferation; hematopoiesis; wound healing; angiogenesis;
 KW chromosome mapping; tissue typing; pharmacogenomic.
 XX
 OS Homo sapiens.
 XX
 PN WO2003040325-A2.
 XX
 PD 15-MAY-2003.
 XX
 XX
 PF 05-NOV-2002; 2002WO-US035464.
 XX
 PR 05-NOV-2001; 2001US-0338626P.
 PR 06-NOV-2001; 2001US-0333072P.
 PR 09-NOV-2001; 2001US-0348283P.
 PR 15-NOV-2001; 2001US-0335610P.
 PR 16-NOV-2001; 2001US-0338543P.
 PR 20-NOV-2001; 2001US-0331630P.
 PR 20-NOV-2001; 2001US-0331641P.
 PR 21-NOV-2001; 2001US-0332152P.
 PR 27-NOV-2001; 2001US-0333461P.
 PR 28-NOV-2001; 2001US-0333912P.
 PR 28-NOV-2001; 2001US-0334027P.
 PR 29-NOV-2001; 2001US-0334300P.
 PR 30-NOV-2001; 2001US-0334421P.
 PR 30-NOV-2001; 2001US-0334526P.
 PR 04-DEC-2001; 2001US-0336576P.
 PR 04-DEC-2001; 2001US-0336664P.
 PR 07-DEC-2001; 2001US-0338314P.
 PR 07-DEC-2001; 2001US-0338390P.
 PR 10-DEC-2001; 2001US-0339006P.
 PR 10-DEC-2001; 2001US-0339008P.
 PR 11-DEC-2001; 2001US-0339286P.
 PR 01-FEB-2002; 2002US-0353280P.
 PR 01-FEB-2002; 2002US-0353288P.
 PR 04-FEB-2002; 2002US-0354392P.
 PR 04-FEB-2002; 2002US-0354393P.
 PR 04-FEB-2002; 2002US-0354409P.
 PR 27-FEB-2002; 2002US-0359944P.
 PR 27-FEB-2002; 2002US-0360148P.
 PR 05-MAR-2002; 2002US-0361790P.
 PR 05-MAR-2002; 2002US-0361833P.
 PR 05-MAR-2002; 2002US-0361925P.
 PR 05-MAR-2002; 2002US-0362230P.
 PR 05-MAR-2002; 2002US-0362625P.
 PR 13-MAR-2002; 2002US-0364000P.
 PR 13-MAR-2002; 2002US-0364181P.
 PR 13-MAR-2002; 2002US-0364182P.
 PR 13-MAR-2002; 2002US-0364197P.
 PR 13-MAR-2002; 2002US-0364227P.
 PR 17-MAY-2002; 2002US-0381621P.
 PR 28-MAY-2002; 2002US-0383675P.
 PR 17-JUL-2002; 2002US-0396703P.
 PR 06-AUG-2002; 2002US-0401552P.
 PR 07-AUG-2002; 2002US-0401594P.
 PR 07-AUG-2002; 2002US-0401787P.
 PR 15-AUG-2002; 2002US-0403619P.
 PR 20-AUG-2002; 2002US-040821P.
 PR 23-AUG-2002; 2002US-0405368P.
 PR 23-AUG-2002; 2002US-0405402P.
 PR 23-AUG-2002; 2002US-0405496P.
 PR 23-AUG-2002; 2002US-0405631P.

PT cancer.
 PS Claim 2; Fig 2A-B; 62pp; English.
 XX
 CC This is the amino acid sequence of human mature phosphatidic acid
 CC phosphatase-alpha 2 (PAP-alpha-2), an enzyme that catalyses the
 CC conversion of phosphatidic acid into diacylglycerol. 3 Variants of human
 CC PAP, i.e. PAP-alpha 2 and its alternatively spliced form PAP-alpha 1 (see
 CC AAW79284), PAP-beta (see AAW79286) and PAP-gamma (see AAW79287) have been
 CC identified. The invention provides PAP polynucleotides (see AAV69086-89)
 CC and polypeptides, a method of preparing a PAP polypeptide in a
 CC transformed host cell, and a method of using PAP to dephosphorylate a
 CC substrate, especially lysophosphatidic acid, ceramide 1-phosphate or
 CC sphingosine 1-phosphate, particularly for production of diacylglycerol,
 CC but also monoacylglycerol, ceramide and sphingosine. PAP is able to
 CC control the balance of lipid mediators of cellular activation and signal
 CC transduction. Sequences that encode PAP are potentially useful, in gene
 CC therapy, for treatment of cancer (PAP may be tumour suppressors, PAP-
 CC alpha is expressed at lower levels in cancer cells than in normal cells
 CC of same tissue type), inflammatory disease and diabetes-associated
 CC obesity
 XX
 SQ Sequence 285 AA;
 Query Match 54.1%; Score 59; DB 2; Length 285;
 Best Local Similarity 50.0%; Pred. No. 0.85;
 Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 1 EGYIYRCRGDDSKVQEAR 20
 :|||: |||: :|||:
 Db 146 DGYIYICRGNAERVKEGR 165
 RESULT 17
 AAY24916
 ID AAY24916 standard; protein; 285 AA.
 XX
 AC AAY24916;
 XX
 DT 26-AUG-1999 (first entry)
 XX
 DE Human phosphatase HPA-1.
 XX
 KW Human; phosphatase; HPA-1; HPA-2; immune disorder; AIDS; allergy;
 KW Acquired Immune Deficiency Syndrome; Addison's disease; cancer;
 KW adenocarcinoma; leukemia; lymphoma.
 XX
 OS Homo sapiens.
 XX
 PN WO9931225-A2.
 XX
 PD 24-JUN-1999.
 XX
 PF 02-DEC-1998; 98WO-US025559.
 XX
 PR 17-DEC-1997; 97US-00992035.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Shah P, Hillman JL, Corley NC, Lal P;
 XX WPI; 1999-395175/33.
 DR N-PSDB; AAX83616.
 XX
 CC New human phosphatases which comprise 285 and 370 amino acid residues or
 PT their fragments, polynucleotides encoding enzymes, and antibodies that
 PT bind to enzymes.
 XX
 CC Claim 1; Fig 1; 80pp; English.
 PS
 XX The present sequence represents a human phosphatase designated HPA-1. HPA
 CC proteins have anti-HIV, antiallergic and cytostatic activity. HPA
 CC antagonists form pharmaceutical compositions for treating or preventing

CC an immune disorder (e.g. Acquired Immune Deficiency Syndrome (AIDS),
 CC Addison's disease and allergies) or cancer (e.g. adenocarcinoma, leukemia
 CC and lymphoma). Polynucleotides complementary to polynucleotides encoding
 CC HPAs are useful for detecting these sequences in order to diagnose
 CC disorders associated with HPA. Neutralizing antibodies against HPA have
 CC therapeutic use
 XX
 SQ Sequence 285 AA;
 Query Match 54.1%; Score 59; DB 2; Length 285;
 Best Local Similarity 50.0%; Pred. No. 0.85;
 Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 1 EGYIYRCRGDDSKVQEAR 20
 :|||: |||: :|||:
 Db 146 DGYIYICRGNAERVKEGR 165
 RESULT 18
 ADM72102
 ID ADM72102 standard; protein; 285 AA.
 XX
 AC ADM72102;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Human tau-related polypeptide PPAP2A.
 XX
 KW Tau; PPAP2A; PPAP2B; IHPK3; IHPK2; FLJ20530; DJ434014.5; EZFL1;
 KW Loc127424; Loc113179; KIAA0826; neuroprotective; neurotropic;
 KW antiparkinsonian; tau-protein kinase; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2004022708-A2.
 XX
 PD 18-MAR-2004.
 XX
 PF 04-SEP-2003; 2003WO-US027590.
 XX
 PR 09-SEP-2002; 2002US-0408877P.
 XX
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 XX
 PI Feany MB, Shulman JW;
 XX WPI; 2004-248456/23.
 DR
 XX New substantially pure Tau-related polypeptides and polynucleotides,
 PT useful for diagnosing and/or treating neurological conditions with
 PT aberrant expression of the Tau-related polypeptide, such as Alzheimer's
 PT disease.
 XX
 PS Claim 1; SEQ ID NO 1; 62pp; English.
 XX
 CC The invention relates to tau-related polypeptide consisting essentially
 CC of an amino acid sequence selected from PPAP2A, PPAP2B, IHPK1, IHPK3,
 CC IHPK2, FLJ20530, DJ434014.5, EZFL1, Loc113179 and KIAA0826
 CC (ADM72102-ADM72112 respectively). The methods and compositions of the
 CC present invention are useful for the diagnosis and/or treatment of
 CC neurological diseases or conditions associated with aberrant expression
 CC or activity of the Tau-related polypeptide, such as Alzheimer's disease
 CC and Parkinson's disease. The present sequence represents a human tau-
 CC related polypeptide homologue PPAP2A.
 XX
 SQ Sequence 285 AA;
 Query Match 54.1%; Score 59; DB 8; Length 285;
 Best Local Similarity 50.0%; Pred. No. 0.85;
 Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 1 EGYIYRCRGDDSKVQEAR 20
 :|||: |||: :|||:

Db 146 DGYIEYICRGNAERVKEGR 165

RESULT 19

ADN95452
ID ADN95452 standard; protein; 289 AA.

AC ADN95452;

DT 01-JUL-2004 (first entry)

DE Human BEC/LEC-related protein sequence SeqID375.

XX growth; differentiation; blood endothelial cell; BEC;
KW lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;
KW lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytostatic;
KW vasotropic; antiinflammatory; gene therapy; endothelial cell disorder;
KW inflammatory disease; cancer metastasis; lymphatic system; human.

XX Homo sapiens.

OS WO2003080640-A1.

PN 02-OCT-2003.

PD 07-MAR-2003; 2003WO-US006900.

PF 07-MAR-2002; 2002US-0363019P.

PR (LUDW-) LUDWIG INST CANCER RES.

XX (LICN) LICENTIA LTD.

PI Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;

XX WPI; 2003-876899/81.

DR N-PSDB; ADN95453.

XX Example 1; SEQ ID NO 375; 176pp; English.

CC This invention relates to a method of differentially modulating the
CC growth or differentiation of blood endothelial cells (BEC) or lymphatic
CC endothelial cells (LEC) comprising contacting endothelial cells with a
CC composition comprising an agent that differentially modulates blood or
CC lymphatic endothelial cells. Treating hereditary lymphoedema comprises
CC identifying a human subject with lymphoedema and with a mutation in at
CC least one allele of a gene encoding a LEC protein, where the mutation
CC correlates with lymphoedema in human subjects, and with the proviso that
CC the LEC protein is not VEGFR-3; and administering to the subject a
CC composition comprising a lymphatic growth agent selected from VEGF-C or
CC VEGF-D polypeptides and polynucleotides. The invention may be useful for
CC the development of compounds with an antiangiogenic, cytostatic,
CC vasotropic or antiinflammatory activity or for gene therapy. The method
CC is useful in modulating the growth or differentiation of blood
CC endothelial cells or lymphatic endothelial cells, in treating hereditary
CC lymphoedema, in screening for an endothelial cell disorder or
CC predisposition to the disorder or in monitoring the efficacy or toxicity
CC of a drug on endothelial cells. The agent is useful in manufacturing a
CC medicament for the differential modulation of blood vessel endothelial
CC cell or lymphatic vessel endothelial cell growth or differentiation. The
CC lymphatic growth agent may also be used in manufacturing a medicament for
CC the treatment of hereditary lymphoedema resulting from a mutation in a
CC LEC gene or of other diseases involving the lymphatic vessels, such as
CC various inflammatory diseases and cancer metastasis via the lymphatic
CC system. The present sequence is that of a human LEC/BEC differentially
CC expressed protein which is related to the method of the invention. Note:
CC This sequence does not appear in the specification but was obtained by
CC the indexer using the source data given in table 14 of the specification.

XX Sequence 289 AA;

Query Match 54.1%; Score 59; DB 7; Length 289;

Best Local Similarity 50.0%; Pred. No. 0.86; Mismatches 5; Indels 0; Gaps 0;

QY 1 EGYIQNYRCRGDDSKVQEAR 20
:||||:||||:|
Db 150 DGYIEYICRGNAERVKEGR 169

RESULT 20

ADL06556

ID ADL06556 standard; protein; 289 AA.

XX AC ADL06556;

XX 20-MAY-2004 (first entry)

XX Human tumour-associated antigenic target (TAT) polypeptide #55.

XX Human; tumour-associated antigenic target; TAT; cell death; tumour;
KW cancer; cytostatic.

XX Homo sapiens.

XX WO2004016225-A2.

XX 26-FEB-2004.

XX 19-AUG-2003; 2003WO-US025892.

XX 19-AUG-2002; 2002US-0404809P.

XX 21-AUG-2002; 2002US-0405645P.

XX 23-SEP-2002; 2002US-0413192P.

XX 15-OCT-2002; 2002US-0419008P.

XX 15-NOV-2002; 2002US-0426847P.

XX 02-JUL-2003; 2003US-0484959P.

XX (GETH) GENENTECH INC.

XX Desauvage FJ, Frantz G, Hillan KJ, Polakis P, Polson A, Smith V;

XX Spencer SD, Wu TD, Zhang Z;

XX WPI; 2004-257144/24.

XX N-PSDB; ADL06477.

XX New antibody that binds to a tumor-associated antigenic target (TAT)
PT polypeptide, useful for preparing a composition for diagnosing or
PT treating cancer.

XX Claim 2; SEQ ID NO 136; 319pp; English.

CC The present invention relates to the isolation of human tumour-associated
CC antigenic target (TAT) polynucleotide and polypeptide sequences. Also
CC disclosed is an antibody that binds to a TAT polypeptide. The antibody is
CC a monoclonal antibody, an antibody fragment, a chimeric antibody or a
CC humanised antibody. It is conjugated to a growth inhibitory agent. It is
CC produced in bacteria or in CHO cells and induces death of a cell to which
CC it binds. The antibody is useful for preparing a composition for
CC diagnosing or treating tumours and cancer. The present sequence
CC represents a human TAT polypeptide of the invention.

XX Sequence 289 AA;

Query Match 54.1%; Score 59; DB 8; Length 289;

Best Local Similarity 50.0%; Pred. No. 0.86;

Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EGYIQNYRCRGDDSKVQEAR 20
:||||:||||:|

Db 150 DGYIEYICRGNAERVKEGR 169

RESULT 21

ADR66929

ID ADR66929 standard; protein; 369 AA.

XX

AC ADR66929;
 XX
 DT 02-DEC-2004 (first entry)
 DE
 XX Human prostatic carcinoma derived DNA SEQ ID 227 #4.
 XX
 KW human, cytostatic; diagnosis; prostatic cancer;
 KW differential expression analysis.
 XX
 OS Homo sapiens.
 XX
 XX WO2004076614-A2.
 XX
 PD 10-SEP-2004.
 XX
 XX 22-FEB-2004; 2004WO-DE000433.
 XX
 PF 27-FEB-2003; 2003DE-01009985.
 PR 14-MAY-2003; 2003DE-01022134.
 XX
 XX (HINZ/) HINZMANN B.
 PA (DAHL/) DAHL E.
 PA (ROSE/) ROSENTHAL A.
 PA (HERM/) HERMANN K.
 PA (PILA/) PILARSKY C.
 XX
 XX Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;
 PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;
 PI Xinzhong L, Staub E;
 XX
 XX WPI; 2004-653386/63.
 DR
 XX
 XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,
 PT useful for diagnosis, treatment and in screening for specific binding
 PT agents.
 XX
 XX Claim 2; Page 1582; 1607pp; German.
 PS
 XX
 CC This invention describes novel cytostatic polynucleotide and polypeptide
 CC sequences which can be used in a method for diagnosing prostatic cancer
 CC or the risk of developing prostatic cancer. Diagnosis is based on
 CC determining over transcription or over expression of the sequences in
 CC prostatic tissue. Screening for inhibitors of the sequences or detection
 CC substances involves a binding assay, any compounds that bind are
 CC selected, optionally after deconvolution of mixtures. Detection of a
 CC predetermined minimum level of the reporter indicates the presence of
 CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
 CC short-interfering RNA or ribozymes; an organic molecule of molecular
 CC weight below 5000, preferably 300, that binds to the polypeptide; an
 CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
 CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human
 CC (monoclonal) antibody directed against Ab or any of the above derivatised
 CC with a reporter group, cell toxin, immunostimulatory molecules and/or
 CC radioisotope. The polynucleotides are identified in human prostatic
 CC cancer by differential expression analysis, using DNA microarrays,
 CC between normal and tumorous tissues, with (over)expression being detected
 CC by quantitative PCR. Analysis of prostatic cancer samples showed that
 CC CD24 was upregulated in many of them. Sections of tissue, isolated from
 CC prostatic cancer patients, or subjects at risk, were incubated
 CC sequentially with anti-human CD4 murine monoclonal antibodies;
 CC biotinylated second antibody; streptavidin-conjugated horseradish
 CC peroxidase and then diaminobenzidine as colour former (brown). The
 CC samples were counterstained with hemalum (blue). Malignant cells stained
 CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
 CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
 CC lymph node metastases were also stained. ADR5805-ADR66954 represent the
 CC polynucleotide and polypeptide sequences used in the method of the
 CC invention.
 XX
 XX Sequence 369 AA;
 SQ
 Query Match 54.1%; Score 59; DB 8; Length 369;
 Best Local Similarity 50.0%; Pred. No. 1.1;

Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 1 EGYQNYRCRGDDSKVQEAR 20
 :|||: |||: |||:
 Db 230 DGYIEYICRGNAERVKGR 249

RESULT 22
 ADR66031
 ID ADR66031 standard; protein; 369 AA.
 XX
 AC ADR66031;
 XX
 XX 02-DEC-2004 (first entry)
 DT
 XX Human prostatic carcinoma derived protein SEQ ID 227 #1.
 DE
 XX human; cytostatic; diagnosis; prostatic cancer;
 KW differential expression analysis.
 XX
 OS Homo sapiens.
 XX
 XX WO2004076614-A2.
 PN
 XX 10-SEP-2004.
 PD
 XX 22-FEB-2004; 2004WO-DE000433.
 PF
 XX 27-FEB-2003; 2003DE-01009985.
 PR 14-MAY-2003; 2003DE-01022134.
 XX
 XX (HINZ/) HINZMANN B.
 PA (DAHL/) DAHL E.
 PA (ROSE/) ROSENTHAL A.
 PA (HERM/) HERMANN K.
 PA (PILA/) PILARSKY C.
 XX
 XX Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;
 PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;
 PI Xinzhong L, Staub E;
 XX
 XX WPI; 2004-653386/63.
 DR
 XX
 XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,
 PT useful for diagnosis, treatment and in screening for specific binding
 PT agents.
 XX
 XX Claim 2; Page 622; 1607pp; German.
 PS
 CC This invention describes novel cytostatic polynucleotide and polypeptide
 CC sequences which can be used in a method for diagnosing prostatic cancer
 CC or the risk of developing prostatic cancer. Diagnosis is based on
 CC determining over transcription or over expression of the sequences in
 CC prostatic tissue. Screening for inhibitors of the sequences or detection
 CC substances involves a binding assay, any compounds that bind are
 CC selected, optionally after deconvolution of mixtures. Detection of a
 CC predetermined minimum level of the reporter indicates the presence of
 CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
 CC short-interfering RNA or ribozymes; an organic molecule of molecular
 CC weight below 5000, preferably 300, that binds to the polypeptide; an
 CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
 CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human
 CC (monoclonal) antibody directed against Ab or any of the above derivatised
 CC with a reporter group, cell toxin, immunostimulatory molecules and/or
 CC radioisotope. The polynucleotides are identified in human prostatic
 CC cancer by differential expression analysis, using DNA microarrays,
 CC between normal and tumorous tissues, with (over)expression being detected
 CC by quantitative PCR. Analysis of prostatic cancer samples showed that
 CC CD24 was upregulated in many of them. Sections of tissue, isolated from
 CC prostatic cancer patients, or subjects at risk, were incubated
 CC sequentially with anti-human CD4 murine monoclonal antibodies;
 CC biotinylated second antibody; streptavidin-conjugated horseradish
 CC peroxidase and then diaminobenzidine as colour former (brown). The
 CC samples were counterstained with hemalum (blue). Malignant cells stained
 CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
 CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
 CC lymph node metastases were also stained. ADR5805-ADR66954 represent the
 CC polynucleotide and polypeptide sequences used in the method of the
 CC invention.
 XX
 XX Sequence 369 AA;
 SQ
 Query Match 54.1%; Score 59; DB 8; Length 369;
 Best Local Similarity 50.0%; Pred. No. 1.1;

CC samples were counterstained with hemalum (blue). Malignant cells stained
 CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
 CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
 CC lymph node metastases were also stained. ADR65805-ADR66954 represent the
 CC polynucleotide and polypeptide sequences used in the method of the
 CC invention.
 XX
 SQ Sequence 369 AA;
 Query Match 54.1%; Score 59; DB 8; Length 369;
 Best Local Similarity 50.0%; Pred. No. 1.1;
 Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 1 EGYIQNYRCRGDSDSKVQEAR 20
 :|||: |||: :||: |
 Db 230 DGYIEYICRGNAERVKEGR 249
 :|||: |||: :||: |
 RESULT 23
 ADR66930
 ID ADR66930 standard; protein; 371 AA.
 XX
 AC ADR66930;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Human prostatic carcinoma derived DNA SEQ ID 228 #4.
 XX
 KW human; cytostatic; diagnosis; prostatic cancer;
 KW differential expression analysis.
 XX
 OS Homo sapiens.
 XX
 PN WO2004076614-A2.
 XX
 PD 10-SEP-2004.
 XX
 PF 22-FEB-2004; 2004WO-DE000433.
 XX
 PR 27-FEB-2003; 2003DE-01009985.
 PR 14-MAY-2003; 2003DE-01022134.
 XX
 PA (HINZ/) HINZMANN B.
 PA (DAHL/) DAHL E.
 PA (ROSE/) ROSENTHAL A.
 PA (HERM/) HERMANN K.
 PA (PILA/) PILARSKY C.
 XX
 PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;
 PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;
 PI Xinzhang L, Staub E;
 XX
 DR WPI; 2004-653386/63.
 XX
 PT New nucleic acids, and encoded proteins, from prostatic cancer tissue,
 PT useful for diagnosis, treatment and in screening for specific binding
 agents.
 XX
 PS Claim 2; Page 1583; 1607pp; German.
 XX
 CC This invention describes novel cytostatic polynucleotide and polypeptide
 CC sequences which can be used in a method for diagnosing prostatic cancer
 CC or the risk of developing prostatic cancer. Diagnosis is based on
 CC determining over transcription or over expression of the sequences in
 CC prostatic tissue. Screening for inhibitors of the sequences or detection
 CC substances involves a binding assay, any compounds that bind are
 CC selected, optionally after deconvolution of mixtures. Detection of a
 CC predetermined minimum level of the reporter indicates the presence of
 CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
 CC short-interfering RNA or ribozymes; an organic molecule of molecular
 CC weight below 5000, preferably 300, that binds to the polypeptide; an
 CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
 CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human

CC (monoclonal) antibody directed against Ab or any of the above derivatised
 CC with a reporter group, cell toxin, immunostimulatory molecules and/or
 CC radioisotope. The polynucleotides are identified in human prostatic
 CC cancer by differential expression analysis, using DNA microarrays,
 CC between normal and tumorous tissues, with overexpression being detected
 CC by quantitative PCR. Analysis of prostatic cancer samples showed that
 CC CD24 was upregulated in many of them. Sections of tissue, isolated from
 CC prostatic cancer patients, or subjects at risk, were incubated
 CC sequentially with anti-human CD4 murine monoclonal antibodies;
 CC biotinylated second antibody; streptavidin-conjugated horseradish
 CC peroxidase and then diaminobenzidine as colour former (brown). The
 CC samples were counterstained with hemalum (blue). Malignant cells stained
 CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
 CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
 CC lymph node metastases were also stained. ADR65805-ADR66954 represent the
 CC polynucleotide and polypeptide sequences used in the method of the
 CC invention.
 XX
 SQ Sequence 371 AA;
 Query Match 54.1%; Score 59; DB 8; Length 371;
 Best Local Similarity 50.0%; Pred. No. 1.1;
 Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 1 EGYIQNYRCRGDSDSKVQEAR 20
 :|||: |||: :||: |
 Db 232 DGYIEYICRGNAERVKEGR 251
 :|||: |||: :||: |
 RESULT 24
 ADR66032
 ID ADR66032 standard; protein; 371 AA.
 XX
 AC ADR66032;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Human prostatic carcinoma derived protein SEQ ID 228 #1.
 XX
 KW human; cytostatic; diagnosis; prostatic cancer;
 KW differential expression analysis.
 XX
 OS Homo sapiens.
 XX
 PN WO2004076614-A2.
 XX
 PD 10-SEP-2004.
 XX
 PF 22-FEB-2004; 2004WO-DE000433.
 XX
 PR 27-FEB-2003; 2003DE-01009985.
 PR 14-MAY-2003; 2003DE-01022134.
 XX
 PA (HINZ/) HINZMANN B.
 PA (DAHL/) DAHL E.
 PA (ROSE/) ROSENTHAL A.
 PA (HERM/) HERMANN K.
 PA (PILA/) PILARSKY C.
 XX
 PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;
 PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;
 PI Xinzhang L, Staub E;
 XX
 DR WPI; 2004-653386/63.
 XX
 PT New nucleic acids, and encoded proteins, from prostatic cancer tissue,
 PT useful for diagnosis, treatment and in screening for specific binding
 agents.
 XX
 PS Claim 2; Page 623; 1607pp; German.
 XX
 CC This invention describes novel cytostatic polynucleotide and polypeptide
 CC sequences which can be used in a method for diagnosing prostatic cancer

CC or the risk of developing prostatic cancer. Diagnosis is based on
 CC determining over transcription or over expression of the sequences in
 CC prostatic tissue. Screening for inhibitors of the sequences or detection
 CC substances involves a binding assay, any compounds that bind are
 CC selected, optionally after deconvolution of mixtures. Detection of a
 CC predetermined minimum level of the reporter indicates the presence of
 CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
 CC short-interfering RNA or ribozymes; an organic molecule of molecular
 CC weight below 5000, preferably 300, that binds to the polypeptide; an
 CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
 CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human
 CC (monoclonal) antibody directed against Ab or any of the above derivatised
 CC with a reporter group, cell toxin, immunostimulatory molecules and/or
 CC radioisotope. The polynucleotides are identified in human prostatic
 CC cancer by differential expression analysis, using DNA microarrays,
 CC between normal and tumorous tissues, with (over)expression being detected
 CC by quantitative PCR. Analysis of prostatic cancer samples showed that
 CC CD24 was upregulated in many of them. Sections of tissue, isolated from
 CC prostatic cancer patients, or subjects at risk, were incubated
 CC sequentially with anti-human CD4 murine monoclonal antibodies;
 CC biotinylated second antibody; streptavidin-conjugated horseradish
 CC peroxidase and then diaminobenzidine as colour former (brown). The
 CC samples were counterstained with hemalum (blue). Malignant cells stained
 CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
 CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
 CC lymph node metastases were also stained. ADR65805-ADR66954 represent the
 CC polynucleotide and polypeptide sequences used in the method of the
 CC invention.

XX SQ Sequence 371 AA;

Query Match 54.1%; Score 59; DB 8; Length 371;

Best Local Similarity 50.0%; Pred. No. 1.1;

Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EGYIONVRCRGDDSKVQEAR 20

DB 232 DGYIEYICRGNAERVKGR 251

RESULT 25

ADS24124

ID ADS24124 standard; protein; 847 AA.

XX AC ADS24124;

XX DT 02-DEC-2004 (first entry)

XX DE Bacterial polypeptide #13157.

XX KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.

XX OS Bacteria.

XX PN US2003233675-A1.

XX PD 18-DEC-2003.

XX PF 20-FEB-2003; 2003US-00369493.

XX PR 21-FEB-2002; 2002US-0360039P.

XX PA (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.

XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX DR WPI; 2004-061375/06.

XX PT New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.

XX PS Claim 1; SEQ ID NO 13157; 122pp; English.

XX CC The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 847 AA;

Query Match 45.0%; Score 49; DB 8; Length 847;

Best Local Similarity 53.3%; Pred. No. 1e+02;

Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 GYIONVRCRGDDSKV 16

DB 181 GFIOKRCRGQDIEI 195

RESULT 26

ADS24139

ID ADS24139 standard; protein; 1327 AA.

XX AC ADS24139;

XX DT 02-DEC-2004 (first entry)

XX DE Bacterial polypeptide #13172.

XX KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.

XX OS Bacteria.

XX PN US2003233675-A1.

XX PD 18-DEC-2003.

XX PF 20-FEB-2003; 2003US-00369493.

XX

PR 21-FEB-2002; 2002US-0360039P.
XX (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
DR
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 13172; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 1327 AA;
Query Match 45.0%; Score 49; DB 8; Length 1327;
Best Local Similarity 53.3%; Pred. No. 1.6e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 2 GYIQNYRCRGDDSKV 16
DB 255 GFIQRCRGQDIEI 269
RESULT 27
ADB74255
ID ADB74255 standard; protein; 705 AA.
XX
AC ADB74255;
XX
DT 04-DEC-2003 (first entry)
XX
DE Mycobacterium tuberculosis non-naturally occurring peptide #3.
XX
KW Non-naturally occurring peptide; anion pump protein; tuberculosis;
KW hypersensitivity reaction; tuberculostatic.
XX
OS Mycobacterium tuberculosis.
XX
PN US6583266-B1.
XX
PD 24-JUN-2003.
XX

PF 16-SEP-1994; 94US-00311731.
XX
PR 19-AUG-1993; 93US-00109181.
PR 22-OCT-1993; 93US-00142558.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Smith DR, Mao J;
XX WPI; 2003-656441/62.
DR N-PSDB; ADB74252.
XX
PT New Mycobacterium tuberculosis anion pump peptide useful for as
PT tuberculosis vaccine and diagnosis of tuberculosis infection.
XX
XX Disclosure; SEQ ID NO 4; 26pp; English.
XX
CC The invention relates to a non-naturally occurring peptide of
CC Mycobacterium tuberculosis comprising an amino acid sequence
CC corresponding to an anion pump protein. The invention also relates to a
CC non-naturally occurring nucleic acid corresponding to a DNA sequence of
CC Mycobacterium tuberculosis or Mycobacterium leprae. The new peptide is
CC useful as a vaccine against Mycobacterium tuberculosis or Mycobacterium
CC leprae or for screening for new tuberculosis drugs. Purified proteins
CC derived from the sequences of the invention may elicit a specific immune
CC response. The peptide may also be used to detect hypersensitivity
CC reactions of individuals exposed to Mycobacterium tuberculosis or
CC Mycobacterium leprae. The proteins and peptides may be affixed to solid
CC supports to detect antibodies typical of hypersensitivity reactions, from
CC a patient's sera. This sequence represents Mycobacterium tuberculosis non
CC -naturally occurring peptide of the invention. Note: The sequence data
CC for this patent did not form part of the printed specification but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 705 AA;
Query Match 42.7%; Score 46.5; DB 7; Length 705;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 5; Mismatches 2; Indels 1; Gaps 1;
QY 1 EGYIQNYRCRGDDSKV 16
DB 378 DGWV-TYRCRADTTEV 392
RESULT 28
ABB62735
ID ABB62735 standard; protein; 340 AA.
XX
AC ABB62735;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 14997.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE) PE CORP NY.
PA
XX Venter JC, Adams M, Li PWD, Myers EW;
PI

Sequences AAU39105-AAU68017 represent *Propionibacterium* acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by *P. acnes*. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hysterositis and osteomyelitis), uveitis and endophthalmitis. *P. acnes* is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of *P. acnes* in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for *P. acnes* proteins. These antibodies can be used to downregulate expression and activity of *P. acnes* polypeptides and therefore treat *P. acnes* infections. The antibodies may also be used as diagnostic agents for determining *P. acnes* presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

Sequence 84 AA;
xx
SQ

```

Query Match      41.3%;   Score 45;   DB 4;   Length 84;
Best Local Similarity 37.5%;   Pred. No. 37;
Matches 6;   Conservative 7;   Mismatches 3;   Indels 0;   Gaps 0

```

RESULT	30	
ABM56755		
ID	ABM56755	standard; protein; 84 AA.
XX	AC	
XX	ABM56755;	
XX		
XX		
DT	20-OCT-2003	(first entry)
XX		
DE	Propionibacterium	acnes predicted ORF-encoded polypeptide #21431.
XX		
XX	Acne vulgaris;	antiseborrheic; dermatological; antibacterial;
KW	immunostimulant;	immune response; vaccine.
XX		
OS	Propionibacterium	acnes.

XX	WO2003033515-A1.	
XX	PN	
XX	XX	
XX	PD	
XX	XX	24-APR-2003.
XX	XX	
XX	11-OCT-2002;	2002WO-US032727.
XX	XX	
XX	15-OCT-2001;	2001US-00978825.
XX	PR	
XX	XX	(CORI-) CORIXA CORP.
PA	XX	
XX	MITCHAM JL,	Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
PI	PI	Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
PI	PI	Barth B, Vallieue-Douglass J;
XX	XX	
DR	WPI;	2003-381785/36.
DR	N-PSDB;	ACF64537.
XX	XX	
PT	PT	New Propionibacterium acnes polypeptides and polynucleotides encoding the
PT	PT	polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
XX	XX	or for stimulating an immune response specific for a P. acnes protein.
XX	XX	
PS	Example 1;	SEQ ID NO 21431; 1481pp; English.
XX	XX	
CC	CC	The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
CC	CC	encoding a Propionibacterium acnes protein. The invention also relates to
CC	CC	polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to

CC immunogenic fragments of *P. acnes* polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a *P. acnes*
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition (comprising *P. acnes* polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of *P. acnes* in a
 CC patient; and a method for inhibiting the development of *P. acnes* in a
 CC patient. The *P. acnes* polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating *P. acnes*
 CC vulgaris, or for stimulating an immune response specific for *P. acnes*
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against *P. acnes*, or for treating *P. acnes*,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the *P. acnes* polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 84 AA;

Query Match 41.3%; Score 45; DB 6; Length 84;
 Best Local Similarity 37.5%; Pred. No. 37;
 Matches 6; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 5 QNYRCRGDDSKVQEAR 20
 :|||::: :|||::: :|||::: :|||:::
 Db 35 RHYACGEGVRQDSR 50

RESULT 31

ADL92508
 ID ADL92508 standard; protein; 135 AA.

XX AC ADL92508;

XX DT 20-MAY-2004 (first entry)

XX DE iMab111 VAP protein fragment.

XX KW immunoglobulin superfamily; beta-barrel; cytostatic; antimicrobial;
 XX cancer; microbial infection; protein-coordinate data.

XX OS Unidentified.

XX PN US2003215914-A1.

XX PD 20-NOV-2003.

XX PF 10-DEC-2002; 2002US-00316194.

XX PR 10-DEC-2001; 2001US-00016516.

XX PA (HOUT/) HOUTZAGER E.

XX PA (VIJN/) VIJN I M C.

XX PA (SIJN/) SIJMONS P C.

XX PI Houtzager E, VijN IMC, Sijmons PC;

XX DR WPI; 2004-021843/02.

XX PT New proteinaceous molecule comprising a binding peptide and a core
 PT comprising a beta-barrel, useful for preparing a composition for
 PT diagnosing or treating a condition involving unwanted proteins, cells or
 PT microorganisms e.g., cancer.

XX PS Example 3; Page 30; 84pp; English.

XX This invention describes a novel proteinaceous molecule (e.g. from an
 CC immunoglobulin superfamily origin) which comprises a binding peptide and
 CC a core comprising a beta-barrel of at least 4 strands. The invention also
 CC describes a method for identifying the proteinaceous molecule, cells
 CC comprising the isolated proteinaceous molecule, a method for producing a
 CC nucleic acid encoding the proteinaceous molecule capable of displaying at
 CC least one desired peptide sequence, displaying a desired peptide
 CC sequence, producing a library including artificial binding peptides,
 CC separating a substance from a mixture, a pharmaceutical composition
 CC comprising the proteinaceous molecule for treating a pathological
 CC condition involving unwanted proteins, cells or microorganisms, a
 CC diagnostic assay comprising the isolated proteinaceous molecule, a gene
 CC delivery vehicle comprising a nucleic acid encoding the isolated
 CC proteinaceous molecule and a nucleic acid encoding a gene of interest and
 CC a chromatography column comprising the proteinaceous molecule and a
 CC packaging material. The alteration of the molecule comprises a post-
 CC translational modification. The products of the invention have cytostatic
 CC and antimicrobial activity. The proteinaceous molecule is useful for
 CC preparing a composition for diagnosing or treating a pathological
 CC condition involving unwanted proteins, cells or microorganisms, e.g.,
 CC cancer or microbial infections.

XX SQ Sequence 135 AA;

Query Match 41.3%; Score 45; DB 8; Length 135;
 Best Local Similarity 53.3%; Pred. No. 61;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 GYQNYRCRGDDSKV 16
 |||::: :|||::: :|||::: :|||:::
 Db 119 GYDSHYRCQGTDTV 133

RESULT 32

ADR41823
 ID ADR41823 standard; protein; 135 AA.

XX AC ADR41823;

XX DT 04-NOV-2004 (first entry)

XX DE Versatile affinity protein iMab111.

XX KW cosmetic; target; softener; hair; perfume; deodorant; mouth wash;
 KW cleaning; hair dye; lipstick; rouge; skin colouring; affinity region;
 KW versatile affinity protein; VAP; protein co-ordinate data.

XX OS Lama glama.

XX PN WO2004069211-A2.

XX PD 19-AUG-2004.

XX PF 10-DEC-2003; 2003WO-NL000876.

XX PR 10-DEC-2002; 2002EP-00080206.

XX PR 10-DEC-2002; 2002US-0432906P.

XX PA (LMAB-) L-MABS BV.

XX PI Houtzager E, VijN IMC, Sijmons PC, Valinotti T, Mudge G, Padel A;

XX DR WPI; 2004-604350/58.

XX PT Applying cosmetic substance to desired target molecule, involves
 PT providing conjugate of proteinaceous substance having specific affinity
 PT for target molecule linked to cosmetic substance.

XX PS Claim 18; Fig 22; 213pp; English.

XX CC The invention relates to a novel method for applying a cosmetic substance
 CC to a desired target molecule. The method comprises providing a conjugate

CC of a proteinaceous substance having specific affinity for the target
 CC molecule linked to a cosmetic substance, where the resulting connection
 CC between cosmetic substance and target molecule can be disrupted upon the
 CC presence of a chemical and/or physical signal. The invention further
 CC comprises: a conjugate obtained by the method; a cosmetic composition
 CC comprising the conjugate; a detergent and/or softener composition
 CC comprising the conjugate; and a di- or multivalent proteinaceous
 CC substance having specific affinity for two or more target molecules
 CC present in hair, where epitopes are recognised on two or more target
 CC molecules may be the same or different. The method is useful for applying
 CC a cosmetic substance to a desired target molecule. The di- or multivalent
 CC proteinaceous substance is useful for a perfume, a deodorant, a mouth
 CC wash, cleaning, hair dye, a lipstick, rouge or another skin colouring
 CC composition. This sequence represents a versatile affinity protein (VAP)
 CC of the invention.

XX

SQ Sequence 135 AA;

Query Match 41.3%; Score 45; DB 8; Length 135;
 Best Local Similarity 53.3%; Pred. No. 61;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 GYIQNYRCRGDDSKV 16
 || :|||:|
 Db 119 GYDSHYRCQGTDTV 133

RESULT 33

AAW99087

ID AAW99087 standard; protein; 822 AA.

XX

AC AAW99087;

XX

DT 13-MAY-1999 (first entry)

XX

DE Human serine protease BSSP-3.

XX

KW Serine protease; BSSP-3; brain tissue.

XX

OS Homo sapiens.

XX

PN WO9905290-A1.

XX

PD 04-FEB-1999.

XX

PF 24-JUL-1998; 98WO-JP003324.

XX

PR 24-JUL-1997; 97JP-00213969.

XX

PA (SUNR) SUNTORY LTD.

XX

PI Tsuruoka N, Yamashiro K, Yamaguchi N;

XX

DR WPI: 1999-142942/12.

XX

DR N-PSDB; AAX19024.

XX

PT New serine protease expressed in brain tissue - used in screening for

XX

PS potential serine protease inhibitors for drug use.

XX

PS Claim 1; Page 61-65; 69pp; Japanese.

XX

CC The present sequence is a serine protease designated BSSP-3, which is
 CC isolated from human brain tissue. Transformants may be used to produce
 CC the enzyme or its partial sequences. Products from the present invention
 CC are used for screening for potential peptide or non-peptide serine
 CC protease inhibitors or expression regulators for use as drugs

XX

SQ Sequence 822 AA;

Query Match

Best Local Similarity 41.3%; Score 45; DB 2; Length 822;

Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

XX

RESULT 35

QY 3 YIQNYRCRGDDSKV 16

Db 233 YMSNVRCRGDEENI 246

XX

RESULT 35

QY 3 YIQNYRCRGDDSKV 16
 || :|||:|
 Db 180 YMSNVRCRGDEENI 193

RESULT 34

AAW83361

ID AAW83361 standard; protein; 875 AA.

XX

AC AAW83361;

XX

DT 17-FEB-1999 (first entry)

XX

DE Human neurotrypsin.

XX

KW Human; neurotrypsin; tumour inhibition; neurological disease;
 KW lung disease; gene therapy; drug development; stroke; brain injury;
 KW neurodegeneration; neuroinflammatory disease; multiple sclerosis;
 KW epilepsy; hypoxia; ischaemia; nerve transection; neovascularisation;
 KW emphysema; bronchitis.

XX

OS Homo sapiens.

XX

PN WO9849322-A1.

XX

PD 05-NOV-1998.

XX

PF 24-APR-1998; 98WO-IB000625.

XX

PR 26-APR-1997; 97CH-00000966.

XX

PA (SOND/) SONDEREGGER P.

XX

PI Sonderegger P;

XX

DR WPI: 1999-009438/01.

XX

DR N-PSDB; AAV72589.

XX

PT New human and murine neurotrypsin - used, e.g. for inhibiting tumours,
 PT treatment of neurological or lung disease, including by gene therapy and
 PT in drug development.

XX

PS Claim 1; Page 20-24; 50pp; English.

XX

CC The present sequence represents human neurotrypsin. Neurotrypsin proteins
 CC and polynucleotides can be used: (i) to inhibit tumours, including
 CC metastases, e.g. of brain or retina; (ii) to minimise tissue damage
 CC caused by stroke or brain injury (having a protective effect on the
 CC penumbra zone); (iii) to treat or prevent neurodegeneration,
 CC neuroinflammatory disease (e.g. multiple sclerosis) or epilepsy; (iv) to
 CC increase survival of damaged neurons (e.g. in cases of hypoxia,
 CC ischaemia, nerve transection) and to stimulate regeneration and/or
 CC restoration of synapses; (v) to treat or prevent retinal disorders (e.g.
 CC degeneration or neovascularisation); (vi) to prevent apoptosis (or other
 CC causes of cell death) in the nervous system; (vii) to regenerate brain
 CC and/or nervous tissue; (viii) to treat pain; (ix) to improve brain
 CC performance, including learning and memory; (x) to treat or prevent a
 CC wide range of psychiatric disorders; and (xi) to treat brain or lung
 CC injury associated with protease expression (specifically emphysema or
 CC bronchitis)

XX

SQ Sequence 875 AA;

Query Match

Best Local Similarity 41.3%; Score 45; DB 2; Length 875;

Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

XX

QY 3 YIQNYRCRGDDSKV 16

Db 233 YMSNVRCRGDEENI 246

XX

RESULT 35

ADQ21226
 ID ADQ21226 standard; protein; 875 AA.
 AC ADQ21226;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4046.
 XX
 KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2004048938-A2.
 XX
 PD 10-JUN-2004.
 XX
 PF 26-NOV-2003; 2003WO-US038193.
 XX
 PR 26-NOV-2002; 2002US-0429739P.
 XX
 PA (PROT-) PROTEIN DESIGN LABS INC.
 XX
 PI Aziz N, Ginsburg WM, Zlotnik A;
 XX
 DR WPI; 2004-441208/41.
 XX
 PT Early detection of soft tissue sarcoma comprises determining expression
 of a gene in a first soft tissue sample and a normal soft tissue sample
 PT and comparing the gene expression, also useful in treating soft tissue
 PT sarcoma.
 XX
 PS Example 2; SEQ ID NO 4046; 210pp; English.
 XX
 CC The invention relates to a novel method for detecting soft tissue sarcoma
 CC which comprises obtaining a first soft tissue sample from an individual
 CC and a normal soft tissue sample from the same or different individual,
 CC determining the expression of a gene in both samples and comparing the
 CC expression of the gene in both soft tissue samples, where a higher level
 CC of protein expression in the first soft tissue sample indicates the
 CC presence of soft tissue sarcoma. The method of the invention has
 CC cytostatic applications and may be useful for detecting soft tissue
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
 CC acid sequences may be useful in diagnostic and screening applications.
 CC The current sequence is that of a human soft tissue sarcoma-upregulated
 CC protein of the invention. The current sequence is not shown within the
 CC specification per se but was submitted in CD format by the inventor.
 XX
 SQ Sequence 875 AA;
 XX
 Query Match 41.3%; Score 45; DB 8; Length 875;
 Best Local Similarity 50.0%; Pred. No. 4.5e+02;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 3 YIQNYRCRGDDSKV 16
 Db 233 YWSNVRCRGDEENI 246
 DE
 RESULT 36
 ADQ89082
 ID ADQ89082 standard; protein; 875 AA.
 XX
 AC ADQ89082;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Human urological disorder related protein 14063 SEQ:34.
 XX
 KW urological disorder; uropathic; cytostatic; urinary incontinence;
 KW benign prostatic hyperplasia; human.
 XX
 OS Homo sapiens.

XX
 PN WO2004065576-A2.
 XX
 PD 05-AUG-2004.
 XX
 PF 14-JAN-2004; 2004WO-US000750.
 XX
 PR 15-JAN-2003; 2003US-0440318P.
 PR 04-FEB-2003; 2003US-0444783P.
 PR 27-MAR-2003; 2003US-0457901P.
 PR 08-MAY-2003; 2003US-0468775P.
 PR 19-MAY-2003; 2003US-0471614P.
 PR 16-JUN-2003; 2003US-0478742P.
 PR 18-JUL-2003; 2003US-0488529P.
 PR 30-JUL-2003; 2003US-0491156P.
 PR 02-SEP-2003; 2003US-0499594P.
 PR 26-SEP-2003; 2003US-0506332P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Karicheti V, Silos-Santiago I, Eliasof SD;
 XX
 DR WPI; 2004-562167/54.
 DR N-PSDB; ADQ89081.
 XX
 PT Use of polypeptides related to urological disorders, e.g. 44390, 54181,
 PT 211 or for identifying a compound capable of treating a urological
 PT disorder or identifying and treating a subject having a urological
 PT disorder.
 XX
 PS Claim 1; SEQ ID NO 34; 542pp; English.
 XX
 CC The present invention describes the use of polypeptides related to
 CC urological disorders for identifying a compound capable of treating a
 CC urological disorder, identifying a subject having a urological disorder,
 CC or treating a subject having a urological disorder. Also described: (1) a
 CC method for identifying a compound capable of treating a urological
 CC disorder; (2) a method for identifying a subject having a urological
 CC disorder; and (3) a method for treating a subject having a urological
 CC disorder. The compound has uropathic and cytostatic activities. The
 CC polypeptides related to urological disorders are useful for identifying a
 CC compound capable of treating a urological disorder, identifying a subject
 CC having a urological disorder, or treating a subject having a urological
 CC disorder. Disorders include urinary incontinence and benign prostatic
 CC hyperplasia. The present sequence represents a human urological disorder
 CC related protein, which is used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 875 AA;
 XX
 Query Match 41.3%; Score 45; DB 8; Length 875;
 Best Local Similarity 50.0%; Pred. No. 4.5e+02;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 3 YIQNYRCRGDDSKV 16
 Db 233 YWSNVRCRGDEENI 246
 DE
 RESULT 37
 ABUS4593
 ID ABUS4593 standard; protein; 191 AA.
 XX
 AC ABUS4593;
 XX
 DT 03-JUN-2003 (first entry)
 XX
 DE Human NOVX polypeptide #52.
 XX
 KW Human; NOVX; metabolic disorder; cardiomyopathy; diabetes; ASD;
 KW hypertension; congenital heart defect; aortic stenosis; valve disease;
 KW atrial septal defect; atrioventricular canal defect; ductus arteriosus;
 KW pulmonary stenosis; subaortic stenosis; ventricular septal defect; VSD;

KW tuberosus sclerosis; scleroderma; atherosclerosis; infectious disease;
KW obesity; anorexia; neurodegenerative disorder; Alzheimer's disease;
KW Parkinson's disease; immune disorder; haematopoietic disorder;
KW haemophilia; hypercoagulation; Crohn's disease; cancer.
XX Homo sapiens.
OS
XX WO200281498-A2.
XX 17-OCT-2002.
XX
XX 03-APR-2002; 2002WO-US010780.
XX
PR 03-APR-2001; 2001US-0281086P.
PR 03-APR-2001; 2001US-0281136P.
PR 05-APR-2001; 2001US-0281863P.
PR 05-APR-2001; 2001US-0281906P.
PR 06-APR-2001; 2001US-0282020P.
PR 10-APR-2001; 2001US-0282930P.
PR 10-APR-2001; 2001US-0282934P.
PR 12-APR-2001; 2001US-0283512P.
PR 13-APR-2001; 2001US-0283710P.
PR 17-APR-2001; 2001US-0284234P.
PR 19-APR-2001; 2001US-0285325P.
PR 20-APR-2001; 2001US-0285381P.
PR 20-APR-2001; 2001US-0285609P.
PR 23-APR-2001; 2001US-0285748P.
PR 23-APR-2001; 2001US-0285890P.
PR 24-APR-2001; 2001US-0286068P.
PR 25-APR-2001; 2001US-0286292P.
PR 27-APR-2001; 2001US-0287213P.
PR 02-MAY-2001; 2001US-0288257P.
PR 29-MAY-2001; 2001US-0294164P.
PR 30-MAY-2001; 2001US-0294484P.
PR 18-JUN-2001; 2001US-0298952P.
PR 19-JUN-2001; 2001US-0299237P.
PR 19-JUN-2001; 2001US-0299276P.
PR 12-SEP-2001; 2001US-0318750P.
PR 25-SEP-2001; 2001US-0324800P.
PR 25-SEP-2001; 2001US-0324802P.
PR 27-SEP-2001; 2001US-0325684P.
PR 17-OCT-2001; 2001US-0330143P.
PR 14-NOV-2001; 2001US-0332131P.
PR 14-NOV-2001; 2001US-0332240P.
PR 14-NOV-2001; 2001US-0332779P.
PR 21-NOV-2001; 2001US-0332115P.
PR 04-DEC-2001; 2001US-0337621P.
PR 03-JAN-2002; 2002US-0345783P.
PR 16-JAN-2002; 2002US-0350251P.
PR 02-APR-2002; 2002US-00114270.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Guo X, Kekuda R, Miller CE, Malvankar UM, Spytek KA;
XX Pattarajan M, Liu X, Gusev VY, Li L, Vernet CAM, Zerhusen BP;
XX Gorman L, Shenoy SG, Pena CEA, Smithson G, Burgess CE, Gerlach V;
XX Padigar M, Shinkets RA, Gangilli EA, Taupier RJ, Casman SJ, Ji W;
XX Anderson DW, Leite MW, Rastelli L, Edinger SR, Stone DJ;
XX Macdougall JR, Rothenberg MB, Mazur A, Millet I, Peyman JA;
XX Ellerman K;
XX
XX WPI: 2003-046858/04.
XX N-PSDB; ABX72221.
XX
XX New isolated NOVX polypeptide useful for treating atherosclerosis,
XX metabolic disorders, diabetes, obesity, infectious disease, anorexia,
XX neurodegenerative disorders, Alzheimer's disease and cancer.
XX
XX Claim 1; Page 205; 666pp; English.
XX
XX The invention relates to human polypeptides, termed NOVX, and the
XX polynucleotides encoding them. The polypeptides and polynucleotides are
XX useful for diagnosing disease, and screening for potential therapeutic

CC agents. The sequences are useful for treating metabolic disorders,
CC cardiomyopathy, diabetes, hypertension, congenital heart defects, aortic
CC stenosis, atrial septal defect (ASD), atrioventricular canal defect,
CC ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular
CC septal defect (VSD), valve diseases, tuberosus sclerosis, scleroderma,
CC atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative
CC disorders, Alzheimer's disease, Parkinson's disease, immune disorders,
CC haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease
CC and cancer. Sequences ABU54542-ABU54647 represent human NOVX polypeptides
CC of the invention
XX
XX Sequence 191 AA;
XX
XX Query Match 40.4%; Score 44; DB 6; Length 191;
XX Best Local Similarity 43.8%; Pred. No. 1.3e+02;
XX Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 4 IONYRCRGDDSKVQEA 19
XX Db 137 LQLYRCREDAAIYQA 152
XX
XX RESULT 38
XX ADE58277
XX ID ADE58277 standard; protein; 385 AA.
XX AC ADE58277;
XX XX
XX 29-JAN-2004 (first entry)
XX
XX Human Protein Q01459, SEQ ID NO 4148.
XX
XX Human; pain; neuronal tissue; gene therapy;
XX spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNI; Chung.
XX
XX Homo sapiens.
XX
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX
XX (GEHO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI: 2003-268312/26.
XX GENBANK; Q01459.
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a

CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIFO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 385 AA;
 Query Match 40.4%; Score 44; DB 7; Length 385;
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YIQNYRCRG 11
 |||||
 Db 342 YIQNYRLRG 350

RESULT 39

ADM04173
 ID ADM04173 standard; protein; 485 AA.

XX AC ADM04173;

XX DT 20-MAY-2004 (first entry)

XX DE Human protein of the invention SEQ ID NO:2859.

XX KW human; gene therapy; diagnostic marker; pharmaceutical.

XX OS Homo sapiens.

XX PN EP1347046-A1.

XX PD 24-SEP-2003.

XX PF 12-APR-2002; 2002EP-00008400.

XX PR 22-MAR-2002; 2002JP-00137785.

XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Kio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

XX DR WPI; 2003-723558/69.

XX DR N-PSDB; ADM01730.

XX PT New polynucleotides and polypeptides are useful in gene therapy, for
 PT developing a diagnostic marker or medicines for regulating their
 PT expression and activity, or as a target of gene therapy.

XX PS Claim 1; SEQ ID NO 2858; 305pp; English.

XX CC The invention relates to a novel human polynucleotide and the encoded
 CC polypeptide. A polynucleotide of the invention may have a use in gene
 CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
 CC as a primer for synthesizing the polynucleotide or as a probe for
 CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
 CC useful in gene therapy, for developing a diagnostic marker or medicines
 CC for regulating their expression and activity, or as a target of gene
 CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
 CC are useful as pharmaceutical agents. The present sequence represents a

CC protein sequence of the invention.

XX SQ Sequence 485 AA;

Query Match 40.4%; Score 44; DB 7; Length 485;
 Best Local Similarity 53.8%; Pred. No. 3.4e+02;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 YIQNYRCRGDDSK 15

||:|:|:|:|

Db 466 YLYNWRCPGTDS 478

RESULT 40

AAAY79209
 ID AAAY79209 standard; protein; 498 AA.

XX AC AAAY79209;

XX DT 19-JUN-2000 (first entry)

XX DE Human transferase TRNSFS-1.

XX KW Transferase; TRNSFS-1; human; antitumour; cancer;
 KW gastrointestinal disorder; developmental disorder; genetic disorder;
 KW neurological disorder; reproductive disorder; smooth muscle disorder;
 KW immunological disorder; inflammation; diagnosis; therapy;
 KW myristoyl CoA:protein N-myristoyltransferase.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Modified-site 64 /note= "potential O-phosphorylation"

FT Modified-site 68 /note= "potential O-phosphorylation"

FT Peptide 150..228 /note= "myristoyl-CoA protein N-myristoyltransferase signature"

FT Modified-site 166 /note= "potential O-phosphorylation"

FT Modified-site 220 /note= "potential O-phosphorylation"

FT Peptide 240..285 /note= "myristoyl-CoA protein N-myristoyltransferase signature"

FT Modified-site 240 /note= "potential O-phosphorylation"

FT Peptide 246..254 /note= "myristoyl-CoA protein N-myristoyltransferase signature"

FT Modified-site 258 /note= "potential O-phosphorylation"

FT Modified-site 270 /note= "potential O-phosphorylation"

FT Peptide 286..362 /note= "myristoyl-CoA protein N-myristoyltransferase signature"

FT Modified-site 295 /note= "potential O-phosphorylation"

FT Modified-site 319 /note= "potential N-glycosylation"

FT Modified-site 325 /note= "potential O-phosphorylation"

FT Modified-site 350 /note= "potential O-phosphorylation"

FT Modified-site 350 /note= "potential O-phosphorylation"

FT Modified-site 417 /note= "potential O-phosphorylation"

FT Peptide 436..488 /note= "myristoyl-CoA protein N-myristoyltransferase signature"

FT FT


```

Db          59  GFIQKRCGQDIIEI 73
RESULT 44
ABU62071
ID  ABU62071 standard; protein; 1907 AA.
XX
AC  ABU62071;
XX
DT  04-SEP-2003 (first entry)
XX
DE  Human skeletal muscle alpha-kinase (SK).
XX
KW  Human; mammalian kinase; melanoma alpha-kinase; MK; HK; KK; SK; IK;
KW  heart alpha-kinase; kidney alpha-kinase; skeletal muscle alpha-kinase;
KW  lymphocyte alpha-kinase; alpha-kinase catalytic domain;
KW  ion channel domain; enzyme.
XX
OS  Homo sapiens.
XX
PN  US2002177205-A1.
XX
PD  28-NOV-2002.
XX
PF  10-APR-2001; 2001US-00832292.
XX
PR  03-AUG-2000; 2000US-00632131.
XX
PA  (RYAZ/) RYAZANOV A.
XX
PI  Ryzanov A;
XX
DR  WPI; 2003-352609/33.
DR  N-PSDB; ACD26093.
XX
PT  Novel mammalian alpha-kinase proteins, including melanoma, kidney, heart,
PT  skeletal muscle or lymphocyte alpha-kinase protein useful for treating an
PT  animal in need of increased activity of mammalian alpha-kinase.
XX
PS  Claim 26; Fig 10B; 69pp; English.
XX
CC  The present invention relates to the isolation of novel mammalian kinases
CC  designated melanoma alpha-kinase (MK), heart alpha-kinase (HK), kidney
CC  alpha-kinase (KK), skeletal muscle alpha-kinase (SK), and lymphocyte
CC  alpha-kinase (LK), and the polynucleotide sequences encoding them. The
CC  alpha-kinase proteins are characterised by the presence of at least two
CC  domains, one being an alpha-kinase catalytic domain and other being an
CC  ion channel domain. The proteins are useful for treating an animal in
CC  need of increased activity of melanoma, kidney, heart, skeletal muscle or
CC  lymphocyte alpha-kinase. An antibody to the kinase is useful for
CC  detecting the presence of an melanoma, kidney, heart, skeletal muscle or
CC  lymphocyte alpha-kinase in a sample. ABU62065-ABU62072 represent the
CC  alpha-kinases of the invention
XX
SQ  Sequence 1907 AA;
Query Match          40.4%; Score 44; DB 6; Length 1907;
Best Local Similarity 43.8%; Pred. No. 1.5e+03;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY  4  IQNYRCGDDSKVQEA 19
    : ||||| : : :
Db  339  LQLYRCREDAAIYQA 354

RESULT 45
ABG23434
ID  ABG23434 standard; protein; 152 AA.
XX
AC  ABG23434;
XX
DT  18-FEB-2002 (first entry)
XX
DE  Novel human secretory protein, Seq ID No 610.
XX

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```

DE  Novel human diagnostic protein #23425.
XX
KW  Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW  food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS  Homo sapiens.
XX
PN  WO200175067-A2.
XX
PD  11-OCT-2001.
XX
PF  30-MAR-2001; 2001WO-US0008631.
XX
PR  31-MAR-2000; 2000US-00540217.
PR  23-AUG-2000; 2000US-00649167.
XX
PA  (HYSE-) HYSEQ INC.
XX
PI  Drmanac RT, Liu C, Tang YT;
XX
DR  WPI; 2001-639362/73.
DR  N-PSDB; AAS87621.
XX
PT  New isolated polynucleotide and encoded polypeptides, useful in
PT  diagnostics, forensics, gene mapping, identification of mutations
PT  responsible for genetic disorders or other traits and to assess
PT  biodiversity.
XX
PS  Claim 20; SEQ ID NO 53793; 103pp; English.
XX
CC  The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC  sequences. (I) is useful as hybridisation probes, polymerase chain
CC  reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC  and in recombinant production of (II). The polynucleotides are also used
CC  in diagnostics as expressed sequence tags for identifying expressed
CC  genes. (I) is useful in gene therapy techniques to restore normal
CC  activity of (II) or to treat disease states involving (II). (II) is
CC  useful for generating antibodies against it, detecting or quantitating a
CC  polypeptide in tissue, as molecular weight markers and as a food
CC  supplement. (II) and its binding partners are useful in medical imaging
CC  of sites expressing (II). (I) and (II) are useful for treating disorders
CC  involving aberrant protein expression or biological activity. The
CC  polypeptide and polynucleotide sequences have application in
CC  diagnostics, forensics, gene mapping, identification of mutations
CC  responsible for genetic disorders or other traits to assess biodiversity
CC  and to produce other types of data and products dependent on DNA and
CC  amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC  amino acid sequences of the invention. Note: The sequence data for this
CC  patent did not appear in the printed specification, but was obtained in
CC  electronic format directly from WIPO at
CC  ftp.wipo.int/pub/published_pct_sequences
XX
SQ  Sequence 152 AA;
Query Match          39.4%; Score 43; DB 4; Length 152;
Best Local Similarity 58.3%; Pred. No. 1.4e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY  4  IQNYRCRGDDSK 15
    : ||||| :
Db  66  LDNHRCRGDLTK 77

RESULT 46
AAU28253
ID  AAU28253 standard; protein; 237 AA.
XX
AC  AAU28253;
XX
DT  18-DEC-2001 (first entry)
XX
DE  Novel human secretory protein, Seq ID No 610.
XX

```

SQL	Sequence 237 AA;
	Query Match 39.4%; Score 43; DB 4; Length 237; Best Local Similarity 58.3%; Pred.No. 2.3e+02; Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY	4 IQNYRCRGDSDK 15 : : :
Db	3 LDNHRCRGDLTK 14
 RESULT 47	
ADSI2199	ADSI2199 standard; protein; 237 AA.
XX	ADSI2199;
XX	16-DEC-2004 (first entry)
DT	Human therapeutic contig protein - SEQ ID 2436.
DE	antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary; inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell; aplastic anaemia; cancer; wound healing; gene therapy.
XX	Homo sapiens.
OS	
XX	Key Location/Qualifiers
FH	Misc-difference 1..237 /label= Unknown, OTHER
FT	/note= "OTHER = In-frame STOP codon"
FT	
PX	WO2004080148-A2.
PN	
XX	23-SEP-2004.
PD	
XX	30-SEP-2003; 2003WO-US030720.
PF	
XX	02-OCT-2002; 2002US-0416186P.
PR	
XX	(NUVE-) NUVELO INC.
PA	
PI	Tang YT, Asundi V, Ren F, Zhang J, Zhang J, Wehrman T, Wang Z, Ma Y; Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P; WPI: 2004-668857/65. DR N-PSDB; ADSI1601.
XX	New polynucleotide, useful in preparing a composition for diagnosing or treating inflammatory, neurodegenerative or stem cell disorders, e.g., aplastic anemia or cancer for promoting wound healing.
PT	
XX	Example 2; SEQ ID NO 2436; 718pp; English.
PS	
CC	The invention relates to a novel isolated polynucleotide and the encoded polypeptide. The molecules of the invention demonstrate antiinflammatory, neuroprotective, antianaemic, cytostatic and vulnerary activities and may be useful in preparing a composition for diagnosing or treating inflammatory, haematopoietic, immune, neurodegenerative or stem cell disorders, such as aplastic anaemia or cancer, as well as for promoting wound healing. The molecules may also be utilised during gene therapy procedures. The current sequence is that of a human therapeutic contig protein of the invention.
XX	
SQ	Sequence 237 AA;
	Query Match 39.4%; Score 43; DB 8; Length 237; Best Local Similarity 58.3%; Pred.No. 2.3e+02; Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY	4 IQNYRCRGDSDK 15 : : :
Db	3 LDNHRCRGDLTK 14

```

RESULT 48
ADN72921
ID   ADN72921 standard; protein; 371 AA.
AC   ADN72921;
XX
XX   15-JUL-2004 (first entry)
XX
XX   Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 816.
XX
XX   plant; transgenic; E2Fa/Dpa transcription factor; growth regulator;
XX   animal feed product; thale cress; cell wall biosynthesis;
XX   nitrogen metabolism; carbon metabolism.
XX
XX   Arabidopsis thaliana.
XX
XX   WO2004035798-A2.
XX
XX   29-APR-2004.
XX
XX   20-OCT-2003; 2003WO-EP011658.
XX
XX   18-OCT-2002; 2002EP-00079408.
XX
XX   (CROP-) CROPDESIGN NV.
XX
XX   Inze D, De Veylder L, Vlieghe K;
XX
XX   WPI; 2004-348466/32.
XX
XX   N-PSDB; ADN72920.
XX
XX
XX   Altering plant characteristics, useful for producing plants for enzyme or
XX   pharmaceutical production comprises modifying in a plant, expression of
XX   one or more nucleic acids and/or modifying level or activity of one or
XX   more proteins.
XX
XX   Claim 1; SEQ ID NO 816; 134pp; English.
XX
XX   This invention relates to a novel method for altering one or more plant
XX   characteristics. Specifically, it refers to identifying genes that are up
XX   - or down-regulated in transgenic plants overexpressing the heterodimeric
XX   E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to
XX   alter plant characteristics accordingly. The present invention describes
XX   generating transgenic plants for the production of growth regulators,
XX   enzymes, therapeutics, pharmaceuticals and animal feed products, where
XX   the altered plant characteristics are selected from increased yield or
XX   biomass, enhanced survival capacity, stress tolerance, plant architecture
XX   or physiology, altered endoreplication, biochemistry, signal
XX   transduction, storage lipid mobilisation and/or altered photosynthesis,
XX   each relative to the corresponding wild type plants. Accordingly, these
XX   sequences can also be useful as positive or negative selectable markers
XX   during transformation of cells or tissues. The identified genes play a
XX   role in a variety of biological processes such as DNA replication, cell
XX   wall biosynthesis, nitrogen and/or carbon metabolism or they function as
XX   transcription factors. This polypeptide sequence is thale cress protein
XX   expressed by a gene upregulated 1.3 fold or more in plants overexpressing
XX   the E2Fa/Dpa transcription factor, given in an exemplification of the
XX   invention.
XX
XX   Query Match          39.4%; Score 43; DB 8; Length 371;
XX   Best Local Similarity 47.1%; Pred. No. 3.7e+02;
XX   Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
XX
XX   Qy      4 IQNYRCRGDSKVQEAR 20
XX          :||| :||| :||| :|||
XX   Db      301 VQNCRCDSENVVWEFR 317
XX
XX   RESULT 49

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ADJ50947
ID   ADJ50947 standard; protein; 421 AA.
XX
XX   ADJ50947;
XX
XX   06-MAY-2004 (first entry)
XX
XX   Human novel protein NOV4b.
XX
XX   Human; NOVX; autoimmune disease; Alzheimer's disease; stroke; allergy;
XX   Parkinson's disease; Huntington's disease; multiple sclerosis; anxiety;
XX   pain; diabetes; graft versus host disease; pancreatitis; obesity; ulcer;
XX   anaemia; cancer; viral infection; bacterial infection;
XX   parasitic infection.
XX
XX   Homo sapiens.
XX
XX   US2004030096-A1.
XX
XX   12-FEB-2004.
XX
XX   01-AUG-2002; 2002US-00210281.
XX
XX   02-AUG-2001; 2001US-0309501P.
XX   03-AUG-2001; 2001US-0310291P.
XX   08-AUG-2001; 2001US-0310951P.
XX   09-AUG-2001; 2001US-0311292P.
XX   13-AUG-2001; 2001US-0311979P.
XX   14-AUG-2001; 2001US-0312203P.
XX   17-AUG-2001; 2001US-0313201P.
XX   20-AUG-2001; 2001US-0313643P.
XX   20-AUG-2001; 2001US-0313702P.
XX   21-AUG-2001; 2001US-0314031P.
XX   23-AUG-2001; 2001US-0314466P.
XX   28-AUG-2001; 2001US-0315403P.
XX   29-AUG-2001; 2001US-0315853P.
XX   05-MAR-2002; 2002US-0361775P.
XX   05-MAR-2002; 2002US-0361832P.
XX
XX   (GORM/) GORMAN L.
XX   (ZERR/) ZERHUSEN B D.
XX   (EDIN/) EDINGER S R.
XX   (PADI/) PADIGARU M.
XX   (GUOX/) GUO X.
XX   (KEKU/) KEKUDA R.
XX   (ZHON/) ZHONG M.
XX   (PATT/) PATTURAJAN M.
XX   (MILL/) MILLER C E.
XX   (JIWW/) JI W.
XX   (PENA/) PENA C E A.
XX   (BURG/) BURGESS C E.
XX   (SCIO/) SCIORE P.
XX   (STON/) STONE D J.
XX   (TAUP/) TAUPIER R J.
XX   (CASM/) CASMAN S J.
XX   (ROTH/) ROTHENBERG M E.
XX   (MALY/) MALYANKAR U M.
XX   (BOLD/) BOLDOG F L.
XX
XX   Gorman L, Zerhusen BD, Edinger SR, Padigaru M, Guo X, Kekuda R;
XX   Zhong M, Patturajan M, Miller CE, Ji W, Pena CE, Burgess CE;
XX   Sciore P, Stone DJ, Taupier RJ, Casman SU, Rothenberg ME;
XX   Malyankar UM, Boldog FL;
XX
XX   WPI: 2004-168942/16.
XX   N-PSDB; ADJ50946.
XX
XX   New NOVX polypeptides and polynucleotides, useful in diagnosing, treating
XX   or preventing diseases or conditions, e.g. autoimmune disease,
XX   Alzheimer's disease, diabetes, graft versus host disease, cancer or viral
XX   or bacterial infections.
XX
XX   Claim 2; SEQ ID NO 12; 342pp; English.

```


CC parasitic infections (many more diseases and disorders are listed in the
 CC specification). The present sequence represents a NOVX protein.

XX
 SQ Sequence 424 AA;

Query Match 39.4%; Score 43; DB 8; Length 424;
 Best Local Similarity 58.3%; Pred. No. 4.3e+02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 IQNYRCRGDDSK 15

Db 196 LDNHRCRGDLTK 207

Search completed: September 7, 2005, 19:54:42
 Job time : 167.186 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 7, 2005, 20:04:06 ; Search time 161 Seconds
(without alignments)
12.231 Million cell updates/sec

Title: US-10-812-238B-41

Perfect score: 32

Sequence: 1 CRGDD 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1774312 seqs, 393823214 residues

Total number of hits satisfying chosen parameters: 1774312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*

2: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pep.*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*

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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*

8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*

9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*

10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*

11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*

12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*

13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*

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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*

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20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*

21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	32	100.0	6	17	US-10-812-238A-32	Sequence 32, App
2	32	100.0	10	17	US-10-812-238A-20	Sequence 20, App
3	32	100.0	13	17	US-10-812-238A-23	Sequence 23, App
4	32	100.0	20	17	US-10-812-238A-2	Sequence 2, Appl
5	32	100.0	43	16	US-10-437-963-157113	Sequence 157113,
6	32	100.0	74	16	US-10-425-115-262985	Sequence 262985,
7	32	100.0	77	16	US-10-437-963-170560	Sequence 170560,
8	32	100.0	81	16	US-10-437-963-113416	Sequence 113416,
9	32	100.0	152	15	US-10-389-566-938	Sequence 938, Ap
10	32	100.0	155	16	US-10-425-115-261512	Sequence 261512,
11	32	100.0	156	16	US-10-437-963-160624	Sequence 160624,

85	28	87.5	140	15	US-10-276-774-1857	Sequence 1857, Ap	158	27	84.4	57	16	US-10-425-115-130978	Sequence 190978,
86	28	87.5	147	15	US-10-424-599-180302	Sequence 180302,	159	27	84.4	72	16	US-10-425-115-315720	Sequence 315720,
87	28	87.5	158	15	US-10-424-599-162278	Sequence 162278,	160	27	84.4	72	15	US-10-424-599-222350	Sequence 222350,
88	28	87.5	160	15	US-10-085-198-96	Sequence 96, Appl	161	27	84.4	93	15	US-10-424-599-225782	Sequence 225782,
89	28	87.5	160	16	US-10-085-198-98	Sequence 98, Appl	162	27	84.4	105	16	US-10-425-115-251759	Sequence 251759,
90	28	87.5	160	16	US-10-729-473-7	Sequence 7, Appl	163	27	84.4	106	16	US-10-425-115-195840	Sequence 195840,
91	28	87.5	184	16	US-10-425-115-296818	Sequence 296818,	164	27	84.4	120	15	US-10-424-599-130435	Sequence 190435,
92	28	87.5	193	16	US-10-425-115-204748	Sequence 204748	165	27	84.4	122	15	US-10-283-132A-62268	Sequence 62268, A
93	28	87.5	220	16	US-10-437-963-144344	Sequence 144344,	166	27	84.4	127	16	US-10-425-115-226461	Sequence 226461,
94	28	87.5	223	16	US-10-425-115-336315	Sequence 336315,	167	27	84.4	128	16	US-10-425-115-298115	Sequence 298115,
95	28	87.5	229	16	US-10-425-115-218457	Sequence 218457,	168	27	84.4	133	16	US-10-425-115-283941	Sequence 283941,
96	28	87.5	263	16	US-10-437-963-140042	Sequence 140042,	169	27	84.4	135	16	US-10-425-115-349300	Sequence 349300,
97	28	87.5	283	20	US-11-021-951-169	Sequence 169, App	170	27	84.4	148	15	US-10-424-599-161914	Sequence 161914,
98	28	87.5	294	16	US-10-425-115-331100	Sequence 331100,	171	27	84.4	158	16	US-10-437-963-109741	Sequence 109741,
99	28	87.5	323	9	US-09-764-898-181	Sequence 181, App	172	27	84.4	159	16	US-10-437-963-126010	Sequence 126010,
100	28	87.5	342	16	US-10-437-963-157655	Sequence 157655,	173	27	84.4	161	16	US-10-767-701-43187	Sequence 43187, A
101	28	87.5	348	16	US-10-739-930-8397	Sequence 8397, Ap	174	27	84.4	164	15	US-10-282-122A-43151	Sequence 43151, A
102	28	87.5	362	16	US-10-737-450-58	Sequence 58, Appl	175	27	84.4	186	16	US-10-767-701-32566	Sequence 32566, A
103	28	87.5	390	15	US-10-108-260A-4719	Sequence 4719, Ap	176	27	84.4	198	16	US-10-425-115-357665	Sequence 357665,
104	28	87.5	416	16	US-10-370-715B-150	Sequence 150, App	177	27	84.4	214	9	US-09-198-559-1	Sequence 1, Appl
105	28	87.5	417	15	US-10-453-478-18	Sequence 18, Appl	178	27	84.4	214	13	US-10-091-613-1	Sequence 1, Appl
106	28	87.5	421	15	US-10-368-438-10	Sequence 10, Appl	179	27	84.4	214	15	US-10-211-462-55	Sequence 55, Appl
107	28	87.5	435	8	US-08-459-455-51	Sequence 51, Appl	180	27	84.4	214	15	US-10-211-462-95	Sequence 95, Appl
108	28	87.5	435	9	US-09-354-697-9	Sequence 9, Appl	181	27	84.4	219	9	US-09-791-171-14	Sequence 14, Appl
109	28	87.5	435	10	US-09-851-873-97	Sequence 97, Appl	182	27	84.4	219	10	US-09-804-980-14	Sequence 14, Appl
110	28	87.5	435	14	US-10-280-670-9	Sequence 9, Appl	183	27	84.4	219	16	US-10-620-246-14	Sequence 14, Appl
111	28	87.5	435	18	US-10-973-858-16	Sequence 16, Appl	184	27	84.4	220	9	US-09-828-644-77	Sequence 77, Appl
112	28	87.5	441	8	US-08-459-455-43	Sequence 43, Appl	185	27	84.4	225	9	US-09-764-868-1102	Sequence 1102, Ap
113	28	87.5	445	16	US-10-767-701-41046	Sequence 41046, A	186	27	84.4	225	15	US-10-276-774-2405	Sequence 2405, Ap
114	28	87.5	446	9	US-09-306-226-30	Sequence 30, Appl	187	27	84.4	230	15	US-10-320-797-3036	Sequence 3036, Ap
115	28	87.5	451	9	US-09-888-243-28	Sequence 28, Appl	188	27	84.4	247	17	US-10-741-600-1591	Sequence 1591, Ap
116	28	87.5	452	14	US-10-205-219-52	Sequence 52, Appl	189	27	84.4	247	17	US-10-741-600-1592	Sequence 1592, Ap
117	28	87.5	456	16	US-10-437-963-124603	Sequence 124603,	190	27	84.4	263	16	US-10-755-889-294	Sequence 294, App
118	28	87.5	457	16	US-10-481-179-8	Sequence 8, Appl	191	27	84.4	280	13	US-10-115-899-5	Sequence 5, Appl
119	28	87.5	466	15	US-10-369-493-2996	Sequence 2996, Ap	192	27	84.4	280	13	US-10-115-899-8	Sequence 8, Appl
120	28	87.5	468	16	US-10-408-765A-1807	Sequence 1807, Ap	193	27	84.4	280	15	US-10-203-532-6	Sequence 6, Appl
121	28	87.5	469	15	US-10-166-334-8	Sequence 8, Appl	194	27	84.4	280	16	US-10-868-270-1	Sequence 1, Appl
122	28	87.5	469	15	US-10-678-986-1	Sequence 1, Appl	195	27	84.4	280	16	US-10-868-270-6	Sequence 6, Appl
123	28	87.5	469	16	US-10-408-765A-1346	Sequence 1346, Ap	196	27	84.4	291	17	US-10-624-727-53	Sequence 53, Appl
124	28	87.5	469	16	US-10-408-765A-2300	Sequence 2300, Ap	197	27	84.4	291	17	US-10-624-727-61	Sequence 61, Appl
125	28	87.5	470	15	US-10-369-493-2942	Sequence 2942, Ap	198	27	84.4	299	9	US-09-815-242-10205	Sequence 10205, A
126	28	87.5	477	14	US-10-018-6	Sequence 6, Appl	199	27	84.4	299	15	US-10-282-122A-56595	Sequence 56595, A
127	28	87.5	524	15	US-10-424-599-213918	Sequence 213918,	200	27	84.4	326	16	US-10-425-115-352784	Sequence 352784,
128	28	87.5	530	14	US-10-053-637-12	Sequence 12, Appl	201	27	84.4	341	15	US-10-282-122A-62115	Sequence 62115, A
129	28	87.5	550	16	US-10-425-115-206001	Sequence 206001,	202	27	84.4	342	16	US-10-437-963-185725	Sequence 185725,
130	28	87.5	580	9	US-09-738-626-6264	Sequence 6264, Ap	203	27	84.4	343	15	US-10-282-122A-64623	Sequence 64623, A
131	28	87.5	586	16	US-10-437-963-174585	Sequence 174585,	204	27	84.4	353	16	US-10-778-557-76	Sequence 76, Appl
132	28	87.5	616	15	US-10-108-260A-2508	Sequence 2508, Ap	205	27	84.4	357	15	US-10-282-122A-64960	Sequence 64960, A
133	28	87.5	629	16	US-10-375-010-24	Sequence 24, Appl	206	27	84.4	395	10	US-09-949-427-2	Sequence 2, Appl
134	28	87.5	659	16	US-10-643-795A-141	Sequence 141, App	207	27	84.4	395	10	US-09-949-428-2	Sequence 2, Appl
135	28	87.5	659	17	US-10-482-029-295	Sequence 295, App	208	27	84.4	448	16	US-10-437-963-183864	Sequence 183864,
136	28	87.5	659	17	US-10-948-518-141	Sequence 141, App	209	27	84.4	455	17	US-10-831-070-116	Sequence 116, App
137	28	87.5	722	14	US-10-222-668-4	Sequence 4, Appl	210	27	84.4	489	16	US-10-437-963-104970	Sequence 104970,
138	28	87.5	730	14	US-10-067-633-58	Sequence 58, Appl	211	27	84.4	492	16	US-10-437-963-192093	Sequence 192093,
139	28	87.5	739	16	US-10-437-963-141439	Sequence 141439,	212	27	84.4	496	16	US-10-425-115-304877	Sequence 304877,
140	28	87.5	746	16	US-10-437-963-118707	Sequence 118707,	213	27	84.4	526	16	US-10-481-179-2	Sequence 2, Appl
141	28	87.5	809	16	US-10-489-425-12	Sequence 12, Appl	214	27	84.4	547	16	US-10-437-963-114235	Sequence 114235,
142	28	87.5	822	9	US-09-147-947-6	Sequence 6, Appl	215	27	84.4	552	16	US-10-425-115-216188	Sequence 216188,
143	28	87.5	842	9	US-09-815-242-11950	Sequence 11950, A	216	27	84.4	553	10	US-09-927-239C-1	Sequence 1, Appl
144	28	87.5	842	15	US-10-282-122A-66544	Sequence 66544, A	217	27	84.4	553	17	US-10-703-986-1	Sequence 1, Appl
145	28	87.5	875	16	US-10-757-262-34	Sequence 34, Appl	218	27	84.4	559	14	US-10-163-587A-11	Sequence 11, Appl
146	28	87.5	875	16	US-10-723-860-4046	Sequence 4046, Ap	219	27	84.4	559	14	US-10-205-219-38	Sequence 38, Appl
147	28	87.5	875	17	US-10-843-299-2	Sequence 2, Appl	220	27	84.4	559	14	US-10-369-378-23	Sequence 23, Appl
148	28	87.5	963	15	US-10-464-368-86	Sequence 86, Appl	221	27	84.4	575	15	US-10-104-047-3176	Sequence 3176, Ap
149	28	87.5	963	16	US-10-479-875-5	Sequence 5, Appl	222	27	84.4	595	15	US-10-425-114-63271	Sequence 63271, A
150	28	87.5	1013	16	US-10-437-963-130025	Sequence 130025,	223	27	84.4	602	14	US-10-161-051-143	Sequence 143, App
151	28	87.5	1075	16	US-10-425-115-274886	Sequence 274886,	224	27	84.4	605	9	US-09-782-980-62	Sequence 62, Appl
152	28	87.5	1280	14	US-10-087-887-86	Sequence 86, Appl	225	27	84.4	605	16	US-10-408-765A-632	Sequence 632, App
153	28	87.5	1806	15	US-10-369-493-5622	Sequence 5622, Ap	226	27	84.4	605	16	US-10-706-791-21	Sequence 21, Appl
154	28	87.5	2043	15	US-10-120-801-81	Sequence 81, Appl	227	27	84.4	605	16	US-10-806-018-62	Sequence 62, Appl
155	27	84.4	34	9	US-09-925-297-883	Sequence 883, App	228	27	84.4	658	16	US-10-408-765A-2647	Sequence 2647, Ap
156	27	84.4	50	16	US-10-425-115-367125	Sequence 367125,	229	27	84.4	686	16	US-10-437-963-128149	Sequence 128149,
157	27	84.4	54	17	US-10-926-683-957	Sequence 957, App	230	27	84.4	713	16	US-10-437-963-113424	Sequence 113424,

231	27	84.4	736	15	US-10-250-613-10	Sequence 10, Appl	304	26	81.2	9	10	US-09-791-524-124	Sequence 124, App
232	27	84.4	1011	15	US-10-422-536-111	Sequence 11, Appl	305	26	81.2	9	11	US-09-995-388-47	Sequence 47, Appl
233	27	84.4	1011	15	US-10-232-351-9	Sequence 9, Appl	306	26	81.2	9	13	US-10-013-009-1	Sequence 1, Appl
234	27	84.4	1036	16	US-10-437-963-192091	Sequence 87, Appl	307	26	81.2	9	13	US-10-033-769-10	Sequence 10, Appl
235	27	84.4	1059	15	US-10-334-143-87	Sequence 87, Appl	308	26	81.2	9	13	US-10-081-258-10	Sequence 10, Appl
236	27	84.4	1137	10	US-09-949-427-405	Sequence 405, App	309	26	81.2	9	13	US-10-080-854-8	Sequence 8, Appl
237	27	84.4	1137	10	US-09-949-428-405	Sequence 405, App	310	26	81.2	9	13	US-10-059-749-56	Sequence 56, Appl
238	27	84.4	2174	14	US-10-087-887-87	Sequence 87, Appl	311	26	81.2	9	13	US-10-038-972A-10	Sequence 10, Appl
239	26	81.2	5	9	US-09-813-484-24	Sequence 24, Appl	312	26	81.2	9	14	US-10-304-160-3	Sequence 3, Appl
240	26	81.2	5	9	US-09-912-609-9	Sequence 9, Appl	313	26	81.2	9	14	US-10-264-374-1	Sequence 1, Appl
241	26	81.2	5	9	US-09-364-597A-37	Sequence 37, Appl	314	26	81.2	9	14	US-10-032-221B-35	Sequence 35, Appl
242	26	81.2	5	14	US-10-046-801-24	Sequence 24, Appl	315	26	81.2	9	14	US-10-375-992-1	Sequence 1, Appl
243	26	81.2	5	14	US-10-304-160-2	Sequence 2, Appl	316	26	81.2	9	15	US-10-269-575-1	Sequence 1, Appl
244	26	81.2	5	17	US-10-838-289-65	Sequence 65, Appl	317	26	81.2	9	15	US-10-269-575-2	Sequence 2, Appl
245	26	81.2	6	9	US-09-912-609-10	Sequence 10, Appl	318	26	81.2	9	15	US-10-269-575-3	Sequence 3, Appl
246	26	81.2	6	9	US-09-912-609-13	Sequence 13, Appl	319	26	81.2	9	15	US-10-296-879-5	Sequence 5, Appl
247	26	81.2	6	9	US-09-364-597A-7	Sequence 7, Appl	320	26	81.2	9	15	US-10-296-879-28	Sequence 28, Appl
248	26	81.2	6	17	US-10-838-289-66	Sequence 66, Appl	321	26	81.2	9	15	US-10-609-217-449	Sequence 449, App
249	26	81.2	6	17	US-10-838-289-67	Sequence 67, Appl	322	26	81.2	9	15	US-10-609-217-450	Sequence 450, App
250	26	81.2	7	9	US-09-364-597A-13	Sequence 13, Appl	323	26	81.2	9	15	US-10-609-217-451	Sequence 451, App
251	26	81.2	7	9	US-09-364-597A-14	Sequence 14, Appl	324	26	81.2	9	15	US-10-609-217-452	Sequence 452, App
252	26	81.2	7	9	US-09-364-597A-30	Sequence 30, Appl	325	26	81.2	9	15	US-10-609-217-1076	Sequence 1076, Ap
253	26	81.2	7	9	US-09-840-277-59	Sequence 59, Appl	326	26	81.2	9	15	US-10-363-208-166	Sequence 166, App
254	26	81.2	7	10	US-09-791-524-148	Sequence 148, App	327	26	81.2	9	15	US-10-652-244-20	Sequence 20, Appl
255	26	81.2	7	14	US-10-264-374-220	Sequence 220, App	328	26	81.2	9	15	US-10-632-388-449	Sequence 449, App
256	26	81.2	7	15	US-10-609-217-444	Sequence 444, App	329	26	81.2	9	15	US-10-632-388-450	Sequence 450, App
257	26	81.2	7	15	US-10-632-388-444	Sequence 444, App	330	26	81.2	9	15	US-10-632-388-451	Sequence 451, App
258	26	81.2	7	15	US-10-651-723-444	Sequence 444, App	331	26	81.2	9	15	US-10-632-388-452	Sequence 452, App
259	26	81.2	7	15	US-10-645-761-444	Sequence 444, App	332	26	81.2	9	15	US-10-632-388-1076	Sequence 1076, Ap
260	26	81.2	7	15	US-10-666-696-444	Sequence 444, App	333	26	81.2	9	15	US-10-668-955-44	Sequence 44, Appl
261	26	81.2	7	15	US-10-653-048-444	Sequence 444, App	334	26	81.2	9	15	US-10-651-723-449	Sequence 449, App
262	26	81.2	7	15	US-10-653-048-444	Sequence 444, App	335	26	81.2	9	15	US-10-651-723-450	Sequence 450, App
263	26	81.2	7	16	US-10-264-374-220	Sequence 220, App	336	26	81.2	9	15	US-10-651-723-451	Sequence 451, App
264	26	81.2	7	18	US-10-818-246-2	Sequence 2, Appl	337	26	81.2	9	15	US-10-651-723-452	Sequence 452, App
265	26	81.2	8	9	US-09-813-484-19	Sequence 19, Appl	338	26	81.2	9	15	US-10-651-723-1076	Sequence 1076, Ap
266	26	81.2	8	9	US-09-813-484-20	Sequence 20, Appl	339	26	81.2	9	15	US-10-645-761-449	Sequence 449, App
267	26	81.2	8	9	US-09-813-484-21	Sequence 21, Appl	340	26	81.2	9	15	US-10-645-761-450	Sequence 450, App
268	26	81.2	8	9	US-09-424-656-5	Sequence 5, Appl	341	26	81.2	9	15	US-10-645-761-451	Sequence 451, App
269	26	81.2	8	9	US-09-364-597A-27	Sequence 27, Appl	342	26	81.2	9	15	US-10-645-761-452	Sequence 452, App
270	26	81.2	8	13	US-10-013-009-4	Sequence 4, Appl	343	26	81.2	9	15	US-10-645-761-1076	Sequence 1076, Ap
271	26	81.2	8	14	US-10-137-435-5	Sequence 5, Appl	344	26	81.2	9	15	US-10-666-696-449	Sequence 449, App
272	26	81.2	8	14	US-10-046-801-19	Sequence 19, Appl	345	26	81.2	9	15	US-10-666-696-450	Sequence 450, App
273	26	81.2	8	14	US-10-046-801-20	Sequence 20, Appl	346	26	81.2	9	15	US-10-666-696-451	Sequence 451, App
274	26	81.2	8	14	US-10-046-801-21	Sequence 21, Appl	347	26	81.2	9	15	US-10-666-696-452	Sequence 452, App
275	26	81.2	8	14	US-10-083-861B-7	Sequence 7, Appl	348	26	81.2	9	15	US-10-666-696-1076	Sequence 1076, Ap
276	26	81.2	8	15	US-10-296-879-5	Sequence 5, Appl	349	26	81.2	9	15	US-10-653-048-449	Sequence 449, App
277	26	81.2	8	15	US-10-296-879-27	Sequence 27, Appl	350	26	81.2	9	15	US-10-653-048-450	Sequence 450, App
278	26	81.2	8	17	US-10-753-729-1	Sequence 1, Appl	351	26	81.2	9	15	US-10-653-048-451	Sequence 451, App
279	26	81.2	9	8	US-08-865-579-56	Sequence 56, Appl	352	26	81.2	9	15	US-10-653-048-452	Sequence 452, App
280	26	81.2	9	9	US-09-746-731-56	Sequence 56, Appl	353	26	81.2	9	15	US-10-653-048-1076	Sequence 1076, Ap
281	26	81.2	9	9	US-09-765-086-1	Sequence 1, Appl	354	26	81.2	9	15	US-10-264-374-1	Sequence 1, Appl
282	26	81.2	9	9	US-09-952-768-44	Sequence 44, Appl	355	26	81.2	9	16	US-10-375-992-1	Sequence 1, Appl
283	26	81.2	9	9	US-09-912-609-31	Sequence 31, Appl	356	26	81.2	9	16	US-10-697-535-1	Sequence 1, Appl
284	26	81.2	9	9	US-09-845-160-5	Sequence 5, Appl	357	26	81.2	9	16	US-10-815-514-33	Sequence 33, Appl
285	26	81.2	9	9	US-09-245-603A-16	Sequence 16, Appl	358	26	81.2	9	16	US-10-729-156-4	Sequence 4, Appl
286	26	81.2	9	9	US-09-364-597A-15	Sequence 15, Appl	359	26	81.2	9	16	US-10-877-930-33	Sequence 33, Appl
287	26	81.2	9	9	US-09-364-597A-16	Sequence 16, Appl	360	26	81.2	9	17	US-10-835-151-1	Sequence 1, Appl
288	26	81.2	9	9	US-09-364-597A-17	Sequence 17, Appl	361	26	81.2	9	17	US-10-835-151-17	Sequence 17, Appl
289	26	81.2	9	9	US-09-364-597A-18	Sequence 18, Appl	362	26	81.2	9	17	US-10-655-755-12	Sequence 12, Appl
290	26	81.2	9	9	US-09-364-597A-33	Sequence 33, Appl	363	26	81.2	9	17	US-10-838-289-87	Sequence 87, Appl
291	26	81.2	9	9	US-09-364-597A-34	Sequence 34, Appl	364	26	81.2	9	17	US-10-838-289-267	Sequence 267, App
292	26	81.2	9	9	US-09-995-388-47	Sequence 47, Appl	365	26	81.2	9	17	US-10-912-764-34	Sequence 34, Appl
293	26	81.2	9	9	US-09-954-697-94	Sequence 94, Appl	366	26	81.2	9	17	US-10-917-709-2	Sequence 2, Appl
294	26	81.2	9	9	US-09-734-628-1	Sequence 1, Appl	367	26	81.2	9	17	US-10-363-205-9	Sequence 9, Appl
295	26	81.2	9	9	US-09-971-798-5	Sequence 5, Appl	368	26	81.2	9	17	US-10-363-205-78	Sequence 78, Appl
296	26	81.2	9	9	US-09-969-192-3	Sequence 3, Appl	369	26	81.2	9	17	US-10-363-205-84	Sequence 84, Appl
297	26	81.2	9	9	US-09-840-277-14	Sequence 14, Appl	370	26	81.2	9	17	US-10-363-205-120	Sequence 102, App
298	26	81.2	9	9	US-09-840-277-22	Sequence 22, Appl	371	26	81.2	9	17	US-10-363-205-220	Sequence 220, App
299	26	81.2	9	9	US-09-840-277-38	Sequence 38, Appl	372	26	81.2	9	17	US-10-363-205-273	Sequence 273, App
300	26	81.2	9	9	US-09-840-277-52	Sequence 52, Appl	373	26	81.2	9	17	US-10-607-595-211	Sequence 211, App
301	26	81.2	9	9	US-09-840-277-62	Sequence 62, Appl	374	26	81.2	9	17	US-10-873-594-33	Sequence 33, Appl
302	26	81.2	9	9	US-09-840-277-63	Sequence 63, Appl	375	26	81.2	9	18	US-10-645-784-449	Sequence 449, App
303	26	81.2	9	10	US-09-801-485-2	Sequence 2, Appl	376	26	81.2	9	18	US-10-645-784-450	Sequence 450, App

377	26	81.2	9	18	US-10-645-784-451	Sequence 451, App	450	15	16	US-10-442-658-11	Sequence 11, Appl
378	26	81.2	9	18	US-10-645-784-452	Sequence 452, App	451	16	10	US-09-801-485-10	Sequence 10, Appl
379	26	81.2	9	18	US-10-645-784-1076	Sequence 1076, App	452	16	15	US-10-353-522A-7	Sequence 7, Appl
380	26	81.2	9	18	US-10-800-399-20	Sequence 20, Appl	453	16	17	US-10-917-709-10	Sequence 10, Appl
381	26	81.2	10	9	US-09-780-142-2	Sequence 2, Appl	454	16	9	US-09-757-908A-16	Sequence 16, Appl
382	26	81.2	10	9	US-09-424-656-6	Sequence 6, Appl	455	18	10	US-09-801-485-8	Sequence 8, Appl
383	26	81.2	10	9	US-09-845-160-14	Sequence 6, Appl	456	18	10	US-09-801-485-9	Sequence 9, Appl
384	26	81.2	10	9	US-09-364-597A-5	Sequence 14, Appl	457	18	15	US-10-430-685-26	Sequence 26, Appl
385	26	81.2	10	9	US-09-870-203A-43	Sequence 43, Appl	458	18	17	US-10-917-709-8	Sequence 8, Appl
386	26	81.2	10	14	US-10-116-067-5	Sequence 5, Appl	459	18	17	US-10-917-709-9	Sequence 9, Appl
387	26	81.2	10	14	US-10-137-435-6	Sequence 6, Appl	460	19	15	US-10-353-522A-3	Sequence 3, Appl
388	26	81.2	10	14	US-10-013-815-21	Sequence 21, Appl	461	19	15	US-10-353-522A-4	Sequence 4, Appl
389	26	81.2	10	14	US-10-429-496-2	Sequence 2, Appl	462	20	9	US-09-205-658-27	Sequence 27, Appl
390	26	81.2	10	14	US-10-429-428-2	Sequence 4, Appl	463	20	9	US-09-844-353A-27	Sequence 27, Appl
391	26	81.2	10	15	US-10-269-575-4	Sequence 4, Appl	464	20	10	US-09-963-693-27	Sequence 27, Appl
392	26	81.2	10	15	US-10-403-337-30	Sequence 30, Appl	465	20	15	US-10-272-437A-10	Sequence 10, Appl
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394	26	81.2	10	15	US-10-296-879-6	Sequence 6, Appl	467	21	14	US-10-661-156-525	Sequence 525, App
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399	26	81.2	11	9	US-09-424-656-7	Sequence 7, Appl	472	23	14	US-10-162-043-5	Sequence 5, Appl
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ALIGNMENTS

RESULT 1
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; Sequence 32, Application US/10812238A
; Publication No. US20050002904A1
; GENERAL INFORMATION:
; APPLICANT: Wary, Kishore, K.
; APPLICANT: Humtsoe, Joseph O.
; TITLE OF INVENTION: Uses of Vascular Endothelial Growth Factor
; TITLE OF INVENTION: and Type I Collagen Inducible Protein (VCIP)
; FILE REFERENCE: D6563
; CURRENT APPLICATION NUMBER: US/10/812,238A
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,164
; PRIOR FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 32
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: a peptide containing a RGD sequence
US-10-812-238A-32

Query Match 100.0%; Score 32; DB 17; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
Db 1 CRGDD 5

RESULT 2
US-10-812-238A-20
; Sequence 20, Application US/10812238A
; Publication No. US20050002904A1
; GENERAL INFORMATION:
; APPLICANT: Wary, Kishore, K.
; APPLICANT: Humtsoe, Joseph O.
; TITLE OF INVENTION: Uses of Vascular Endothelial Growth Factor
; TITLE OF INVENTION: and Type I Collagen Inducible Protein (VCIP)
; FILE REFERENCE: D6563
; CURRENT APPLICATION NUMBER: US/10/812,238A
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,164
; PRIOR FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: a peptide containing RGD sequence
US-10-812-238A-20

Query Match 100.0%; Score 32; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
Db 4 CRGDD 8

RESULT 3
US-10-812-238A-23
; Sequence 23, Application US/10812238A
; Publication No. US20050002904A1
; GENERAL INFORMATION:
; APPLICANT: Wary, Kishore, K.
; APPLICANT: Humtsoe, Joseph O.
; TITLE OF INVENTION: Uses of Vascular Endothelial Growth Factor
; TITLE OF INVENTION: and Type I Collagen Inducible Protein (VCIP)
; FILE REFERENCE: D6563
; CURRENT APPLICATION NUMBER: US/10/812,238A
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,164
; PRIOR FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 23
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: a peptide containing RGD sequence
US-10-812-238A-23

Query Match 100.0%; Score 32; DB 17; Length 13;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
Db 4 CRGDD 8

RESULT 4
US-10-812-238A-2

; Sequence 2, Application US/10812238A
; Publication No. US20050002904A1

; GENERAL INFORMATION:
; APPLICANT: Wary, Kishore, K.
; APPLICANT: Huntsoe, Joseph O.
; TITLE OF INVENTION: Uses of Vascular Endothelial Growth Factor
; TITLE OF INVENTION: and Type I Collagen Inducible Protein (VCIP)
; FILE REFERENCE: D6563
; CURRENT APPLICATION NUMBER: US/10/812,238A
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,164
; PRIOR FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 2
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: peptide used to raise anti-VCIP-RGD antibody
US-10-812-238A-2

Query Match 100.0%; Score 32; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 9 CRGDD 13

RESULT 5

US-10-437-963-157113
; Sequence 157113, Application US/10437963

; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 157113
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(43)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_56716C.1.pep
US-10-437-963-157113

Query Match 100.0%; Score 32; DB 16; Length 43;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 30 CRGDD 34

RESULT 6

US-10-425-115-262985

; Sequence 262985, Application US/10425115
; Publication No. US20040214272A1

; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 262985
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_171454C.1.pep
US-10-425-115-262985

Query Match 100.0%; Score 32; DB 16; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 44 CRGDD 48

RESULT 7

US-10-437-963-170560

; Sequence 170560, Application US/10437963
; Publication No. US20040123343A1

; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 170560
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_68875C.1.pep
US-10-437-963-170560

Query Match 100.0%; Score 32; DB 16; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 36 CRGDD 40

RESULT 8

US-10-437-963-113416

; Sequence 113416, Application US/10437963
; Publication No. US20040123343A1

; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 113416
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_17205C.1.pep
US-10-437-963-113416

Query Match 100.0%; Score 32; DB 16; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 35 CRGDD 39
|||||

RESULT 9
US-10-389-566-938
; Sequence 938, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 938
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (88)..(88)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (152)..(152)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-389-566-938

Query Match 100.0%; Score 32; DB 15; Length 152;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 49 CRGDD 53
|||||

RESULT 10
US-10-425-115-261512
; Sequence 261512, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 261512
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_170112C.1.pep
US-10-425-115-261512

Query Match 100.0%; Score 32; DB 16; Length 155;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 74 CRGDD 78
|||||

RESULT 11
US-10-437-963-160624
; Sequence 160624, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 160624
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_59888C.1.pep
US-10-437-963-160624

Query Match 100.0%; Score 32; DB 16; Length 156;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 35 CRGDD 39
|||||

RESULT 12
US-10-424-599-245759
; Sequence 245759, Application US/10424599

; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 245759
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(192)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_63952C.1.pep
US-10-424-599-245759

Query Match 100.0%; Score 32; DB 15; Length 192;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
|||
Db 37 CRGDD 41

RESULT 13
US-10-424-599-254290
; Sequence 254290, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 254290
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(203)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_71648C.1.pep
US-10-424-599-254290

Query Match 100.0%; Score 32; DB 15; Length 203;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
|||
Db 177 CRGDD 181

RESULT 14
US-10-437-963-199332
; Sequence 199332, Application US/10437963
; Publication No. US20040123343A1

; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 199332
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_94907C.1.pep
US-10-437-963-199332

Query Match 100.0%; Score 32; DB 16; Length 207;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
|||
Db 126 CRGDD 130

RESULT 15
US-10-437-963-128934
; Sequence 128934, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 128934
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_3123C.1.pep
US-10-437-963-128934

Query Match 100.0%; Score 32; DB 16; Length 248;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
|||
Db 21 CRGDD 25

RESULT 16
US-10-437-963-204891
; Sequence 204891, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

```
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 204891
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(253)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_99933C.1.pep
US-10-437-963-204891

Query Match      100.0%; Score 32; DB 16; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDD 5
Db      86 CRGDD 90

RESULT 17
US-10-732-923-5779
; Sequence 5779, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 5779
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(267)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-732-923-5779

Query Match      100.0%; Score 32; DB 17; Length 267;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDD 5
Db      220 CRGDD 224

RESULT 18
US-10-437-963-103596
; Sequence 103596, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
```

```
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 103596
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_101009C.1.pep
US-10-437-963-103596

Query Match      100.0%; Score 32; DB 16; Length 293;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDD 5
Db      43 CRGDD 47

RESULT 19
US-10-369-493-15738
; Sequence 15738, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 15738
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Xanthomonas campestris
US-10-369-493-15738

Query Match      100.0%; Score 32; DB 15; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDD 5
Db      200 CRGDD 204

RESULT 20
US-10-369-493-16124
; Sequence 16124, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
```

```
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 16124
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Xanthomonas campestris
US-10-369-493-16124

Query Match      100.0%; Score 32; DB 15; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDD 5
Db      200 CRGDD 204

RESULT 21
US-10-369-493-15371
; Sequence 15371, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 15371
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Xanthomonas campestris
US-10-369-493-15371

Query Match      100.0%; Score 32; DB 15; Length 302;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDD 5
Db      203 CRGDD 207

RESULT 22
US-10-655-601-2
; Sequence 2, Application US/10655601
; Publication No. US20040137522A1
; GENERAL INFORMATION:
; APPLICANT: Feany, Mel B.
; APPLICANT: Shulman, Joshua M.
; TITLE OF INVENTION: Genes and Proteins Altering Tau-Related Neuropathy
; FILE REFERENCE: 7570/73251
; CURRENT APPLICATION NUMBER: US/10/655,601
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```
US-10-655-601-2

Query Match      100.0%; Score 32; DB 16; Length 311;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDD 5
Db      181 CRGDD 185

RESULT 23
US-10-812-238A-13
; Sequence 13, Application US/10812238A
; Publication No. US20050002904A1
; GENERAL INFORMATION:
; APPLICANT: Wary, Kishore, K.
; APPLICANT: Humtsoe, Joseph O.
; TITLE OF INVENTION: Uses of Vascular Endothelial Growth Factor
; TITLE OF INVENTION: and Type I Collagen Inducible Protein (VCIP)
; FILE REFERENCE: D6563
; CURRENT APPLICATION NUMBER: US/10/812,238A
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/459,164
; PRIOR FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 13
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: human VCIP
US-10-812-238A-13

Query Match      100.0%; Score 32; DB 17; Length 311;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDD 5
Db      181 CRGDD 185

RESULT 24
US-10-437-963-132805
; Sequence 132805, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 132805
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_34738C.1.pep
US-10-437-963-132805

Query Match      100.0%; Score 32; DB 16; Length 393;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 175 CRGDD 179

RESULT 25
US-10-282-122A-43293
; Sequence 43293, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43293
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-282-122A-43293

Query Match 100.0%; Score 32; DB 15; Length 400;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 41 CRGDD 45

RESULT 26
US-10-282-122A-59506
; Sequence 59506, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
```

```
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59506
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-10-282-122A-59506

Query Match 100.0%; Score 32; DB 15; Length 400;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 41 CRGDD 45

RESULT 27
US-10-282-122A-73186
; Sequence 73186, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
```

```
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73186
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Salmonella paratyphi A
US-10-282-122A-73186

Query Match      100.0%; Score 32; DB 15; Length 400;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDD 5
Db      41 CRGDD 45
      |||||

RESULT 28
US-10-282-122A-75975
; Sequence 75975, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
```

```
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75975
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Salmonella typhi
US-10-282-122A-75975

Query Match      100.0%; Score 32; DB 15; Length 400;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDD 5
Db      41 CRGDD 45
      |||||

RESULT 29
US-10-425-115-214055
; Sequence 214055, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 214055
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_126814C.1.pep
US-10-425-115-214055

Query Match      100.0%; Score 32; DB 16; Length 438;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDD 5
Db      281 CRGDD 285
      |||||

RESULT 30
US-10-437-963-103600
; Sequence 103600, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
```

; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 103600
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_101012C.1.pep
US-10-437-963-103600

Query Match 100.0%; Score 32; DB 16; Length 469;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 201 CRGDD 205

RESULT 31
US-10-437-963-111036
; Sequence 111036, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 111036
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_15051C.1.pep
US-10-437-963-111036

Query Match 100.0%; Score 32; DB 16; Length 495;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 232 CRGDD 236

RESULT 32
US-10-369-493-2069
; Sequence 2069, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 2069
; LENGTH: 1116
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-10-369-493-2069

Query Match 100.0%; Score 32; DB 15; Length 1116;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 677 CRGDD 681

RESULT 33
US-10-424-599-257727
; Sequence 257727, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 257727
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_74751C.1.pep
US-10-424-599-257727

Query Match 90.6%; Score 29; DB 15; Length 51;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 13 CRGDD 17

RESULT 34
US-10-424-599-228943
; Sequence 228943, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 228943
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_48762C.1.pep
US-10-424-599-228943

Query Match 90.6%; Score 29; DB 15; Length 62;
Best Local Similarity 80.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
|:|
Db 7 CKGDD 11

RESULT 35

US-10-437-963-124025
; Sequence 124025, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 124025
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; LOCATION: (1)..(343)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_26803C.1.pap
US-10-437-963-124025

Query Match 90.6%; Score 29; DB 16; Length 112;
Best Local Similarity 80.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
|:|
Db 45 CKGDD 49

RESULT 36

US-10-425-115-353920
; Sequence 353920, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 353920
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_85948C.1.pap
US-10-425-115-353920

Query Match 90.6%; Score 29; DB 16; Length 144;
Best Local Similarity 80.0%; Pred. No. 9.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
|:|
Db 53 CKGDD 57

RESULT 37

US-10-425-115-285895
; Sequence 285895, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 285895
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(343)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_23837C.1.pap
US-10-425-115-285895

Query Match 90.6%; Score 29; DB 16; Length 343;
Best Local Similarity 80.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
|:|
Db 218 CKGDD 222

RESULT 38

US-10-424-599-228246
; Sequence 228246, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 228246
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_48134C.1.pap
US-10-424-599-228246

Query Match 90.6%; Score 29; DB 15; Length 360;
Best Local Similarity 80.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
|:|
Db 7 CKGDD 11

RESULT 39

US-10-424-599-153174
; Sequence 153174, Application US/10424599
; Publication No. US20040031072A1

```
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 153174
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_109340C.1.pep
US-10-424-599-153174

Query Match          90.6%; Score 29; DB 15; Length 370;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDD 5
Db      312 CKGDD 316

RESULT 40
US-10-424-599-151975
; Sequence 151975, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 151975
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(381)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_108257C.1.pep
US-10-424-599-151975

Query Match          90.6%; Score 29; DB 15; Length 381;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDD 5
Db      140 CKGDD 144

RESULT 41
US-10-425-115-330473
; Sequence 330473, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
```

```
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 330473
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_64492C.1.pep
US-10-425-115-330473

Query Match          90.6%; Score 29; DB 16; Length 393;
Best Local Similarity 80.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDD 5
Db      323 CKGDD 327

RESULT 42
US-10-425-115-194403
; Sequence 194403, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 194403
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_108879C.1.pep
US-10-425-115-194403

Query Match          90.6%; Score 29; DB 16; Length 399;
Best Local Similarity 80.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDD 5
Db      370 CKGDD 374

RESULT 43
US-10-183-687-481
; Sequence 481, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Cahoon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kinney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changjiang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
```


; APPLICANT: Tarczynski, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: BBI458 US NA
; CURRENT APPLICATION NUMBER: US/10/183,687
; PRIOR FILING DATE: 2002-06-27
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 481
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Glycine max
US-10-183-687-481

Query Match 90.6%; Score 29; DB 15; Length 412;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
|:|
Db 325 CKGDD 329

RESULT 44

US-10-739-930-6640
; Sequence 6640, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:

; APPLICANT: KOVALIC, DAVID K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 6640
; LENGTH: 427
; TYPE: PRT

; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: Clone ID: ARATH-23APRO3-C6231_1.p
US-10-739-930-6640

Query Match 90.6%; Score 29; DB 16; Length 427;
Best Local Similarity 80.0%; Pred. No. 2.5e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
|:|
Db 184 CKGDD 188

RESULT 45

US-10-437-963-123766
; Sequence 123766, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 123766

; LENGTH: 483
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_26569C.1.p
US-10-437-963-123766

Query Match 90.6%; Score 29; DB 16; Length 483;
Best Local Similarity 80.0%; Pred. No. 2.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
|:|
Db 289 CKGDD 293

RESULT 46

US-10-433-757-9
; Sequence 9, Application US/10433757
; Publication No. US20050101529A1
; GENERAL INFORMATION:

; APPLICANT: INCYTE CORPORATION; YUE, Henry;
; APPLICANT: AZIMZAI, Yalda; KALLICK, Deborah A.;
; APPLICANT: BAUGHN, Mariah R.; GRIFFIN, Jennifer A.;
; APPLICANT: SHARNAKAR, Anita; LAL, Preeti G.;
; APPLICANT: CHAWLA, Narinder K.; HAFALIA, April J.A.;
; APPLICANT: GANDHI, Ameena R.; AU-YOUNG, Janice K.;
; APPLICANT: ELLIOTT, Vicki S.; RAMKUMAR, Javalaxmi;
; APPLICANT: THANGAVELU, Kavitha; LU, Yan;
; APPLICANT: WARREN, Bridget A.; LU, Dzung Aina M.;
; APPLICANT: LEE, Ernestine A.; TRIBOULEY, Catherine M.;
; APPLICANT: ARVIZO, Chandra S.; DELEGANE, Angele M.;
; APPLICANT: YAO, Monique G.; KHAN, Farrah A.;
; APPLICANT: SANJANWALA, Madhusudan M.
; TITLE OF INVENTION: PROTEIN MODIFICATION AND MAINTENANCE MOLECULES
; FILE REFERENCE: PI-0310 USN
; CURRENT APPLICATION NUMBER: US/10/433,757
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/46964
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/264,623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 60/262,851
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/260,110
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/257,803
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 60/254,399
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PERL Program
; SEQ ID NO 9
; LENGTH: 508
; TYPE: PRT

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7485421CD1
US-10-433-757-9

Query Match 90.6%; Score 29; DB 17; Length 508;
Best Local Similarity 80.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
|:|
Db 261 CKGDD 265

RESULT 47

US-10-044-205A-14
; Sequence 14, Application US/10044205A

```
; Publication No. US20020123464A1
; GENERAL INFORMATION:
; APPLICANT: KAPPELLER-LIBERMANN, Rosana
; TITLE OF INVENTION: BANDARU, Rajasekhar
; TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Protei
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 10147-5201
; CURRENT APPLICATION NUMBER: US/10/044,205A
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/242,428
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: US 60/241,884
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/241,877
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Cyprinus carpio
US-10-044-205A-14

Query Match          90.6%; Score 29; DB 13; Length 549;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDD 5
Db      438 CRGDD 442

RESULT 48
US-09-872-153-18
; Sequence 18, Application US/09872153
; Patent No. US20020082207A1
; GENERAL INFORMATION:
; APPLICANT: Hirst, Shannon K.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.531
; CURRENT APPLICATION NUMBER: US/09/872,153
; CURRENT FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-872-153-18

Query Match          90.6%; Score 29; DB 9; Length 593;
Best Local Similarity 80.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDD 5
Db      346 CRGDD 350

RESULT 49
US-10-723-860-3727
; Sequence 3727, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nataasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
```

```
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3727
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-3727

Query Match          90.6%; Score 29; DB 16; Length 593;
Best Local Similarity 80.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDD 5
Db      346 CRGDD 350

RESULT 50
US-10-437-963-121532
; Sequence 121532, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 121532
; LENGTH: 813
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_24548C.1.pep
US-10-437-963-121532

Query Match          90.6%; Score 29; DB 16; Length 813;
Best Local Similarity 80.0%; Pred. No. 4.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDD 5
Db      17 CRGDD 21

RESULT 51
US-09-888-615-66
; Sequence 66, Application US/09888615
; Patent No. US20020064856A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/09/888,615
; CURRENT FILING DATE: 2001-06-26
```

; PRIOR APPLICATION NUMBER: 60/214,047
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 953
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-615-66

Query Match 90.6%; Score 29; DB 9; Length 953;
Best Local Similarity 80.0%; Pred. No. 5e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
|:|
Db 695 CKGDD 699

RESULT 52

US-10-311-035-21
; Sequence 21, Application US/10311035
; Publication No. US20040023243A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: YUE, Henry

; APPLICANT: ELLIOTT, Vicki

; APPLICANT: GANDHI, Ameena R.

; APPLICANT: LAL, Preeti

; APPLICANT: AU-YOUNG, Janice

; APPLICANT: TRIBOULEY, Catherine M.

; APPLICANT: DELEGEANS, Angelo M.

; APPLICANT: BAUGHN, Mariah R.

; APPLICANT: NGUYEN, Dannie B.

; APPLICANT: LEE, Ernestine A.

; APPLICANT: HAFALIA, April

; APPLICANT: KHAN, Farrah A.

; APPLICANT: CHAWLA, Narinder K.

; APPLICANT: YAO, Monique G.

; APPLICANT: LU, Dyung Aina M.

; APPLICANT: ARVIZU, Chandra S.

; APPLICANT: TANG, Y. Tom

; APPLICANT: WALSH, Roderick T.

; APPLICANT: AZIMZAI, Yalda

; APPLICANT: LU, Yan

; APPLICANT: RAMKUMAR, Jayalaximi

; APPLICANT: XU, Yuming

; APPLICANT: REDDY, Roopa

; APPLICANT: DAS, Depopriya

; APPLICANT: KEARNEY, Liam

; APPLICANT: KALLICK, Deborah A.

; TITLE OF INVENTION: Proteases

; FILE REFERENCE: PI-0123 PCT

; CURRENT APPLICATION NUMBER: US/10/311,035

; CURRENT FILING DATE: 2002-12-10

; PRIOR APPLICATION NUMBER: 60/212,336; 60/213,955; 60/215,396; 60/216,821; 60/218,946

; PRIOR FILING DATE: 2000-06-16; 2000-06-22; 2000-06-29; 2000-07-07; 2000-07-14

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PERL Program

; SEQ ID NO 21

; LENGTH: 953

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No. US20040023243A1 6817347CD1

US-10-311-035-21

Query Match 90.6%; Score 29; DB 15; Length 953;
Best Local Similarity 80.0%; Pred. No. 5e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5

Db 695 CKGDD 699
|:|
|:|

RESULT 53

US-10-437-963-123768

; Sequence 123768, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 123768

; LENGTH: 988

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_26570C.1.pep

US-10-437-963-123768

Query Match 90.6%; Score 29; DB 16; Length 988;

Best Local Similarity 80.0%; Pred. No. 5.2e+03;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5

|:|
|:|

Db 601 CKGDD 605

RESULT 54

US-08-865-579-74

; Sequence 74, Application US/08865579

; Publication No. US20010006779A1

; GENERAL INFORMATION:

; APPLICANT: Alnemri, Emad S.

; APPLICANT: Fernandes-Alnemri, Tereesa

; APPLICANT: Litwack, Gerald

; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids

; TITLE OF INVENTION: Encoding Same and Methods of Use

; NUMBER OF SEQUENCES: 87

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell & Flores LLP

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: United States

; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/865,579

; FILING DATE: 29-MAY-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-ID 2180

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 535-9001

;

TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-865-579-74

Query Match 87.5%; Score 28; DB 8; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 5 CRGDE 9

RESULT 55
US-09-746-731-74
; Sequence 74, Application US/09746731
; Publication No. US20010016345A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; Fernandes-Alnemri, Teresa
; Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/746,731
; FILING DATE: 22-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9849
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 74:

US-09-746-731-74

Query Match 87.5%; Score 28; DB 9; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 5 CRGDE 9

RESULT 56
US-09-952-768-59
; Sequence 59, Application US/09952768
; Patent No. US20020035242A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; Fernandes-Alnemri, Teresa
; Litwack, Gerald
; Armstrong, Robert
; Tomaselli, Kevin
; TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,
; NUCLEIC ACIDS ENCODING AND METHODS OF USE
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: Suite 6300, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/952,768
; FILING DATE: 10-Sep-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Christiansen, William T.
; REGISTRATION NUMBER: 44,614
; REFERENCE/DOCKET NUMBER: 480140.424C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..9
; OTHER INFORMATION: /note= "ICH-1"
; SEQUENCE DESCRIPTION: SEQ ID NO: 59:

US-09-952-768-59

Query Match 87.5%; Score 28; DB 9; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 5 CRGDE 9

RESULT 57
US-09-954-697-112
; Sequence 112, Application US/09954697
; Patent No. US20020106631A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 112

```
;
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-954-697-112

Query Match      87.5%; Score 28; DB 9; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CRGDD 5
Db 5 CRGDE 9

RESULT 58
US-10-059-749-74
; Sequence 74, Application US/10059749
; Publication No. US20020183504A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
;               Fernandes-Alnemri, Teresa
;               Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
;               Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/059,749
; FILING DATE: 29-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 74:
US-10-059-749-74

Query Match      87.5%; Score 28; DB 13; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CRGDD 5
Db 5 CRGDE 9

RESULT 59
US-10-668-955-59
; Sequence 59, Application US/10668955
; Publication No. US20040054148A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
;               Fernandes-Alnemri, Teresa
;               Litwack, Gerald
;               Armstrong, Robert
;               Tomaselli, Kevin
; TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,
;               NUCLEIC ACIDS ENCODING AND METHODS OF USE
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: Suite 6300, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/668,955
; FILING DATE: 22-Sep-2003
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Laherty, Carol D.
; REGISTRATION NUMBER: 51,909
; REFERENCE/DOCKET NUMBER: 480140.424D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..9
; OTHER INFORMATION: /note= "ICH-1"
; SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-10-668-955-59

Query Match      87.5%; Score 28; DB 15; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CRGDD 5
Db 5 CRGDE 9

RESULT 60
US-10-812-238A-22
; Sequence 22, Application US/10812238A
; Publication No. US20050002904A1
; GENERAL INFORMATION:
; APPLICANT: Wary, Kishore, K.
; APPLICANT: Humtsoe, Joseph O.
; TITLE OF INVENTION: Uses of Vascular Endothelial Growth Factor
; TITLE OF INVENTION: and Type I Collagen Inducible Protein (VCIP)
; FILE REFERENCE: D6563
; CURRENT APPLICATION NUMBER: US/10/812,238A
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US 60/458,164
; PRIOR FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
```

; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: a peptide containing a mutated RGD sequence
US-10-812-238A-22

Query Match 87.5%; Score 28; DB 17; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
|||:
Db 4 CRGED 8

RESULT 61
US-10-133-128-62
; Sequence 62, Application US/10133128
; Publication No. US20030082630A1
; GENERAL INFORMATION:
; APPLICANT: KOLKMAN, JOOST A.
; TITLE OF INVENTION: COMBINATORIAL LIBRARIES OF MONOMER DOMAINS
; FILE REFERENCE: 0319.410US
; CURRENT APPLICATION NUMBER: US/10/133,128
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: 60/374,107
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 60/333,359
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 60/337,209
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/286,823
; PRIOR FILING DATE: 2001-04-26
; NUMBER OF SEQ ID NOS: 244
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-133-128-62

Query Match 87.5%; Score 28; DB 14; Length 35;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
|||:
Db 1 CRGDE 5

RESULT 62
US-10-289-660-62
; Sequence 62, Application US/10289660
; Publication No. US20030157561A1
; GENERAL INFORMATION:
; APPLICANT: KOLKMAN, JOOST A.
; APPLICANT: STEMMER, WILLEM P.C.
; TITLE OF INVENTION: COMBINATORIAL LIBRARIES OF MONOMER DOMAINS
; FILE REFERENCE: 0319.510US
; CURRENT APPLICATION NUMBER: US/10/289,660
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: 10/133,128
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: 60/374,107
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 60/333,359
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 60/337,209
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/286,823
; PRIOR FILING DATE: 2001-04-26

; NUMBER OF SEQ ID NOS: 244
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-289-660-62

Query Match 87.5%; Score 28; DB 14; Length 35;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
|||:
Db 1 CRGDE 5

RESULT 63
US-10-693-057-62
; Sequence 62, Application US/10693057
; Publication No. US20040175756A1
; GENERAL INFORMATION:
; APPLICANT: Kolkman, Joost A.
; APPLICANT: Stemmer, Willem P.C.
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: Methods for Using Combinatorial Libraries
; TITLE OF INVENTION: of Monomer Domains
; FILE REFERENCE: 022013-000170US
; CURRENT APPLICATION NUMBER: US/10/693,057
; CURRENT FILING DATE: 2003-10-24
; PRIOR APPLICATION NUMBER: US 60/286,823
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/337,209
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/333,359
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 60/374,107
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US 10/133,128
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 10/289,660
; PRIOR FILING DATE: 2002-11-06
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human ApoER2 A domain
US-10-693-057-62

Query Match 87.5%; Score 28; DB 16; Length 35;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
|||:
Db 1 CRGDE 5

RESULT 64
US-10-693-056-62
; Sequence 62, Application US/10693056
; Publication No. US20050048512A1
; GENERAL INFORMATION:
; APPLICANT: Kolkman, Joost A.
; APPLICANT: Stemmer, Willem P.C.
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: Combinatorial Libraries of Monomer Domains
; FILE REFERENCE: 022013-000160US
; CURRENT APPLICATION NUMBER: US/10/693,056
; CURRENT FILING DATE: 2003-10-24

; PRIOR APPLICATION NUMBER: US 60/286,823
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/337,209
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/333,359
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 60/374,107
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US 10/133,128
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 10/289,660
; PRIOR FILING DATE: 2002-11-06
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human ApoER2 A domain
US-10-693-056-62

Query Match 87.5%; Score 28; DB 17; Length 35;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 1 CRGDE 5

RESULT 65
US-10-840-723-62
; Sequence 62, Application US/10840723
; Publication No. US2005053973A1
; GENERAL INFORMATION:
; APPLICANT: Kolkman, Joost A.
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Freskgard, Per-Ola
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: Novel Proteins With Targeted Binding
; FILE REFERENCE: 022013-000180US
; CURRENT APPLICATION NUMBER: US/10/840,723
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 60/286,823
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/337,209
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/333,359
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 60/374,107
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US 10/133,128
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 10/289,660
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: US 10/693,056
; PRIOR FILING DATE: 2003-10-24
; PRIOR APPLICATION NUMBER: US 10/693,057
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 665
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human ApoER2 A domain
US-10-840-723-62

Query Match 87.5%; Score 28; DB 17; Length 35;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 1 CRGDE 5

RESULT 66
US-10-871-602-62
; Sequence 62, Application US/10871602
; Publication No. US2005089932A1
; GENERAL INFORMATION:
; APPLICANT: Kolkman, Joost A.
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Freskgard, Per-Ola
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: Novel Proteins With Targeted Binding
; FILE REFERENCE: 022013-000190US
; CURRENT APPLICATION NUMBER: US/10/871,602
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: US 60/286,823
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/337,209
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/333,359
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 60/374,107
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US 10/133,128
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 10/289,660
; PRIOR FILING DATE: 2002-11-06
; NUMBER OF SEQ ID NOS: 665
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human ApoER2 A domain
US-10-871-602-62

Query Match 87.5%; Score 28; DB 17; Length 35;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 1 CRGDE 5

RESULT 67
US-10-971-679-62
; Sequence 62, Application US/10971679
; Publication No. US20050164301A1
; GENERAL INFORMATION:
; APPLICANT: Kolkman, Joost A.
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: LDL Receptor Class A and EGF Domain
; FILE REFERENCE: 022013-000210US
; CURRENT APPLICATION NUMBER: US/10/971,679
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,391
; PRIOR FILING DATE: 2003-10-24
; PRIOR APPLICATION NUMBER: US 10/693,056
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence

```
;
; FEATURE:
; OTHER INFORMATION: human ApoER2 A domain
US-10-971-679-62

Query Match      87.5%; Score 28; DB 18; Length 35;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 1 CRGDE 5

RESULT 68
US-11-066-697-1545
; Sequence 1545, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1545
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-066-697-1545

Query Match      87.5%; Score 28; DB 20; Length 39;
Best Local Similarity 80.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 7 CQGDD 11

RESULT 69
US-08-865-579-16
; Sequence 16, Application US/08865579
; Publication No. US20010006779A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
```

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-865-579-16

Query Match      87.5%; Score 28; DB 8; Length 46;
Best Local Similarity 80.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 17 CRGDE 21

RESULT 70
US-09-746-731-16
; Sequence 16, Application US/09746731
; Publication No. US20010016345A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/746,731
; FILING DATE: 22-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
```



```
;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-746-731-16
Query Match      87.5%; Score 28; DB 9; Length 46;
Best Local Similarity 80.0%; Pred. No. 5.4e+02; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDD 5
Db      17 CRGDE 21

RESULT 71
US-10-059-749-16
; Sequence 16, Application US/10059749
; Publication No. US20020183504A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; FERNANDEZ-ALNEMRI, TERESA
; LITWACK, GERALD
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/059,749
; FILING DATE: 29-Jan-2002
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/POCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-059-749-16
Query Match      87.5%; Score 28; DB 13; Length 46;
Best Local Similarity 80.0%; Pred. No. 5.4e+02; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDD 5
Db      17 CRGDE 21

RESULT 72
US-09-989-903-58
; Sequence 58, Application US/09989903
; Patent No. US20020146804A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434D1
; CURRENT APPLICATION NUMBER: US/09/989,903
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-989-903-58
Query Match      87.5%; Score 28; DB 9; Length 56;
Best Local Similarity 80.0%; Pred. No. 6.4e+02; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDD 5
Db      31 CRGDE 35

RESULT 73
US-10-068-564-58
; Sequence 58, Application US/10068564
; Publication No. US20030040096A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C2
; CURRENT APPLICATION NUMBER: US/10/068,564
; CURRENT FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-068-564-58
Query Match      87.5%; Score 28; DB 14; Length 56;
Best Local Similarity 80.0%; Pred. No. 6.4e+02; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDD 5
Db      31 CRGDE 35

RESULT 74
US-10-870-765-58
; Sequence 58, Application US/10870765
; Publication No. US20040236081A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434D2
; CURRENT APPLICATION NUMBER: US/10/870,765
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: 10/068,564
; PRIOR FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/989,903
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/187,789
; PRIOR FILING DATE: 1998-11-06
US-10-870-765-58
Query Match      87.5%; Score 28; DB 13; Length 46;
Best Local Similarity 80.0%; Pred. No. 5.4e+02; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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; PRIOR APPLICATION NUMBER: 09/139,600
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-870-765-58

Query Match 87.5%; Score 28; DB 16; Length 56;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 31 CRGDE 35

RESULT 75
US-10-767-701-54704
; Sequence 54704, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 54704
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 14592790.pap
US-10-767-701-54704

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Best Local Similarity 80.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 38 CRGDE 42

Search completed: September 7, 2005, 20:13:46
Job time : 176 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 7, 2005, 19:57:40 ; Search time 163 Seconds
(without alignments)
11.864 Million cell updates/sec

Title: US-10-812-238B-41

Perfect score: 32

Sequence: 1 CRGDD 5

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Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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277	27	84.4	280	2	AAU29606	Aau29606	Human ING	350	27	84.4	1854	5	AAU95500	Lettuce p
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279	27	84.4	280	8	ADH09685	Adh09685	Human hos	352	27	84.4	2174	4	ABP67222	Drosophil
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286	27	84.4	283	4	ABG68798	Abg68798	Drosophil	359	26	81.2	5	AAU11587	Fibrinoge	
287	27	84.4	286	8	ADQ76230	Adq76230	Human cel	360	26	81.2	5	AAU10415	Fibrinoge	
288	27	84.4	291	8	ADQ76278	Adq76278	Human cel	361	26	81.2	5	AAU10414	Fibrinoge	
289	27	84.4	291	8	ADS11076	Ads11076	Human the	362	26	81.2	5	AAU10417	Fibrinoge	
290	27	84.4	299	4	AAU34612	Aau34612	E. coli c	363	26	81.2	5	AAU10418	Fibrinoge	
291	27	84.4	299	6	ABU28671	Abu28671	Protein e	364	26	81.2	5	AAU27031	Peptide 1	
292	27	84.4	326	2	AAU27866	Aau27866	Myxoma vi	365	26	81.2	5	AAU29052	Peptide 1	
293	27	84.4	326	2	AAU85072	Aau85072	Myxoma vi	366	26	81.2	5	AAU59325	GP IIb/II	
294	27	84.4	333	2	AAU88345	Aau88345	Salmonell	367	26	81.2	5	AAU54700	Cyclic RG	
295	27	84.4	341	6	ABU34191	Abu34191	Protein e	368	26	81.2	5	AAU54852	Fibrinoge	
296	27	84.4	343	6	ABU36699	Abu36699	Protein e	369	26	81.2	5	AAU54693	Cyclic RG	
297	27	84.4	351	7	ADF08053	Adf08053	Bacterial	370	26	81.2	5	AAU79093	Alpha5/be	
298	27	84.4	352	3	AAU53165	Aau53165	Macaca mu	371	26	81.2	5	AAU14746	Biologica	
299	27	84.4	357	6	ABU37036	Abu37036	Protein e	372	26	81.2	5	AAU03492	Alpha(5)-	
300	27	84.4	395	5	AAU48926	Aau48926	Regulator	373	26	81.2	5	AAU79645	N-alpha-A	
301	27	84.4	395	5	AAU78131	Aau78131	Mouse HYP	374	26	81.2	5	AAU79649	N-alpha-A	
302	27	84.4	395	5	ABG35302	Abg35302	Mouse HYP	375	26	81.2	5	AAU45510	Targeting	
303	27	84.4	395	6	ADA15041	Ada15041	Mouse HYP	376	26	81.2	5	AAU48499	Integrin	
304	27	84.4	395	7	ADAB95603	Adab95603	Mouse HYP	377	26	81.2	5	AAU64952	Targettin	
305	27	84.4	502	4	ABB70242	Abb70242	Drosophil	378	26	81.2	5	AAU16026	Snake ven	
306	27	84.4	522	4	AAU29022	Aau29022	Mouse PAR	379	26	81.2	5	AAU50594	GP1Ib/III	
307	27	84.4	526	6	ABU26885	Abu26885	Cellobioh	380	26	81.2	5	ADH67975	Compositi	
308	27	84.4	530	4	ABG57868	Abg57868	Drosophil	381	26	81.2	5	AAU39345	Fibrinoge	
309	27	84.4	540	8	ADQ89648	Adq89648	Antagonis	382	26	81.2	5	AAU21570	Integrin-	
310	27	84.4	543	7	ADG30906	Adg30906	Human nov	383	26	81.2	5	ADP25491	Tc-99m la	
311	27	84.4	553	7	ADJ12629	Adj12629	Methanoco	384	26	81.2	5	ADP65898	Platelet	
312	27	84.4	554	4	ABG57866	Abg57866	Drosophil	385	26	81.2	5	AAU54976	Peptide 1	
313	27	84.4	557	3	AAU87913	Aau87913	D. opposi	386	26	81.2	5	AAU95465	GP1Ib/III	
314	27	84.4	559	7	ADB79798	Adb79798	Mouse put	387	26	81.2	5	AAU20607	Targeting	
315	27	84.4	572	4	ABG57867	Abg57867	Drosophil	388	26	81.2	5	AAU17982	Human lig	
316	27	84.4	575	7	ADP65022	Adp65022	Human pro	389	26	81.2	5	ABG30404	Glycoprot	
317	27	84.4	602	5	AAU47598	Aau47598	Drosophil	390	26	81.2	5	ABU59650	Glybronec	

391	26	81.2	5	7	ABUG31172	Targeting	464	7	7	ADJ73093	Integrin
392	26	81.2	5	8	ADJ37781	RGD-conta	465	7	8	ADJ52728	CH1 delet
393	26	81.2	5	8	Adm10985	Ultrason	466	7	8	AdJ51689	CH1 delet
394	26	81.2	6	2	AAR10406	Fibrinose	467	7	8	AdR75515	Target no
395	26	81.2	6	2	AAR10407	Fibrinose	468	7	8	AAR21003	Cyclised
396	26	81.2	6	2	AAR99222	RGD-type	469	8	2	AAR21021	Cyclised
397	26	81.2	6	2	AAR76191	Alphav/be	470	8	2	AAR21004	Cyclised
398	26	81.2	6	2	AARQ3508	Alpha (5) -	471	8	2	AAR99214	RGD-type
399	26	81.2	6	2	AARQ3483	Alpha (5) -	472	8	2	AAR99223	RGD-type
400	26	81.2	6	2	AAR35454	Non-dendr	473	8	2	AAR96333	RGD cycli
401	26	81.2	6	2	AAR35453	Non-dendr	474	8	2	AAR96340	RGD cycli
402	26	81.2	6	2	AAR48528	Integrin	475	8	2	AAR96391	RGD cycli
403	26	81.2	6	2	AAR48582	Integrin	476	8	2	AAR45506	Targeting
404	26	81.2	6	2	AAR48500	Integrin	477	8	2	AAR45505	Targeting
405	26	81.2	6	2	AAY21561	Integrin	478	8	2	AAR45507	Targeting
406	26	81.2	6	2	AAY21586	Integrin	479	8	2	AAR48471	Integrin
407	26	81.2	6	5	ABB78357	Amino aci	480	8	2	AAR48481	Integrin
408	26	81.2	6	5	AAM48797	Tumour-ta	481	8	2	AAR48472	Integrin
409	26	81.2	6	6	ABU59535	Finbronec	482	8	2	AAR48525	Integrin
410	26	81.2	6	6	ABU59538	Finbronec	483	8	2	AAR48524	Integrin
411	26	81.2	6	8	ADJ37783	RGD-conta	484	8	2	AAR48526	Integrin
412	26	81.2	6	8	ADJ37782	RGD-conta	485	8	2	AAR48534	Integrin
413	26	81.2	7	2	AAR10400	Fibrinose	486	8	2	AAR48521	Integrin
414	26	81.2	7	2	AAR21010	Cyclised	487	8	2	AAR66939	Peptide u
415	26	81.2	7	2	AAR21006	Cyclised	488	8	2	AAR66836	Peptide u
416	26	81.2	7	2	AAR57220	Cyclised	489	8	2	AAR66911	Peptide u
417	26	81.2	7	2	AAR99213	RGD-type	490	8	2	ADH67970	Compositi
418	26	81.2	7	2	AAR99219	RGD-type	491	8	2	ADH67971	Compositi
419	26	81.2	7	2	AAR99220	RGD-type	492	8	2	ADH67972	Compositi
420	26	81.2	7	2	AAR99209	RGD-type	493	8	2	AAR96981	Peptide u
421	26	81.2	7	2	AAR99208	RGD-type	494	8	2	AAR97017	Peptide u
422	26	81.2	7	2	AAR99212	RGD-type	495	8	2	AAR96941	Peptide u
423	26	81.2	7	2	AAR79086	Alpha5/be	496	8	2	AAR95405	Integrin
424	26	81.2	7	2	AAR76197	Alpha5/be	497	8	3	AB220604	Targeting
425	26	81.2	7	2	AAR96316	RGD cycli	498	8	3	AB220602	Targeting
426	26	81.2	7	2	AAR96314	RGD cycli	499	8	3	AB220603	Targeting
427	26	81.2	7	2	AAR96323	RGD cycli	500	8	3	AAE17094	Cyclic in
428	26	81.2	7	2	AAR96378	RGD cycli	501	8	5	AAR74977	Transfetr
429	26	81.2	7	2	AAR96398	RGD cycli	502	8	5	AAU74955	Integrin
430	26	81.2	7	2	AAR96337	RGD cycli	503	8	5	ABG30399	Glycoprot
431	26	81.2	7	2	AAR96339	RGD cycli	504	8	5	ABG30401	Glycoprot
432	26	81.2	7	2	AAR96333	RGD cycli	505	8	5	ABG30400	Glycoprot
433	26	81.2	7	2	AAR48532	Integrin	506	8	6	ABP98675	Cyclic RG
434	26	81.2	7	2	AAR48516	Integrin	507	8	6	ABU62647	RGD pepti
435	26	81.2	7	2	AAR48556	Integrin	508	8	7	ABU63167	Targeting
436	26	81.2	7	2	AAR48544	Integrin	509	8	7	ABU63168	Targeting
437	26	81.2	7	2	AAR48473	Integrin	510	8	7	ABU63169	Targeting
438	26	81.2	7	2	AAR48501	Integrin	511	8	8	ADF82864	Integrin
439	26	81.2	7	2	AAR48519	Integrin	512	8	8	ADM10980	Ultrason
440	26	81.2	7	2	AAR48531	Integrin	513	8	8	ADM10981	Ultrason
441	26	81.2	7	2	AAR48555	Integrin	514	8	8	ADM10982	Ultrason
442	26	81.2	7	2	AAR48522	Integrin	515	8	8	ADM96259	Human alp
443	26	81.2	7	2	AAR48596	Integrin	516	8	8	ADS13912	Gene/anti
444	26	81.2	7	2	AAR48529	Integrin	517	8	8	AAR12332	Platelet-
445	26	81.2	7	2	AAR48523	Integrin	518	9	2	AAR12333	Platelet-
446	26	81.2	7	2	AAR66936	Peptide u	519	9	2	AAR21019	Cyclised
447	26	81.2	7	2	AAR66901	Peptide u	520	9	2	AAR21009	Cyclised
448	26	81.2	7	2	AAR66922	Peptide u	521	9	2	AAR21020	Cyclised
449	26	81.2	7	2	AAR66859	Peptide u	522	9	2	AAR29262	Selectin-
450	26	81.2	7	2	AAR66902	Peptide u	523	9	2	AAR79074	Alphav/be
451	26	81.2	7	2	AAR66892	Peptide u	524	9	2	AAR76200	Alphav/be
452	26	81.2	7	2	AAR66921	Peptide u	525	9	2	AAR79073	Alphav/be
453	26	81.2	7	2	AAY43232	RGD-conta	526	9	2	AAR76199	Alphav/be
454	26	81.2	7	2	AAR96912	Peptide u	527	9	2	AAR79089	Alphav/be
455	26	81.2	7	2	AAR96889	Peptide u	528	9	2	AAR79080	Alphav/be
456	26	81.2	7	2	AAR96921	Peptide u	529	9	2	AAR96386	RGD cycli
457	26	81.2	7	2	AAR96914	Peptide u	530	9	2	AAW01131	RGD pepti
458	26	81.2	7	2	AAR96931	Peptide u	531	9	2	AAW60289	Tumour ho
459	26	81.2	7	3	AAI17340	Integrin	532	9	2	AAW48478	Integrin
460	26	81.2	7	3	AAY90212	Alphav in	533	9	2	AAW48480	Integrin
461	26	81.2	7	3	AAY90219	UPAR targ	534	9	2	AAW48520	Integrin
462	26	81.2	7	5	AAU81131	Integrin	535	9	2	AAW48479	Integrin
463	26	81.2	7	5	ABB72939	Integrin	536	9	2	AAW48535	Integrin

537	26	81.2	9	2	AAW48476	Integrin	610	9	7	ADC44955	Adc44955	Endotheli
538	26	81.2	9	2	AAW48477	Integrin	611	9	7	ADF12488	Adf12488	RGD pepti
539	26	81.2	9	2	AAW51235	Cyclic pe	612	9	7	ADF55508	Adf55508	RGD-4C pe
540	26	81.2	9	2	AAW56034	Chimeric	613	9	7	ADJ73101	Adj73101	Integrin
541	26	81.2	9	2	AAW56035	Chimeric	614	9	7	ADJ73100	Adj73100	Integrin
542	26	81.2	9	2	AAW66907	Peptide u	615	9	7	ADJ73099	Adj73099	Integrin
543	26	81.2	9	2	AAW42255	Synthetic	616	9	7	ADJ73115	Adj73115	Integrin
544	26	81.2	9	2	AAW43233	RGD-conta	617	9	7	ADJ73098	Adj73098	Integrin
545	26	81.2	9	2	AAW96977	Peptide u	618	9	8	ADJ52733	Adj52733	CHI delet
546	26	81.2	9	2	AAW93626	NGR recep	619	9	8	ADJ52750	Adj52750	CHI delet
547	26	81.2	9	2	AAW48821	Membrane	620	9	8	ADJ52735	Adj52735	CHI delet
548	26	81.2	9	3	AAW54271	Alpha Vbe	621	9	8	ADJ52734	Adj52734	CHI delet
549	26	81.2	9	3	AAW44970	RGD-4C ta	622	9	8	ADJ52736	Adj52736	CHI delet
550	26	81.2	9	3	AAW17928	TFO-mimet	623	9	8	ADJ51697	Adj51697	CHI delet
551	26	81.2	9	3	AAW17345	Integrin-	624	9	8	ADJ51695	Adj51695	CHI delet
552	26	81.2	9	3	AAW17964	Integrin-	625	9	8	ADJ51694	Adj51694	CHI delet
553	26	81.2	9	3	AAW17346	Integrin-	626	9	8	ADJ51696	Adj51696	CHI delet
554	26	81.2	9	3	AAW17348	Integrin-	627	9	8	ADJ51711	Adj51711	CHI delet
555	26	81.2	9	3	AAW17347	Integrin-	628	9	8	ADJ51516	Adj51516	RGD-conta
556	26	81.2	9	3	AAW90211	Alpha v in	629	9	8	ADM72073	Adm72073	tumour ho
557	26	81.2	9	3	AAO22875	Angiogeni	630	9	8	ADJ59524	Adj59524	Antibody-
558	26	81.2	9	3	AAW21701	Human bre	631	9	8	ADM96257	Adm96257	Human alp
559	26	81.2	9	4	AAW20271	Peptide t	632	10	2	AAW11746	AAw11746	Cyclic pl
560	26	81.2	9	4	AAW50242	Enhanced	633	10	2	AAW11747	AAw11747	Cyclic pl
561	26	81.2	9	4	AAW97086	Integrin-	634	10	2	AAW10181	AAw10181	RGD-contg
562	26	81.2	9	4	AAW66279	Tumour ho	635	10	2	AAW76189	AAw76189	Integrin
563	26	81.2	9	4	AAW08989	ICE pepti	636	10	2	AAW98935	AAw98935	Integrin
564	26	81.2	9	4	AAW11044	RGD-conta	637	10	2	AAW03485	AAw03485	Alpha (5) -
565	26	81.2	9	5	AAW98837	Tumour ho	638	10	2	AAW03419	AAw03419	Fibronect
566	26	81.2	9	5	ABG35079	RGD-4C-be	639	10	2	AAW79650	AAw79650	N-alpha-A
567	26	81.2	9	5	AAW81135	Integrin-	640	10	2	AAW79652	AAw79652	N-alpha-A
568	26	81.2	9	5	AAW81110	Integrin-	641	10	2	AAW79651	AAw79651	N-alpha-A
569	26	81.2	9	5	AAW81094	Integrin-	642	10	2	AAW12863	AAw12863	RGD-bindi
570	26	81.2	9	5	AAW81134	Integrin-	643	10	2	AAW35451	AAw35451	Non-dendr
571	26	81.2	9	5	AAW54051	Alpha-v-b	644	10	2	AAW48516	AAw48516	Integrin
572	26	81.2	9	5	ABP54051	Integrin	645	10	2	AAW48515	AAw48515	Integrin
573	26	81.2	9	5	ABW72944	Integrin	646	10	2	AAW99008	AAw99008	Peptide R
574	26	81.2	9	5	ABW72945	Integrin	647	10	2	AAW21563	AAw21563	Integrin-
575	26	81.2	9	5	ABW72946	Integrin	648	10	2	AAW95406	AAw95406	Integrin-
576	26	81.2	9	5	ABW72947	Integrin	649	10	3	AAW90755	AAw90755	Alphasbet
577	26	81.2	9	5	ABW72961	Integrin	650	10	3	AAW21716	AAw21716	Human tum
578	26	81.2	9	5	ABJ04333	Stem cell	651	10	4	AAW08561	AAw08561	RGD-4C pe
579	26	81.2	9	5	ABJ04622	Bone marr	652	10	5	ABG68408	ABg68408	Transloca
580	26	81.2	9	5	ABJ04451	Stem cell	653	10	5	ABW08397	ABw08397	Cyclic RG
581	26	81.2	9	5	ABJ04359	BRAS11 me	654	10	5	ABW76444	ABw76444	RGD-4C pe
582	26	81.2	9	5	ABJ04427	Stem cell	655	10	5	ABG70755	ABg70755	Targeting
583	26	81.2	9	5	ABJ04569	Bone marr	656	10	5	AAE17113	AAe17113	Cyclic in
584	26	81.2	9	5	ABJ01278	Human cas	657	10	5	AAE17110	AAe17110	Cyclic in
585	26	81.2	9	5	ABW08066	Cyclic RG	658	10	5	AAE17095	AAe17095	Cyclic in
586	26	81.2	9	5	ABG70729	avB3 bind	659	10	5	AAE17097	AAe17097	Cyclic in
587	26	81.2	9	5	ABW76442	RGD-4C pe	660	10	5	AAU74988	AAu74988	RGD conta
588	26	81.2	9	5	AAE17983	Human lig	661	10	5	AAU74979	AAu74979	Transfect
589	26	81.2	9	5	ABW78354	Amino aci	662	10	5	AAU74983	AAu74983	Transfect
590	26	81.2	9	5	ABG70754	Targeting	663	10	6	AAE35396	AAe35396	Peptide c
591	26	81.2	9	5	AAE17109	Cyclic in	664	10	6	AAE32514	AAe32514	West nile
592	26	81.2	9	5	AAE17108	Cyclic in	665	10	7	AAO23409	AAo23409	Human Ad5
593	26	81.2	9	5	AAU75609	Synthetic	666	10	7	ABR56197	ABr56197	RGD pepti
594	26	81.2	9	5	AAU79138	Synthetic	667	10	7	ADC33483	Adc33483	Synthetic
595	26	81.2	9	5	AAU98972	Adeno-agg	668	10	8	ADJ82865	Adj82865	Integrin-
596	26	81.2	9	5	AAU74978	Transfect	669	10	8	ADJ37784	Adj37784	RGD-conta
597	26	81.2	9	5	AAW48795	Tumour-ta	670	10	8	ADO80847	Ado80847	Synthetic
598	26	81.2	9	5	ABW79525	RGD motif	671	10	8	ADR75421	Adr75421	target mo
599	26	81.2	9	5	ABG31063	Alpha v b	672	10	8	ADR75430	Adr75430	Target mo
600	26	81.2	9	5	AAW78427	Cyclic pe	673	10	8	ADJ17359	Adj17359	Peptide a
601	26	81.2	9	5	AAW51995	Drug targ	674	10	8	ADJ13913	Adj13913	Gene/anti
602	26	81.2	9	5	AAW51996	Integrin	675	11	2	AAW76194	AAw76194	Integrin
603	26	81.2	9	5	AAW51997	Integrin	676	11	2	AAW11184	AAw11184	Free pept
604	26	81.2	9	6	ABG73024	Integrin	677	11	2	AAW60299	AAw60299	tumour ho
605	26	81.2	9	6	ABW84641	Human int	678	11	2	AAW57199	AAw57199	RGD-conta
606	26	81.2	9	6	ABU59556	Tumour an	679	11	2	AAW95408	AAw95408	Integrin-
607	26	81.2	9	6	ABU08571	RGD-conta	680	11	2	AAW95409	AAw95409	Integrin-
608	26	81.2	9	6	ABP60343	Tumour va	681	11	2	AAW95407	AAw95407	Integrin-
609	26	81.2	9	6	ADA20234	Synthetic	682	11	3	AAW54273	AAw54273	Peptide 1

683	26	81.2	11	3	AAV90159	Aay90159 UPAR targ	756	26	81.2	19	6	AAE38405	Aae38405 HIV 1 Tat
684	26	81.2	11	3	AAV58860	Aay58860 Membrane	757	26	81.2	20	3	ADF77514	Adf77514 DAF-7 pro
685	26	81.2	11	4	AAE06294	Aae06294 Double cy	758	26	81.2	20	2	ABO6057	AbO6057 Caenorhab
686	26	81.2	11	5	AAU97578	Aau97578 Synthetic	759	26	81.2	20	4	AAm51432	Aam51432 Peptide K
687	26	81.2	11	5	AAU97580	Aau97580 Synthetic	760	26	81.2	20	6	AAe38386	Aae38386 ErbB2 bin
688	26	81.2	11	5	AAU97577	Aau97577 Synthetic	761	26	81.2	20	7	ADC33480	Adc33480 Peptide K
689	26	81.2	11	5	AAU97579	Aau97579 Synthetic	762	26	81.2	20	7	ADe86004	AdE86004 Human Hu-
690	26	81.2	11	5	AAU97581	Aau97581 Synthetic	763	26	81.2	20	8	ADQ76841	AdQ76841 Mouse alp
691	26	81.2	11	5	AAU87024	Aau87024 Targettin	764	26	81.2	21	2	ADQ76841	AdQ76841 Mouse alp
692	26	81.2	11	5	AAE17096	Aae17096 Cyclic in	765	26	81.2	21	7	ADQ76841	AdQ76841 Mouse alp
693	26	81.2	11	5	AAE17098	Aae17098 Cyclic in	766	26	81.2	21	7	ADQ76841	AdQ76841 Mouse alp
694	26	81.2	11	5	AAO21743	Aao21743 Procytoto	767	26	81.2	21	8	ADN11199	Adn11199 Peptide m
695	26	81.2	11	5	AAE35395	Aae35395 Peptide c	768	26	81.2	21	8	ADN11233	Adn11233 Peptide m
696	26	81.2	11	6	ABP58062	Abp58062 RGD pepi	769	26	81.2	21	8	ADN11234	Adn11234 Peptide m
697	26	81.2	11	6	ABP70218	Abp70218 Amino aci	770	26	81.2	21	8	ADM96250	Adm96250 Human cas
698	26	81.2	11	6	ABR40189	AbR40189 Integrin	771	26	81.2	21	8	ADM96250	Adm96250 Human cas
699	26	81.2	11	7	ADF12487	Adf12487 RGD pepi	772	26	81.2	21	8	ADR41069	Adr41069 Cyclic KD
700	26	81.2	11	7	ADF82866	Adf82866 Integrin-	773	26	81.2	21	8	ADR51117	Adr51117 Duo bindi
701	26	81.2	11	8	ADF82867	Adf82867 Integrin-	774	26	81.2	22	4	AAm15231	Aam15231 Peptide #
702	26	81.2	11	8	ADF82868	Adf82868 Integrin-	775	26	81.2	22	4	ABB34221	Abb34221 Peptide #
703	26	81.2	11	8	ADN11238	Adn11238 Peptide u	776	26	81.2	22	4	AAm27692	Aam27692 Peptide #
704	26	81.2	11	8	ADO80846	Ado80846 Synthetic	777	26	81.2	22	4	ABB29060	Abb29060 Peptide #
705	26	81.2	11	8	ADR12199	Adr12199 RGD-4C pe	778	26	81.2	22	4	ABB19657	Abb19657 Protein #
706	26	81.2	11	8	ADS13914	Ads13914 Gene/anti	779	26	81.2	22	4	AAm67400	Aam67400 Human bon
707	26	81.2	11	8	ADS13915	Ads13915 Gene/anti	780	26	81.2	22	4	AAm55015	Aam55015 Human bra
708	26	81.2	11	8	ADS13916	Ads13916 Gene/anti	781	26	81.2	22	4	ABG49059	Abg49059 Human liv
709	26	81.2	12	2	AAW56052	Aaw56052 Chimeric	782	26	81.2	22	4	AAm02974	Aam02974 Peptide #
710	26	81.2	12	2	AAW50655	Aaw50655 Integrin	783	26	81.2	22	4	AAW5097	Aaw5097 RGD/SV40
711	26	81.2	12	2	AAW95410	Aaw95410 Integrin-	784	26	81.2	22	4	AAW56036	Aaw56036 Chimeric
712	26	81.2	12	4	AAW51437	Aam51437 Carboxyl	785	26	81.2	23	2	AAW96220	Aaw96220 Modified
713	26	81.2	12	5	ABP56215	Abp56215 Chimeric	786	26	81.2	24	2	AAW56044	Aaw56044 Chimeric
714	26	81.2	12	5	ABP56186	Abp56186 Chimeric	787	26	81.2	24	2	AAW56044	Aaw56044 Chimeric
715	26	81.2	12	5	AAE17099	Aae17099 Cyclic in	788	26	81.2	24	3	AAW79875	Aay79875 Integrin-
716	26	81.2	12	5	AAE17103	Aae17103 Cyclic in	789	26	81.2	24	3	AAW83259	Aay83259 Integrin-
717	26	81.2	12	5	AAU74965	Aau74965 RGD conta	790	26	81.2	24	3	AAW96572	Aay96572 Integrin-
718	26	81.2	12	8	ADF82869	Adf82869 Integrin-	791	26	81.2	24	4	AAm60908	Abm60908 RGD pepi
719	26	81.2	12	8	ADF82876	Adf82876 Integrin-	792	26	81.2	24	5	ABO5522	AbO5522 Integrin-
720	26	81.2	12	8	ADF82877	Adf82877 Integrin-	793	26	81.2	24	5	ABP56201	Abp56201 Chimeric
721	26	81.2	12	8	ADS13917	Ads13917 Gene/anti	794	26	81.2	24	5	ABP56184	Abp56184 Chimeric
722	26	81.2	13	2	AAV43226	Aay43226 RGD-Conta	795	26	81.2	24	5	ABP56187	Abp56187 Chimeric
723	26	81.2	13	2	AAV43229	Aay43229 RGD-Conta	796	26	81.2	24	5	ABP56202	Abp56202 Chimeric
724	26	81.2	13	2	AAV48725	Aay48725 Membrane	797	26	81.2	24	7	ADF70993	Adf70993 Phosphope
725	26	81.2	13	3	AAV90168	Aay90168 UPAR targ	798	26	81.2	24	8	ADM82999	Adm82999 Integrin-
726	26	81.2	13	3	AAV90158	Aay90158 UPAR targ	799	26	81.2	25	3	AAE21940	Aae21940 Homing an
727	26	81.2	13	5	AAU98801	Aau98801 Peptide 1	800	26	81.2	25	4	AAE06517	Aae06517 Homing pr
728	26	81.2	13	5	AAU98802	Aau98802 Peptide 1	801	26	81.2	25	5	ABP56213	Abp56213 Chimeric
729	26	81.2	13	6	ABU63060	Abu63060 Peptide 1	802	26	81.2	25	5	ABP56212	Abp56212 Chimeric
730	26	81.2	13	6	ABU63059	Abu63059 Peptide 1	803	26	81.2	25	5	ABP56211	Abp56211 Chimeric
731	26	81.2	14	2	AAW19833	Aaw19833 RGD pepi	804	26	81.2	25	5	ABP56214	Abp56214 Chimeric
732	26	81.2	14	2	AAW56051	Aaw56051 Chimeric	805	26	81.2	25	5	ABP56185	Abp56185 Chimeric
733	26	81.2	14	2	AAW50662	Aaw50662 DAB conta	806	26	81.2	26	2	AAW95403	Aaw95403 Conserved
734	26	81.2	14	3	AAV59625	Aay59625 Maturatio	807	26	81.2	26	3	AAE21937	Aae21937 Homing an
735	26	81.2	14	3	AAU98966	Aau98966 Peptide #	808	26	81.2	26	4	AAE06516	Aae06516 Homing pr
736	26	81.2	14	8	ADM96254	Adm96254 Apoptosis	809	26	81.2	26	5	AAE17092	Aae17092 Cyclic in
737	26	81.2	15	2	AAE62581	Aae62581 Human hep	810	26	81.2	26	5	AAE17092	Aae17092 Cyclic in
738	26	81.2	15	2	AAW56040	Aaw56040 Chimeric	811	26	81.2	26	5	AAU74953	Aau74953 RGD conta
739	26	81.2	15	2	AAV43228	Aay43228 RGD-Conta	812	26	81.2	26	5	AAU48798	Aau48798 Tmour-ta
740	26	81.2	15	2	AAV43222	Aay43222 RGD-Conta	813	26	81.2	26	8	ADS13910	AdS13910 Gene/anti
741	26	81.2	15	3	AAV54372	Aay54372 Peptide i	814	26	81.2	27	2	AAW95402	Aaw95402 Conserved
742	26	81.2	15	3	AAV90167	Aay90167 UPAR targ	815	26	81.2	27	2	AAW95404	Aaw95404 Conserved
743	26	81.2	15	6	ABU59649	Abu59649 PEG conta	816	26	81.2	27	4	AAE47345	Aae47345 DNA bindi
744	26	81.2	15	8	AAO24331	Aao24331 Human Sli	817	26	81.2	27	4	AAE06191	Aae06191 Human gen
745	26	81.2	16	7	ADP03397	Adp03397 GPIIb/III	818	26	81.2	27	5	ABG34015	Abg34015 Human sec
746	26	81.2	16	7	ADF12496	Adf12496 Mouse p35	819	26	81.2	27	5	AAE17120	Aae17120 Integrin-
747	26	81.2	17	2	AAV20690	Aay20690 Human neu	820	26	81.2	27	5	AAE17093	Aae17093 Cyclic in
748	26	81.2	18	2	AAW79487	Aaw79487 Peptide i	821	26	81.2	27	5	AAE17122	Aae17122 Peptide x
749	26	81.2	18	3	AAE49453	Aae49453 Peptide s	822	26	81.2	27	5	AAE17091	Aae17091 Cyclic in
750	26	81.2	18	4	AAE04343	Aae04343 Human dis	823	26	81.2	27	5	AAE17125	Aae17125 Integrin-
751	26	81.2	18	5	AAE23768	Aae23768 Zdscl pro	824	26	81.2	27	5	AAU74970	Aau74970 Alpha V,
752	26	81.2	18	7	ADF12495	Adf12495 Canine p3	825	26	81.2	27	5	AAU74952	Aau74952 RGD conta
753	26	81.2	18	7	ADF12494	Adf12494 Human p35	826	26	81.2	27	5	AAU74954	Aau74954 RGD conta
754	26	81.2	19	5	AAm51998	Aam51998 Integrin	827	26	81.2	27	5	ABO8603	AbO8603 Gene tran
755	26	81.2	19	6	AAE38404	Aae38404 HIV 1 Tat	828	26	81.2	27	6	ABB98397	Abb98397 Integrin

829	26	81.2	27	8	ADSL3911	Gene/anti	Adsl3911	Gene/anti	902	26	81.2	60	4	AAU61298	Propionib
830	26	81.2	27	8	ADSL3909	Gene/anti	Adsl3909	Gene/anti	903	26	81.2	60	5	ABP10154	Human ORF
831	26	81.2	28	2	AAW95401	Conserved	Aaw95401	Conserved	904	26	81.2	60	5	ABP10154	Human ORF
832	26	81.2	28	3	ABP35728	RGD-polyl-	Aab35728	RGD-polyl-	905	26	81.2	60	6	ABM38744	Propionib
833	26	81.2	28	5	AAE17123	Integrin-	Aae17123	Integrin-	906	26	81.2	60	8	ADM96252	Human alp
834	26	81.2	28	5	AAE17050	Cyclic RG	Aae17050	Cyclic RG	907	26	81.2	62	4	ABG07543	Novel hum
835	26	81.2	28	5	AAU74973	Alpha V i	Aau74973	Alpha V i	908	26	81.2	62	4	ABG13743	Novel hum
836	26	81.2	28	5	AAU74951	RGD conta	Aau74951	RGD conta	909	26	81.2	63	3	AAU49443	Murine zd
837	26	81.2	28	8	ADNL1184	Peptide i	Adnl1184	Peptide i	910	26	81.2	63	3	AAU68905	Amino aci
838	26	81.2	28	8	ADSL3908	Gene/anti	Adsl3908	Gene/anti	911	26	81.2	63	4	AAU68187	Human bon
839	26	81.2	29	4	AAE02759	Kalata B1	Aae02759	Kalata B1	912	26	81.2	63	4	AAU58320	Propionib
840	26	81.2	29	5	ABU67204	G-protein	Abe67204	G-protein	913	26	81.2	63	4	AAU55813	Human bra
841	26	81.2	29	6	ABP53985	Human adr	Abp53985	Human adr	914	26	81.2	63	4	AAE04333	Murine di
842	26	81.2	29	8	ADO28725	Human alp	Ado28725	Human alp	915	26	81.2	63	5	AAE23758	Murine zd
843	26	81.2	29	8	ADO05229	Adrenergi	Ado5229	Adrenergi	916	26	81.2	63	5	AAE21091	Mouse T17
844	26	81.2	30	2	AAV48646	N-termina	Aay48646	N-termina	917	26	81.2	63	6	ABM54839	Human ORF
845	26	81.2	32	3	AAV49268	Lactoferr	Aay49268	Lactoferr	918	26	81.2	63	7	ABW00620	Mouse T17
846	26	81.2	35	2	ADF77517	DAP-7 pro	Adf77517	DAP-7 pro	919	26	81.2	64	4	AAU40485	Propionib
847	26	81.2	35	3	AAE06060	Caenorhab	Aay6060	Caenorhab	920	26	81.2	64	6	ABM36984	Propionib
848	26	81.2	39	3	AAU49444	Murine zd	Aay49444	Murine zd	921	26	81.2	65	3	ABM53796	Human col
849	26	81.2	39	4	AAE04334	Murine ma	Aae04334	Murine ma	922	26	81.2	65	4	AAU62810	Propionib
850	26	81.2	39	5	AAE23759	Murine zd	Aae23759	Murine zd	923	26	81.2	65	5	ABP35285	Human ORF
851	26	81.2	39	5	AAE21094	Mouse T17	Aae21094	Mouse T17	924	26	81.2	65	6	ABM59329	Propionib
852	26	81.2	39	7	ABW00621	Mouse mac	Abw00621	Mouse mac	925	26	81.2	65	7	ADD89952	Foot-and-
853	26	81.2	39	8	ABO55221	Human gen	Abos5221	Human gen	926	26	81.2	65	8	ADJ56911	Foot-and-
854	26	81.2	43	2	ADF77515	DAP-7 pro	Adf77515	DAP-7 pro	927	26	81.2	65	8	ABO56543	Human gen
855	26	81.2	43	3	AAE06058	Caenorhab	Aae06058	Caenorhab	928	26	81.2	67	4	AAU63498	Human gen
856	26	81.2	43	4	AAE49744	Antimicro	Aae49744	Antimicro	929	26	81.2	67	6	ABM60017	Propionib
857	26	81.2	45	2	ABR05875	Intermedi	Aab05875	Intermedi	930	26	81.2	68	5	ABP09222	Human ORF
858	26	81.2	45	4	ABG25537	Novel hum	Abg25537	Novel hum	931	26	81.2	69	3	ABP25079	Plant SDF
859	26	81.2	45	7	ADF69847	ACMA-type	Adf69847	ACMA-type	932	26	81.2	69	4	AAU44985	Propionib
860	26	81.2	46	4	AAE08946	ICE pepti	Aae08946	ICE pepti	933	26	81.2	69	4	AAU44985	Propionib
861	26	81.2	46	4	AAE52031	Aspartate	Ades2031	Aspartate	934	26	81.2	69	4	AAU49774	Propionib
862	26	81.2	46	8	ADM97028	Botulinum	Adm97028	Botulinum	935	26	81.2	69	6	ABM46293	Propionib
863	26	81.2	48	4	ABG18211	Novel hum	Abg18211	Novel hum	936	26	81.2	69	6	ABM48570	Propionib
864	26	81.2	49	2	AAW02648	Mutant di	Aaw02648	Mutant di	937	26	81.2	69	6	ABM41504	Propionib
865	26	81.2	50	4	AAW80383	Human hae	Aaw80383	Human hae	938	26	81.2	70	4	AAW82385	Human imm
866	26	81.2	50	4	AAU50635	Propionib	Aau50635	Propionib	939	26	81.2	70	4	AAU53860	Propionib
867	26	81.2	50	4	AAU45429	Propionib	Aau45429	Propionib	940	26	81.2	70	6	ABM50379	Propionib
868	26	81.2	50	6	ABM47154	Propionib	Abm47154	Propionib	941	26	81.2	72	2	AAU44985	Propionib
869	26	81.2	50	6	ABM41948	Propionib	Abm41948	Propionib	942	26	81.2	72	2	AAU44985	Propionib
870	26	81.2	52	4	AAU46051	Propionib	Aau46051	Propionib	943	26	81.2	72	2	AAU44985	Propionib
871	26	81.2	52	6	AAU42570	Propionib	Aau42570	Propionib	944	26	81.2	72	4	AAU42570	Propionib
872	26	81.2	53	4	AAU53004	Propionib	Aau53004	Propionib	945	26	81.2	76	2	AAU72215	HSV-2 str
873	26	81.2	53	6	ABM49523	Propionib	Abm49523	Propionib	946	26	81.2	76	3	AAU72215	HSV-2 str
874	26	81.2	53	6	ABM65238	Propionib	Abm65238	Propionib	947	26	81.2	76	3	AAU72215	HSV-2 str
875	26	81.2	54	4	AAU59762	Propionib	Aau59762	Propionib	948	26	81.2	76	4	AAU59762	Propionib
876	26	81.2	54	6	ABM56281	Propionib	Abm56281	Propionib	949	26	81.2	76	4	ABM56281	Propionib
877	26	81.2	55	4	AAU42049	Propionib	Aau42049	Propionib	950	26	81.2	76	6	ABM53553	Propionib
878	26	81.2	55	4	AAU39246	Propionib	Aau39246	Propionib	951	26	81.2	76	7	ABO69836	Pseudomon
879	26	81.2	55	4	AAU64092	Propionib	Aau64092	Propionib	952	26	81.2	76	7	ABO69836	Pseudomon
880	26	81.2	55	4	AAU56638	Propionib	Aau56638	Propionib	953	26	81.2	77	4	AAU43934	Propionib
881	26	81.2	55	6	ABM60611	Propionib	Abm60611	Propionib	954	26	81.2	77	4	AAU43934	Propionib
882	26	81.2	55	6	ABM35765	Propionib	Abm35765	Propionib	955	26	81.2	77	6	ABM40453	Propionib
883	26	81.2	55	6	ABM38568	Propionib	Abm38568	Propionib	956	26	81.2	77	6	ABM40453	Propionib
884	26	81.2	55	6	ABM53157	Propionib	Abm53157	Propionib	957	26	81.2	79	4	AAW80730	Human imm
885	26	81.2	56	3	AAU25002	Plant SDF	Aau25002	Plant SDF	958	26	81.2	83	5	ABP03980	Human ORF
886	26	81.2	56	3	AAU45593	Arabidops	Aau45593	Arabidops	959	26	81.2	85	5	ABP03980	Human ORF
887	26	81.2	56	4	AAO09402	Human pol	Aao09402	Human pol	960	26	81.2	85	5	ABP05804	Human imm
888	26	81.2	57	3	AAU97990	RGD-proin	Aay97990	RGD-proin	961	26	81.2	86	3	AAU97990	RGD-proin
889	26	81.2	57	8	ABO54720	Human gen	Abo54720	Human gen	962	26	81.2	86	4	AAU40276	Human pol
890	26	81.2	58	3	AAE25001	Plant SDF	Aae25001	Plant SDF	963	26	81.2	86	8	ABO57808	Human gen
891	26	81.2	58	4	AAW21186	Peptide #	Aaw21186	Peptide #	964	26	81.2	87	4	AAU42944	Human pan
892	26	81.2	58	4	ABE43506	Peptide #	Abb43506	Peptide #	965	26	81.2	87	6	ABM39463	Propionib
893	26	81.2	58	4	AAW37401	Peptide #	Aam37401	Peptide #	966	26	81.2	88	4	AAU20304	Human nov
894	26	81.2	58	4	ABE26466	Protein #	Aab26466	Protein #	967	26	81.2	89	3	AAU25479	Pinus rad
895	26	81.2	58	4	AAW64441	Human bra	Aaw64441	Human bra	968	26	81.2	89	3	AAU25479	Pinus rad
896	26	81.2	58	4	ABG58884	Human liv	Aab58884	Human liv	969	26	81.2	89	3	AAU25479	Pinus rad
897	26	81.2	58	5	ABG46265	Human pep	Abg46265	Human pep	970	26	81.2	90	3	AAU25479	Pinus rad
898	26	81.2	58	5	ABP34415	Human ORF	Abp34415	Human ORF	971	26	81.2	90	4	AAU25479	Pinus rad
899	26	81.2	59	3	AAE25081	Plant SDF	Aab25081	Plant SDF	972	26	81.2	90	4	AAU25081	Plant SDF
900	26	81.2	59	3	AAE25000	Plant SDF	Aau25000	Plant SDF	973	26	81.2	90	6	ABM36296	Propionib
901	26	81.2	60	4	AAU42225	Propionib	Aau42225	Propionib	974	26	81.2	90	6	ABM36296	Propionib

975 26 81.2 91 4 AAU48465
 976 26 81.2 91 6 ABM44984
 977 26 81.2 93 8 ADK19706
 978 26 81.2 94 2 AAY35872
 979 26 81.2 96 4 ABG21787
 980 26 81.2 97 4 AAM06515
 981 26 81.2 97 4 AAM06799
 982 26 81.2 99 2 AAY04833
 983 26 81.2 99 4 AAU40436
 984 26 81.2 99 6 AAW36955
 985 26 81.2 101 4 AAO12673
 986 26 81.2 102 5 ADK36904
 987 26 81.2 103 7 ADB64460
 988 26 81.2 106 4 ABG09018
 989 26 81.2 108 3 AAB53252
 990 26 81.2 108 5 ABP04690
 991 26 81.2 108 8 ADS12498
 992 26 81.2 108 8 ADS12482
 993 26 81.2 110 4 ABG26316
 994 26 81.2 110 7 ADE08262
 995 26 81.2 110 8 ADS12494
 996 26 81.2 111 2 AAU44079
 997 26 81.2 111 2 AAW27643
 998 26 81.2 112 4 AAO00116
 999 26 81.2 115 4 AAO06254
 1000 26 81.2 115 4 AAU48996

ALIGNMENTS

RESULT 1
 AAR96393
 ID AAR96393 standard; peptide; 7 AA.
 XX
 AC AAR96393;
 XX
 DT 05-JUL-1996 (first entry)
 XX
 DE RGD cyclic peptide, TL#86, binds alpha-v,beta3 integrin receptor.
 XX
 KW RGD-containing peptide; alpha-v, beta-3 integrin receptor; osteoclast;
 KW matrix; bone; inhibition; bone resorption; promote; endothelial cell;
 KW smooth muscle cell; restenosis; angiogenesis; cyclic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..7
 FT Modified-site 1
 FT Modified-site 7 /note= "Acyl-Cys"
 FT Modified-site 7 /note= "Amidated C-terminal"
 FT
 XX WO9528426-A2.
 XX
 XX 26-OCT-1995.
 XX
 XX 12-APR-1995; 9SWO-US004741.
 XX
 XX 13-APR-1994; 94US-00227316.
 XX 08-SEP-1994; 94US-00303052.
 XX
 XX (LJOL-) LA JOLLA CANCER RES FOUND.
 XX
 XX Cheng S, Ingram R, Mullen D, Tschopp J;
 XX WPI; 1995-373767/48.
 XX
 XX Altering alpha-v, beta-3 integrin receptor-mediated binding of cell to
 PT matrix - using conformationally restrained peptide of RGD type, e.g. for
 PT treating inappropriate angiogenesis or for inhibiting bone resorption.
 XX

AAU48465 Propionib
 ABM44984 Propionib
 ADK19706 Mouse pro
 AAY35872 Chlamydia
 ABG21787 Novel hum
 AAM06515 Human foe
 AAM06799 Human foe
 AAY04833 Mycobacte
 AAU40436 Propionib
 ABM36955 Propionib
 AAO12673 Human pol
 ADK36904 Novel hum
 ADB64460 Human pro
 ABG09018 Novel hum
 AAB53252 Human col
 ABP04690 Human ORF
 ADS12498 Human IGF
 ADS12482 Human IGF
 ABG26316 Novel hum
 ADE08262 Novel pro
 ADS12494 Human IGF
 AAU44079 Human sec
 AAW27643 Secreted
 AAO00116 Human pol
 AAO06254 Human pol
 AAU48996 Propionib

PS Claim 85; Page 79; 99pp; English.
 XX
 CC The sequences given in AAR96301-417 are non-naturally occurring RGD-
 CC containing peptides which alter the alpha-v, beta-3 integrin receptor
 CC binding of a cell to a matrix, such as the binding of an osteoclast to a
 CC matrix such as bone. These peptides inhibit bone resorption and can
 CC inhibit or promote alpha-v, beta-3-mediated cell attachment depending on
 CC whether they are present in the cell in a soluble form or are bound to a
 CC solid substrate. These peptides can be used in the amelioration of the
 CC severity of a pathology involving alpha-v, beta-3 receptor-mediated
 CC binding of a cell, such as an osteoclast, endothelial cell or smooth
 CC muscle cell to a matrix. They are used for treating conditions associated
 CC with restenosis or inappropriate or insufficient angiogenesis, or for
 CC inhibiting osteoclast binding to the matrix

SQ Sequence 7 AA;

Query Match 100.0%; Score 32; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5

Db 1 CRGDD 5

RESULT 2

AAW66831
 ID AAW66831 standard; peptide; 7 AA.
 XX

AC AAW66831;

DT 25-MAR-2003 (revised)

DT 10-DEC-1998 (first entry)

XX Peptide useful for altering bone resorption.

XX bone resorption; pharmacore; angiogenesis; restenosis; integrin receptor;
 KW alpha v beta 3 integrin receptor; osteoclast; cyclic.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1

FT Modified-site 7 /note= "N-terminal acetyl"

FT Modified-site 7 /note= "C-terminal amide"

XX US5807819-A.

XX 15-SEP-1998.

XX 12-APR-1995; 95US-00421698.

XX 15-APR-1994; 94US-00227316.

XX 08-SEP-1994; 94US-00303052.

XX (LJOL-) LA JOLLA CANCER RES CENT.

XX Tschopp JF, Mullen D, Ingram R, Cheng S;

XX WPI; 1998-555601/47.

XX Use of peptide derivatives which can alter integrin receptor binding -
 PT for altering bone resorption, treating angiogenesis or restenosis and
 PT altering integrin receptor mediated interactions.
 XX
 XX Example 2; Fig 2C; 87pp; English.
 XX
 CC A new method is claimed for altering bone resorption. It comprises
 CC administration of a peptide of formula: X1X2X3X4GX5X6X7X8; where X1 =
 CC R1R2N or 0-10 amino acids (optionally protected by acetylation at the N-
 CC terminus); X2 = absent or 1 amino acid; X3 = absent or 1 or 2 amino acids

CC ; X4 = N-Me-Arg; X5 = residue which provides an ionic interaction with an
 CC integrin receptor, or is Msa, Psa or Ifsa; X6 = residue which has an
 CC aliphatic side chain; a non-natural amino acid that is hydrophobic; or
 CC Thr; X7 = a residue capable of forming a bond (i) with a bridging amino
 CC acid of X2, (ii) with X3 when X2 is absent, or (iii) with X4 when X2 and
 CC X3 are absent, to conformationally restrain the peptide; X8 = NR3R4; ORS;
 CC or 0-10 amino acids, optionally protected as an amide at the C-terminus;
 CC R1, R3-R5 = H or alkyl; R2 = H, alkyl, alkyl-CO or phenyl-CO. The
 CC peptides are useful for inhibiting bone resorption, angiogenesis or
 CC restenosis, and for altering integrin receptor-mediated interactions,
 CC especially alpha v beta 3 integrin receptor-mediated binding of cells to
 CC a matrix. They may be used for reducing or inhibiting osteoclast binding
 CC to a matrix. The present sequence represents an example of a circular
 CC peptide disclosed in the specification. (Updated on 25-MAR-2003 to
 CC correct PF field.)
 XX
 XX

Sequence 7 AA;

Query Match 100.0%; Score 32; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 Db 1 CRGDD 5

RESULT 3

AAW96984
 ID AAW96984 standard; peptide; 7 AA.

AC AAW96984;

26-APR-1999 (first entry)

Peptide used to inhibit bone resorption, angiogenesis and restenosis.

RGD-peptide; bone resorption; angiogenesis; restenosis;
 integrin receptor mediated interaction; binding; osteoclast; bone.

Synthetic.

Key Location/Qualifiers
 Modified-site 1 /note= "acetylated residue"
 Modified-site 7 /note= "amidated residue"

US5849865-A.

15-DEC-1998.

12-APR-1995; 95US-00421695.

13-APR-1994; 94US-00227316.

08-SEP-1994; 94US-00303052.

(LJOL-) LA JOLLA CANCER RES FOUND.

Tschopp JF, Mullen D, Ingram R, Cheng S;

WPI; 1999-179486/15.

RGD peptides - that modulate integrin-mediated cell-matrix binding.

Claim 5; Col 137; 90pp; English.

The present peptide represents a non-naturally occurring Arg-Gly-Asp
 (RGP)-containing peptide. The peptide may be useful for reducing or
 inhibiting bone resorption, angiogenesis or restenosis, and for altering
 an integrin receptor mediated interaction. The peptide may also be used
 to inhibit the binding of an osteoclast to bone

Sequence 7 AA;

Query Match 100.0%; Score 32; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 Db 1 CRGDD 5

RESULT 4

AAR96408

ID AAR96408 standard; peptide; 9 AA.

AC AAR96408;

21-OCT-2004 (revised)

05-JUL-1996 (first entry)

RGD cyclic peptide, TL#473, binds alpha-v,beta3 integrin receptor.

RGD-containing peptide; alpha-v, beta-3 integrin receptor; osteoclast;
 matrix; bone; inhibition; bone resorption; promote; endothelial cell;
 smooth muscle cell; restenosis; angiogenesis; cyclic.

Synthetic.

Key Location/Qualifiers
 Modified-site 1 /note= "Acyl-Ala"
 Disulfide-bond 2. .8
 Modified-site 9 /note= "Amidated C-terminal"

WO9528426-A2.

26-OCT-1995.

12-APR-1995; 95WO-US004741.

13-APR-1994; 94US-00227316.

08-SEP-1994; 94US-00303052.

(LJOL-) LA JOLLA CANCER RES FOUND.

Cheng S, Ingram R, Mullen D, Tschopp J;

WPI; 1995-373767/48.

Altering alpha-v, beta-3 integrin receptor-mediated binding of cell to
 matrix - using conformationally restrained peptide of RGD type, e.g. for
 treating inappropriate angiogenesis or for inhibiting bone resorption.

Claim 85; Page 80; 99pp; English.

The sequences given in AAR96301-417 are non-naturally occurring RGD-
 containing peptides which alter the alpha-v, beta-3 integrin receptor
 binding of a cell to a matrix, such as the binding of an osteoclast to a
 matrix such as bone. These peptides inhibit bone resorption and can
 inhibit or promote alpha-v, beta-3-mediated cell attachment depending on
 whether they are present in the cell in a soluble form or are bound to a
 solid substrate. These peptides can be used in the amelioration of the
 severity of a pathology involving alpha-v, beta-3 receptor-mediated
 binding of a cell, such as an osteoclast, endothelial cell or smooth
 muscle cell to a matrix. They are used for treating conditions associated
 with restenosis or inappropriate or insufficient angiogenesis, or for
 inhibiting osteoclast binding to the matrix

Revised record issued on 21-OCT-2004 : Correction to Feature Table Key

Sequence 9 AA;

Sequence 7 AA;

Query Match 100.0%; Score 32; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 DB 2 CRGDD 6

RESULT 5
 AAW66840
 ID AAW66840 standard; peptide; 9 AA.
 XX
 AC AAW66840;
 XX
 DT 25-MAR-2003 (revised)
 DT 10-DEC-1998 (first entry)
 XX
 DE Cyclic peptide.
 XX
 KW bone resorption; pharmacore; angiogenesis; restenosis; integrin receptor;
 KW alpha v beta 3 integrin receptor; osteoclast; cyclic.
 XX
 OS Synthetic.
 PN US5807819-A.
 XX
 PD 15-SEP-1998.
 XX
 PF 12-APR-1995; 95US-00421698.
 XX
 PR 15-APR-1994; 94US-00227316.
 PR 08-SEP-1994; 94US-00303052.
 XX
 PA (LJOL-) LA JOLLA CANCER RES CENT.
 XX
 PI Tschopp JF, Mullen D, Ingram R, Cheng S;
 XX
 DR WPI; 1998-555601/47.
 XX
 PT Use of peptide derivatives which can alter integrin receptor binding -
 PT for altering bone resorption, treating angiogenesis or restenosis and
 PT altering integrin receptor mediated interactions.
 XX
 PS Disclosure; Col 47-48; 87pp; English.
 XX
 CC A new method is claimed for altering bone resorption. It comprises
 CC administration of a peptide of formula: X1X2X3X4X5X6X7X8 ; where X1 =
 CC R1R2N or 0-10 amino acids (optionally protected by acetylation at the N-
 CC terminus); X2 = absent or 1 amino acid; X3 = absent or 1 or 2 amino acids
 CC ; X4 = N-Me-Arg; X5 = residue which provides an ionic interaction with an
 CC integrin receptor, or is Mea, Paa or Tfaa; X6 = residue which has an
 CC aliphatic side chain; a non-natural amino acid that is hydrophobic; or
 CC Thr; X7 = a residue capable of forming a bond (i) with a bridging amino
 CC acid of X2, (ii) with X3 when X2 is absent, or (iii) with X4 when X2 and
 CC X3 are absent, to conformationally restrain the peptide; X8 = NR3R4; OR5;
 CC or 0-10 amino acids, optionally protected as an amide at the C-terminus;
 CC R1, R3-R5 = H or alkyl; R2 = H, alkyl, alkyl-CO or phenyl-CO. The
 CC peptides are useful for inhibiting bone resorption, angiogenesis or
 CC restenosis, and for altering integrin receptor-mediated interactions,
 CC especially alpha v beta 3 integrin receptor-mediated binding of cells to
 CC a matrix. They may be used for reducing or inhibiting osteoclast binding
 CC to a matrix. The present sequence is shown in the specification. (Updated
 CC on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 32; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 DB 2 CRGDD 6

Db 2 CRGDD 6
 RESULT 6
 AAW97003
 ID AAW97003 standard; peptide; 9 AA.
 XX
 AC AAW97003;
 XX
 DT 26-APR-1999 (first entry)
 XX
 DE Peptide used to inhibit bone resorption, angiogenesis and restenosis.
 XX
 KW RGD-peptide; bone resorption; angiogenesis; restenosis;
 KW integrin receptor mediated interaction; binding; osteoclast; bone.
 XX
 OS Synthetic.
 XX
 FH Key
 FT Modified-site 1 Location/Qualifiers
 FT /note= "acetylated residue"
 FT Modified-site 9
 FT /note= "amidated residue"

US5849865-A.
 PN
 PD 15-DEC-1998.
 XX
 PF 12-APR-1995; 95US-00421695.
 XX
 PR 13-APR-1994; 94US-00227316.
 PR 08-SEP-1994; 94US-00303052.
 XX
 PA (LJOL-) LA JOLLA CANCER RES FOUND.
 XX
 PI Tschopp JF, Mullen D, Ingram R, Cheng S;
 XX
 DR WPI; 1999-179486/15.
 XX
 PT RGD peptides - that modulate integrin-mediated cell-matrix binding.
 XX
 PS Claim 6; Col 138; 90pp; English.
 XX
 CC The present peptide represents a non-naturally occurring Arg-Gly-Asp
 CC (RGD)-containing peptide. The peptide may be useful for reducing or
 CC inhibiting bone resorption, angiogenesis or restenosis, and for altering
 CC an integrin receptor mediated interaction. The peptide may also be used
 CC to inhibit the binding of an osteoclast to bone
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 32; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 DB 2 CRGDD 6

RESULT 7
 AAU61299
 ID AAU61299 standard; protein; 92 AA.
 XX
 AC AAU61299;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DE Propionibacterium acnes immunogenic protein #22195.
 XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;

KW dermatological; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX
 PN WO200181581-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 20-APR-2001; 2001WO-US012865.
 XX
 PR 21-APR-2000; 2000US-0199047P.
 PR 02-JUN-2000; 2000US-0208841P.
 PR 07-JUL-2000; 2000US-0216747P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'Maisonneuve J, Zhang Y, Jen S, Carter D;
 XX
 DR WPI; 2001-616774/71.
 DR N-PSDB; AAS59616.
 XX
 XX Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris.
 XX
 PS Example 1; SEQ ID NO 22494; 1069pp; English.
 XX
 XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 92 AA;
 Query Match 100.0%; Score 32; DB 4; Length 92;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRGDD 5
 Db 75 CRGDD 79
 RESULT 8
 ABM57818
 ID ABM57818 standard; protein; 92 AA.
 XX
 AC ABM57818;
 XX
 XX 20-OCT-2003 (first entry)
 DT
 XX Propionibacterium acnes predicted ORF-encoded polypeptide #22494.
 DE
 XX Acne vulgaris; antiseborrheic; dermatological; antibacterial;
 KW immunostimulant; immune response; vaccine.
 XX

OS Propionibacterium acnes.
 XX
 PN WO2003033515-A1.
 XX
 PD 24-APR-2003.
 XX
 PF 11-OCT-2002; 2002WO-US032727.
 XX
 PR 15-OCT-2001; 2001US-00978825.
 XX
 XX (CORI-) CORIXA CORP.
 PA
 PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
 PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
 PI Barth B, Vallieue-Douglas J;
 XX
 DR WPI; 2003-381789/36.
 DR N-PSDB; ACF64545.
 XX
 XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX
 PS Example 1; SEQ ID NO 22494; 1481pp; English.
 XX
 XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the P. acnes polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 92 AA;
 Query Match 100.0%; Score 32; DB 6; Length 92;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRGDD 5
 Db 75 CRGDD 79
 RESULT 9
 ABR41549
 ID ABR41549 standard; protein; 117 AA.
 XX
 AC ABR41549;
 XX
 XX 02-JUN-2003 (first entry)
 DT
 XX Human DTHP nucleic acid synthesis/modification protein.
 DE

XX Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;
KW cancer; cell proliferative disorder; autoimmune disorder;
KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;
KW neurological disorder; gastrointestinal disorder; transport disorder;
KW connective tissue disorder; drug screening; proteome analysis;
KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
KW disease model; toxicological testing; transcript imaging;
KW nucleic acid synthesis; nucleic acid modification.
XX
OS Homo sapiens.
XX
XX WO200297031-A2.
XX
XX 05-DEC-2002.
XX
XX 27-MAR-2002; 2002WO-US010056.
XX
XX 28-MAR-2001; 2001US-0279619P.
XX 29-MAR-2001; 2001US-0280067P.
XX 29-MAR-2001; 2001US-0280068P.
XX 16-MAY-2001; 2001US-0291280P.
XX 17-MAY-2001; 2001US-0291829P.
XX 17-MAY-2001; 2001US-0291849P.
XX 19-JUN-2001; 2001US-0299428P.
XX 20-JUN-2001; 2001US-029976P.
XX 20-JUN-2001; 2001US-0300001P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI Duffour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
PI Daughtery SC, Dam TC, Liu TE, Nguyen DA, Kleefeld Y, Gerstin EH;
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX
XX WPI; 2003-129518/12.
XX N-PSDB; ACC46487.
XX
XX Novel human diagnostic and therapeutic polypeptide useful for identifying
PT test compound which specifically binds to a polypeptide encoded by human
PT diagnostic and therapeutic polynucleotide, and to induce antibodies.
XX
XX Claim 27; SEQ ID NO 1084; 591pp; English.
XX
XX The invention relates to novel human diagnostic and therapeutic
CC polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded
CC proteins (DITHP; ABR41136-ABR41812). The invention also relates to
CC polynucleotide sequences at least 90% identical to the dithp cDNA
CC sequences of the invention; recombinant vectors, host cells and
CC transgenic organisms comprising a dithp nucleic acid sequence; the
CC recombinant production of DITHP proteins; antibodies specific for DITHP
CC proteins; microarrays comprising dithp nucleic acid sequences; methods of
CC detecting dithp nucleotide and protein sequences; methods of screening
CC for compounds which specifically bind a DITHP protein; and methods of
CC assessing the toxicity of test compounds using a dithp hybridisation
CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
CC diagnosis of a wide variety of conditions including cancer and other cell
CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,
CC viral, fungal or parasitic infections; hormonal disorders; metabolic
CC disorders; neurological disorders; gastrointestinal disorders; transport
CC disorders; and connective tissue disorders. They may also be used to
CC screen for modulators of protein activity or gene expression. DITHP
CC proteins can additionally be used in analysis of the proteome of a tissue
CC or cell type and to induce antibodies. The dithp nucleic acids are
CC additionally useful in somatic or germline gene therapy of the disorders
CC mentioned above, as a source of antisense sequences, as a source of
CC probes and primers, in genotyping and identification of individuals, in
CC the generation of transgenic animal models of human disease or knock in
CC humanised animals, in toxicological testing, and in transcript imaging.
XX The present sequence represents a DITHP protein which is involved in
CC nucleic acid synthesis and/or modification. Note: The sequence data for
CC this patent did not form part of the printed specification, but was

CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 117 AA;
XX
XX Query Match 100.0%; Score 32; DB 6; Length 117;
XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CRGDD 5
XX 113 CRGDD 117
XX
XX
XX RESULT 10
XX AAU44177
XX ID AAU44177 standard; protein; 120 AA.
XX
XX AC AAU44177;
XX
XX 27-FEB-2002 (first entry)
XX
XX Propionibacterium acnes immunogenic protein #5073.
XX
XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
XX Propionibacterium acnes.
XX
XX WO200181581-A2.
XX
XX 01-NOV-2001.
XX
XX 20-APR-2001; 2001WO-US012865.
XX
XX 21-APR-2000; 2000US-0199047P.
XX 02-JUN-2000; 2000US-0208841P.
XX 07-JUL-2000; 2000US-0216747P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
XX WPI; 2001-616774/71.
XX N-PSDB; AAS59522.
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris.
XX
XX Example 1; SEQ ID NO 5372; 1069pp; English.
XX
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
CC this patent did not form part of the printed specification, but was

CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 120 AA;

Query Match 100.0%; Score 32; DB 4; Length 120;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 |||||
 Db 105 CRGDD 109

RESULT 11

ABM40696
 ID ABM40696 standard; protein; 120 AA.

XX AC ABM40696;

XX DT 20-OCT-2003 (first entry)

XX Propionibacterium acnes predicted ORF-encoded polypeptide #5372.

XX Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;

XX immunostimulant; immune response; vaccine.

XX Propionibacterium acnes.

XX WO2003033515-A1.

XX PD 24-APR-2003.

XX PF 11-OCT-2002; 2002WO-US032727.

XX PR 15-OCT-2001; 2001US-00978825.

XX PA (CORI-) CORIXA CORP.

XX Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;

PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;

PI Barth B, Valliave-Douglas J;

XX WPI; 2003-381789/36.

DR N-PSDB; ACF64451.

XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.

XX Example 1; SEQ ID NO 5372; 1481pp; English.

XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC polynucleotide of the invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,

CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the P. acnes polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 120 AA;

Query Match 100.0%; Score 32; DB 6; Length 120;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 |||||
 Db 105 CRGDD 109

RESULT 12

ADJ48934
 ID ADJ48934 standard; protein; 152 AA.

XX AC ADJ48934;

XX DT 06-MAY-2004 (first entry)

XX Oil-associated gene related protein #434.

XX oil-associated gene; transgenic; enhanced seed oil; vegetable oil.

XX Unidentified.

XX US2004025202-A1.

XX PD 05-FEB-2004.

XX PF 14-MAR-2003; 2003US-00389566.

XX PR 15-MAR-2002; 2002US-0365301P.

XX PR 26-JUN-2002; 2002US-0391786P.

XX PR 26-JUN-2002; 2002US-0392018P.

XX (LAUR/) LAURIE C C.

PA (RAVA/) RAVANELLO M.

PA (SAVA/) SAVAGE T.

PA (LEDE/) LEDEAUX J R.

PA (ROGE/) ROGERS J A.

XX Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;

XX WPI; 2004-142683/14.

XX Novel recombinant DNA construct comprising a promoter functional in
 PT plants operably linked to an oil-associated gene for producing transgenic
 PT plant seed.

XX Example 3; SEQ ID NO 938; 22pp; English.

XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in plants operably linked to an oil-associated gene.
 CC The construct is useful for transgenic plant seed which has in its genome
 CC the construct, that is functional in the plant to transcribe the oil-
 CC associated gene. The transgenic plant seed grows into a plant having
 CC enhanced seed oil as compared to wild type. The construct is useful for
 CC producing hybrid maize seed. The transgenic plant seed is useful for
 CC producing vegetable oil. The present sequence represents the amino acid
 CC sequence of an oil-associated gene related protein.

XX Sequence 152 AA;

Query Match 100.0%; Score 32; DB 8; Length 152;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 Db |||||
 49 CRGDD 53

RESULT 13
 AAB40710
 ID AAB40710 standard; protein; 154 AA.
 XX
 AC AAB40710;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Human ORFX ORF474 polypeptide sequence SEQ ID NO:948.
 XX
 KW Human; open reading frame, ORFX; detection; cytostatic; hepatotropic;
 KW vulnery; antipsoriatic; antiparkinsonian; neurotropic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
 KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
 KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KW thrombosis; contraceptive.
 XX
 OS Homo sapiens.
 XX
 PN WO200058473-A2.
 XX
 PD 05-OCT-2000.
 XX
 PF 31-MAR-2000; 2000WO-US008621.
 XX
 PR 31-MAR-1999; 99US-0127607P.
 PR 02-APR-1999; 99US-0127636P.
 PR 05-APR-1999; 99US-0127728P.
 PR 30-MAR-2000; 2000US-00540763.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Leach M;
 XX
 XX WPI; 2000-602362/57.
 DR N-PSDB; AAC74919.
 DR
 XX
 PT Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease.
 XX
 PS Claim 11; Page 938; 5507pp; English.
 XX
 CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
 CC antipsoriatic; antiparkinsonian; neurotropic; neuroprotective; osteopathic;
 CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
 CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
 CC dermatological; immunosuppressive; antiinflammatory; antibacterial;
 CC antiviral; antifungal; antirheumatic; antithyroid; and antianemic. The
 CC sequences can be used for determining the presence of or predisposition
 CC to, or preventing or treating pathological conditions associated with an
 CC ORFX-associated disorder. The nucleic acids can be used to express ORFX
 CC proteins in gene therapy vectors. The proteins and nucleic acids may be
 CC used to treat cancers, proliferative disorders, neurodegenerative
 CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
 CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
 CC storage, systemic lupus erythematosus, severe combined immunodeficiency

CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
 CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
 CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
 CC enhance coagulation; to inhibit thrombosis; and as a contraceptive
 XX
 SQ Sequence 154 AA;
 Query Match 100.0%; Score 32; DB 3; Length 154;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRGDD 5
 Db |||||
 50 CRGDD 54

RESULT 14
 ADC39079
 ID ADC39079 standard; protein; 156 AA.
 XX
 AC ADC39079;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Novel human NOVX polypeptide SEQ ID NO: 18.
 KW
 KW antidiabetic; cytostatic; immunomodulator; anorectic; antilipemic;
 KW neurotropic; neuroprotective; immunostimulant; antiparkinsonian; anti-HIV;
 KW antiaschmatic; antiinflammatory; hypotensive; diabetes; obesity; cancer;
 KW hemostatic; osteopathic; gene therapy; NOVX; diabetes; anorexia;
 KW lymphoma; uterus cancer; prostate cancer; dyslipidemia; anorexia;
 KW wasting disorder; Alzheimer's disease; Parkinson's disorder; cachexia;
 KW cardiomyopathy; AIDS; asthma; Crohn's disease; multiple sclerosis;
 KW hypertension; atherosclerosis; hemophilia; graft-versus-host disease;
 KW Albright hereditary osteodystrophy.
 XX
 OS Homo sapiens.
 XX
 PN WO2003010327-A2.
 XX
 PD 06-FEB-2003.
 XX
 PF 02-MAY-2002; 2002WO-US014199.
 XX
 PR 02-MAY-2001; 2001US-0288063P.
 PR 03-MAY-2001; 2001US-0288395P.
 PR 07-MAY-2001; 2001US-0289087P.
 PR 09-MAY-2001; 2001US-0289817P.
 PR 09-MAY-2001; 2001US-0289818P.
 PR 11-MAY-2001; 2001US-0290194P.
 PR 14-MAY-2001; 2001US-0290753P.
 PR 15-MAY-2001; 2001US-0291181P.
 PR 16-MAY-2001; 2001US-0291243P.
 PR 18-MAY-2001; 2001US-0292001P.
 PR 21-MAY-2001; 2001US-0292374P.
 PR 22-MAY-2001; 2001US-0292587P.
 PR 23-MAY-2001; 2001US-0293107P.
 PR 25-MAY-2001; 2001US-0293747P.
 PR 29-MAY-2001; 2001US-0294109P.
 PR 29-MAY-2001; 2001US-0294110P.
 PR 30-MAY-2001; 2001US-0294434P.
 PR 31-MAY-2001; 2001US-0294827P.
 PR 12-JUL-2001; 2001US-0304879P.
 PR 31-JUL-2001; 2001US-0308901P.
 PR 14-AUG-2001; 2001US-0312270P.
 PR 17-AUG-2001; 2001US-0313416P.
 PR 10-SEP-2001; 2001US-0318463P.
 PR 27-SEP-2001; 2001US-0325683P.
 PR 18-OCT-2001; 2001US-0330292P.
 PR 28-NOV-2001; 2001US-0333873P.
 PR 03-DEC-2001; 2001US-0336909P.
 PR 03-DEC-2001; 2001US-0337552P.
 PR 21-FEB-2002; 2002US-0359245P.

PR 01-MAY-2002; 2002US-00136826.
XX (CURA-) CURAGEN CORP.
XX Miller CE, Kekuda R, Malyankar UM, Li L, Pena CBA, Spytek KA;
PI Gorman L, Guo X, Fernandez ER, Smithson G, Stone DJ, Zerhusen BD;
PI Patturajan M, Anderson DW, Mezes PS, Peyman JA, Macdougall JR;
PI Padigar M, Rastelli L, Shenoy SG, Gerlach VL, Shinkets RA, Zhong M;
PI Edinger SR, Ellerman K;
XX WPI; 2003-239445/23.
DR N-PSDB; ADC39078.
XX New NOVX polypeptides and polynucleotides, useful in gene therapy,
PT particularly for treating or preventing a syndrome associated with a
PT human disease e.g. diabetes, obesity, cancer, Alzheimer's disease,
PT hypertension or hemophilia.
XX Claim 1; SEQ ID NO 18; 748pp; English.
XX The invention relates to new isolated NOVX polypeptides, the genes
CC encoding them or sequences having at least 95% identity to the amino acid
CC or nucleotide sequences. The NOVX polypeptide is useful as a therapeutic,
CC particularly in the manufacture of a medicament for treating a syndrome
CC associated with a human disease, which includes a pathology associated
CC with NOVX polypeptide. The NOVX polypeptide is particularly useful for
CC treating, preventing or alleviating pathology associated with NOVX
CC polypeptide in a mammal, e.g. a human. The NOVX nucleic acid and
CC polypeptide are especially useful for treating or preventing e.g.
CC diabetes, obesity, cancers (e.g. lymphoma, uterus cancer or prostate
CC cancer), dyslipidemias, anorexia, wasting disorders, Alzheimer's disease,
CC Parkinson's disorder, cachexia, cardiomyopathy, AIDS, asthma, Crohn's
CC disease, multiple sclerosis, hypertension, atherosclerosis, hemophilia,
CC graft-versus-host disease or Albritght hereditary osteodystrophy. The DNA
CC encoding the protein is useful in gene therapy for treating the above
CC conditions. These are also useful in developing powerful assay system for
CC functional analysis of various human disorders, as well as in diagnostic
CC applications. This sequence represents one of the NOVX proteins of the
CC invention.
XX Sequence 156 AA;
SQ Query Match 100.0%; Score 32; DB 7; Length 156;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRGDD 5
Db 62 CRGDD 66
RESULT 15
ADS26705
ID ADS26705 standard; protein; 301 AA.
XX ADS26705;
AC ADS26705;
XX 02-DEC-2004 (first entry)
XX Bacterial polypeptide #15738.
XX Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX Bacteria.
OS US2003233675-A1.
XX

PD 18-DEC-2003.
XX 20-FEB-2003; 2003US-00369493.
XX 21-FEB-2002; 2002US-0360039P.
XX (CAOV/) CAO Y.
XX (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
PI WPI; 2004-061375/06.
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX Claim 1; SEQ ID NO 15738; 122pp; English.
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition. improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX Sequence 301 AA;
SQ Query Match 100.0%; Score 32; DB 8; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRGDD 5
Db 200 CRGDD 204
RESULT 16
ADS27091
ID ADS27091 standard; protein; 301 AA.
XX ADS27091;
AC ADS27091;
XX 02-DEC-2004 (first entry)
XX Bacterial polypeptide #16124.
DE Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW bacterial polypeptide.

KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.

XX Bacteria.

XX US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.

XX (HINK/) HINKLE G J.

XX (SLAT/) SLATER S C.

XX (CHEN/) CHEN X.

XX (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 16124; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 301 AA;

Query Match 100.0%; Score 32; DB 8; Length 301;

Best Local Similarity 100.0%; Pred. No. 5.9e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5

DB 200 CRGDD 204

RESULT 17

ADS26338

AD ADS26338 standard; protein; 302 AA.

XX ADS26338;

XX 02-DEC-2004 (first entry)

XX

DE Bacterial polypeptide #15371.

XX Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.

XX Bacteria.

XX US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.

XX (HINK/) HINKLE G J.

XX (SLAT/) SLATER S C.

XX (CHEN/) CHEN X.

XX (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 15371; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 302 AA;

Query Match 100.0%; Score 32; DB 8; Length 302;

Best Local Similarity 100.0%; Pred. No. 5.9e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5

DB 203 CRGDD 207

RESULT 18

AAW79286
ID AAW79286 standard; protein; 311 AA.
XX
AC AAW79286;
XX
DT 15-FEB-1999 (first entry)
XX
XX Human phosphatidic acid phosphatase beta.
DE
XX
XX Phosphatidic acid phosphatase beta; PAP-beta; human; dephosphorylation;
KW tumour suppressor; cancer; gene therapy.
KW
XX Homo sapiens.
OS
XX
XX WO9846730-A1.
PN
XX
XX 22-OCT-1998.
PD
XX
XX 16-APR-1998; 98WO-US007928.
PF
XX
XX 17-APR-1997; 97US-00842827.
PR
XX
XX (CELL-) CELL THERAPEUTICS INC.
PA
XX
XX Leung DW, Tompkins CK;
PI
XX
XX WPI; 1998-594568/50.
DR
XX N-PSDB; AAV69088.
XX
XX New nucleic acid encoding human phosphatidic acid phosphatases - used to
PT regulate levels of lipid cellular mediators and in gene therapy of e.g.
PT cancer.
XX
XX Claim 8; Fig 3A-B; 62pp; English.
PS
XX
XX This is the amino acid sequence of human mature phosphatidic acid
CC phosphatase-beta (PAP-beta), an enzyme that catalyses the conversion of
CC phosphatidic acid into diacylglycerol. 3 Variants of human PAP, i.e. PAP-
CC alpha 1 and 2 (see AAW79284-85), PAP-beta (see AAW79286) and PAP-gamma
CC (see AAW79287) have been identified. The invention provides PAP
CC polynucleotides (see AAV69086-89) and polypeptides, a method of preparing
CC PAP in a transformed host cell, and a method of using PAP to
CC dephosphorylate a substrate, especially lysophosphatidic acid, ceramide 1
CC -phosphate or sphingosine 1-phosphate, particularly for production of
CC diacylglycerol, but also monoacylglycerol, ceramide and sphingosine. PAP
CC is able to control the balance of lipid mediators of cellular activation
CC and signal transduction. Sequences that encode PAP are potentially
CC useful, in gene therapy, for treatment of cancer (PAP may be tumour
CC suppressors, PAP-alpha is expressed at lower levels in cancer cells than
CC in normal cells of same tissue type), inflammatory disease and diabetes-
CC associated obesity
XX
XX Sequence 311 AA;
SQ
Query Match 100.0%; Score 32; DB 2; Length 311;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRGDD 5
DB 181 CRGDD 185
RESULT 19
ADE60703
ID ADE60703 standard; protein; 311 AA.
XX
XX ADE60703;
AC
XX
XX 29-JAN-2004 (first entry)
DT
XX
XX Human Protein NP_003704, SEQ ID NO 6615.
DE
XX

KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
XX Homo sapiens.
OS
XX WO2003016475-A2.
PN
XX
XX 27-FEB-2003.
PD
XX
XX 14-AUG-2002; 2002WO-US025765.
PF
XX
XX 14-AUG-2001; 2001US-0312147P.
PR
XX 01-NOV-2001; 2001US-0346382P.
PR
XX 26-NOV-2001; 2001US-0333347P.
PR
XX
XX (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
PA
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
PI
XX
XX WPI; 2003-268312/26.
DR
XX
XX GENBANK; NP_003704.
DR
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
PT
XX
XX Claim 1; Page; 1017pp; English.
PS
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 311 AA;
SQ
Query Match 100.0%; Score 32; DB 7; Length 311;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRGDD 5
DB 181 CRGDD 185
RESULT 20
ADM72103
ID ADM72103 standard; protein; 311 AA.
XX
XX ADM72103;
AC

XX DT 03-JUN-2004 (first entry)
XX PA Human tau-related polypeptide PPAP2B.
XX DE
XX KW Tau; PPAP2A; PPAP2B; IHPK1; IHPK3; IHPK2; FLJ20530; DJ434014.5; EZF1;
KW Loc127424; Loc113179; KIAA0826; neuroprotective; neurotropic;
KW antiparkinsonian; tau-protein kinase; human.
XX OS Homo sapiens.
XX PN WO2004022708-A2.
XX PD 18-MAR-2004.
XX PF 04-SEP-2003; 2003WO-US027590.
XX PR 09-SEP-2002; 2002US-040877P.
XX PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
XX PI Feany MB, Shulman JM;
XX PS Claim 1; SEQ ID NO 2; 62pp; English.
XX DR WPI; 2004-248456/23.
XX DE New substantially pure Tau-related polypeptides and polynucleotides,
PT useful for diagnosing and/or treating neurological conditions with
PT aberrant expression of the Tau-related polypeptide, such as Alzheimer's
PT disease.
XX PS Claim 1; SEQ ID NO 2; 62pp; English.
XX DE The invention relates to tau-related polypeptide consisting essentially
CC of an amino acid sequence selected from PPAP2A, PPAP2B, IHPK1, IHPK3,
CC IHPK2, FLJ20530, DJ434014.5, EZF1, Loc127424, Loc113179 and KIAA0826
CC (ADM72102-ADM72112 respectively). The methods and compositions of the
CC present invention are useful for the diagnosis and/or treatment of
CC neurological diseases or conditions associated with aberrant expression
CC or activity of the Tau-related polypeptide, such as Alzheimer's disease
CC and Parkinson's disease. The present sequence represents a human tau-
CC related polypeptide homologue PPAP2B.
XX SQ Sequence 311 AA;
Query Match 100.0%; Score 32; DB 8; Length 311;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRGDD 5
DB 181 CRGDD 185
RESULT 21
ADN04415
ID ADN04415 standard; protein; 311 AA.
XX AC ADN04415;
XX DT 01-JUL-2004 (first entry)
XX DE Antipsoriatic protein sequence #401.
XX KW antipsoriatic; gene therapy; psoriasis; diagnosis.
XX OS Homo sapiens.
XX PN WO2004028479-A2.
XX PD 08-APR-2004.
XX PF 25-SEP-2003; 2003WO-US030907.
XX

PR 25-SEP-2002; 2002US-0414006P.
XX (GETH) GENENTECH INC.
XX PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
PI Wu TD;
XX WPI; 2004-305105/28.
DR N-PSDB; ADN04414.
XX New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
PT mammal.
XX PS Claim 9; SEQ ID NO 809; 3069pp; English.
XX CC The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polypeptides of the invention.
XX SQ Sequence 311 AA;
Query Match 100.0%; Score 32; DB 8; Length 311;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRGDD 5
DB 181 CRGDD 185
RESULT 22
ADP24274
ID ADP24274 standard; protein; 311 AA.
XX AC ADP24274;
DT 18-NOV-2004 (first entry)
XX DE PRO polypeptide SEQ ID NO:1452.
XX KW PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
KW antiaschmatic; hepatotropic; respiratory; gene therapy; immune system.
XX OS Unidentified.
XX PN WO2004041170-A2.
XX PD 21-MAY-2004.
XX PF 30-OCT-2003; 2003WO-US034312.
XX PR 01-NOV-2002; 2002US-0423394P.
XX PA (GETH) GENENTECH INC.
XX PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
PI Wu TD;
XX WPI; 2004-419628/39.
DR N-PSDB; ADP24273.
XX New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.
XX PS Claim 7; SEQ ID NO 1452; 2940pp; English.
XX DE The invention relates to a novel isolated nucleic acid and the PRO

CC polypeptide encoded by it. A protein of the invention has
 CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
 CC osteopathic, antidiabetic, dermatological, antiporiatic, antiallergic,
 CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its
 CC agonist, antagonist, or antibody that specifically binds to the
 CC polypeptide is useful for treating an immune related disorder such as
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein
 CC of the invention.

XX
 SQ Sequence 311 AA;

Query Match 100.0%; Score 32; DB 8; Length 311;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 |||||
 DB 181 CRGDD 185

RESULT 23

ABO62272
 ID ABO62272 standard; protein; 376 AA.

XX
 AC ABO62272;

XX
 DT 29-JUL-2004 (first entry)

XX Klebsiella pneumoniae polypeptide seqid 8789.

XX
 DE
 KW Recombinant expression vector; transcription regulatory element;
 XX Klebsiella pneumoniae protein; antibacterial; Vaccine.

XX Klebsiella pneumoniae.

OS
 PN US6610836-B1.

XX
 PD 26-AUG-2003.

XX
 PF 27-JAN-2000; 2000US-00489039.

XX
 PR 29-JAN-1999; 99US-0117747P.

XX
 PA (GENO-) GENOME THERAPEUTICS CORP.

XX Breton GL, Osborne M;

XX
 DR WPI; 2003-895346/82.

DR N-PSDB; ACH95823.

XX New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
 PT preparing a vaccine composition against Klebsiella pneumoniae.

XX
 PS Disclosure; SEQ ID NO 8789; 932pp; English.

XX

CC The invention describes a new isolated nucleic acid encoding a Klebsiella
 CC pneumoniae polypeptide. Also described are: a recombinant expression
 CC vector comprising the nucleic acid, operably linked to a transcription
 CC regulatory element; and a cell comprising the recombinant expression
 CC vector. The nucleic acid is useful for preparing a vaccine composition
 CC against Klebsiella pneumoniae. This is the amino acid sequence of a
 CC Klebsiella pneumoniae polypeptide of the invention

XX Sequence 376 AA;

SQ Query Match 100.0%; Score 32; DB 7; Length 376;

Best Local Similarity 100.0%; Pred. No. 7.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 |||||

DB 158 CRGDD 162

RESULT 24

ABU31582

ID ABU31582 standard; protein; 400 AA.

XX
 AC ABU31582;

XX
 DT 19-JUN-2003 (first entry)

XX Protein encoded by Prokaryotic essential gene #17109.

XX
 DE
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Klebsiella pneumoniae.

XX
 PN WO200277183-A2.

XX
 PD 03-OCT-2002.

XX
 PF 21-MAR-2002; 2002WO-US009107.

XX
 PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX
 PA (ELIT-) ELITRA PHARM INC.

XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX
 DR WPI; 2003-029926/02.

DR N-PSDB; ACA35452.

XX
 PT New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

XX
 PS Claim 25; SEQ ID NO 59506; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological

CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 400 AA;

Query Match 100.0%; Score 32; DB 6; Length 400;

Best Local Similarity 100.0%; Pred. No. 7.7e+02; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 |||||
 Db 41 CRGDD 45

RESULT 25

ABU45262
 ID ABU45262 standard; protein; 400 AA.

AC ABU45262;

XX 19-JUN-2003 (first entry)

XX Protein encoded by Prokaryotic essential gene #30789.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Salmonella paratyphi.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX N-PSDB; ACA49132.

XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 73186; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway;
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 400 AA;

Query Match 100.0%; Score 32; DB 6; Length 400;

Best Local Similarity 100.0%; Pred. No. 7.7e+02; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 |||||
 Db 41 CRGDD 45

RESULT 26

ABU48051
 ID ABU48051 standard; protein; 400 AA.

XX AC ABU48051;

XX 19-JUN-2003 (first entry)

XX Protein encoded by Prokaryotic essential gene #33578.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Salmonella typhi.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX N-PSDB; ACA51921.

PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.

XX
XX
XX Claim 25; SEQ ID NO 75975; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
XX Sequence 400 AA;

Query Match 100.0%; Score 32; DB 6; Length 400;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
|||||
Db 41 CRGDD 45

RESULT 27
ABU15369
ID ABU15369 standard; protein; 400 AA.
XX
XX ABU15369;
XX
XX
DT 19-JUN-2003 (first entry)
XX
XX Protein encoded by prokaryotic essential gene #896.
DE
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
XX Escherichia coli.
OS
XX WO200277183-A2.
XX
XX
XX 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US009107.
XX
XX 21-MAR-2001; 2001US-00815242.
XX 06-SEP-2001; 2001US-00948993.
XX 25-OCT-2001; 2001US-0342923P.
XX 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.
XX (SLIT-) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
XX N-PSDB; ACA19239.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
XX for homologous nucleic acids required for cellular proliferation to
XX isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 43293; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
XX Sequence 400 AA;

Query Match 100.0%; Score 32; DB 6; Length 400;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
|||||
Db 41 CRGDD 45

RESULT 28
ABO65513
ID ABO65513 standard; protein; 424 AA.
XX
XX ABO65513;
XX
XX 29-JUL-2004 (first entry)
XX
XX Klebsiella pneumoniae polypeptide seqid 12030.
XX
XX Recombinant expression vector; transcription regulatory element;
XX Klebsiella pneumoniae protein; antibacterial; vaccine.
XX
XX Klebsiella pneumoniae.

XX US6610836-B1.
 XX
 XX 26-AUG-2003.
 XX
 XX 27-JAN-2000; 2000US-00489039.
 XX
 XX 29-JAN-1999; 99US-0117747P.
 XX
 XX (GENO-) GENOME THERAPEUTICS CORP.
 XX
 XX Breton GL, Osborne M;
 XX
 XX WPI; 2003-895346/82.
 XX
 XX N-PSDB; ACH99064.
 XX
 XX New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
 PT preparing a vaccine composition against Klebsiella pneumoniae.
 XX
 XX Disclosure; SEQ ID NO 12030; 932pp; English.
 XX
 XX The invention describes a new isolated nucleic acid encoding a Klebsiella
 CC pneumoniae polypeptide. Also described are: a recombinant expression
 CC vector comprising the nucleic acid, operably linked to a transcription
 CC regulatory element; and a cell comprising the recombinant expression
 CC vector. The nucleic acid is useful for preparing a vaccine composition
 CC against Klebsiella pneumoniae. This is the amino acid sequence of a
 CC Klebsiella pneumoniae polypeptide of the invention
 CC
 XX Sequence 424 AA;
 SQ

Query Match 100.0%; Score 32; DB 7; Length 424;
 Best Local Similarity 100.0%; Pred. No. 8.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CRGDD 5
 Db 65 CRGDD 69
 |||||

RESULT 29
 ABO66647
 ID ABO66647 standard; protein; 488 AA.
 XX
 XX ABO66647;
 XX
 XX 29-JUL-2004 (first entry)
 DT
 XX
 XX Klebsiella pneumoniae polypeptide seqid 13164.
 DE
 XX
 XX Recombinant expression vector; transcription regulatory element;
 KW Klebsiella pneumoniae protein; antibacterial; Vaccine.
 KW
 XX Klebsiella pneumoniae.
 OS
 XX
 XX US6610836-B1.
 XX
 XX 26-AUG-2003.
 XX
 XX 27-JAN-2000; 2000US-00489039.
 XX
 XX 29-JAN-1999; 99US-0117747P.
 XX
 XX (GENO-) GENOME THERAPEUTICS CORP.
 XX
 XX Breton GL, Osborne M;
 XX
 XX WPI; 2003-895346/82.
 XX
 XX N-PSDB; ABD00218.
 XX
 XX New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
 PT preparing a vaccine composition against Klebsiella pneumoniae.
 XX

PS Disclosure; SEQ ID NO 13164; 932pp; English.
 XX
 XX The invention describes a new isolated nucleic acid encoding a Klebsiella
 CC pneumoniae polypeptide. Also described are: a recombinant expression
 CC vector comprising the nucleic acid, operably linked to a transcription
 CC regulatory element; and a cell comprising the recombinant expression
 CC vector. The nucleic acid is useful for preparing a vaccine composition
 CC against Klebsiella pneumoniae. This is the amino acid sequence of a
 CC Klebsiella pneumoniae polypeptide of the invention
 XX
 XX Sequence 488 AA;
 SQ

Query Match 100.0%; Score 32; DB 7; Length 488;
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CRGDD 5
 Db 103 CRGDD 107
 |||||

RESULT 30
 ADN19416
 ID ADN19416 standard; protein; 1116 AA.
 XX
 XX ADN19416;
 AC
 XX 02-DEC-2004 (first entry)
 DT
 XX
 XX Bacterial polypeptide #2069.
 DE
 XX
 XX Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 KW
 XX Bacteria.
 OS
 XX
 XX US2003233675-A1.
 FN
 XX 18-DEC-2003.
 PD
 XX 20-FEB-2003; 2003US-00369493.
 PF
 XX 21-FEB-2002; 2002US-0360039P.
 PR
 XX (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX
 XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 PI
 XX WPI; 2004-061375/06.
 DR
 XX
 XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX
 XX Claim 1; SEQ ID NO 2069; 122pp; English.
 PS
 XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the

CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX
 SQ Sequence 1116 AA;
 Query Match 100.0%; Score 32; DB 8; Length 1116;
 Best Local Similarity 100.0%; Pred. No. 26+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 |||||
 Db 677 CRGDD 681

RESULT 31
 ABB62913
 ID ABB62913 standard; protein; 1837 AA.
 XX
 AC ABB62913;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 15531.

XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.

OS Drosophila melanogaster.

PN WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

PR 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

DR N-PSDB; ABL07016.

XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.

PS Disclosure; SEQ ID NO 15531; 21pp + Sequence Listing; English.

XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
 CC ABB72072). The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1837 AA;

Query Match 100.0%; Score 32; DB 4; Length 1837;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 |||||
 Db 1413 CRGDD 1417

RESULT 32
 AAR96407
 ID AAR96407 standard; peptide; 7 AA.

XX AAR96407;

XX 21-OCT-2004 (revised)

DT 05-JUL-1996 (first entry)

XX RGD cyclic peptide, TL#114, binds alpha-v,beta3 integrin receptor.

XX RGD-containing peptide; alpha-v, beta-3 integrin receptor; osteoclast;
 KW matrix; bone; inhibition; bone resorption; promote; endothelial cell;
 KW smooth muscle cell; restenosis; angiogenesis; cyclic.

XX Synthetic.

XX Key Location/Qualifiers

FH Disulfide-bond 1..7

FT Modified-site 1 /note= "Acyl-Cys"

FT Modified-site 7 /note= "Amidated C-terminal"

FT

XX WO9528426-A2.

XX 26-OCT-1995.

XX 12-APR-1995; 95WO-US004741.

XX 13-APR-1994; 94US-00227316.

PR 08-SEP-1994; 94US-00303052.

XX (LJOL-) LA JOLLA CANCER RES FOUND.

XX Cheng S, Ingram R, Mullen D, Tschopp J;

XX WPI; 1995-373767/48.

XX
 PT Altering alpha-v, beta-3 integrin receptor-mediated binding of cell to
 PT matrix - using conformationally restrained peptide of RGD type, e.g. for
 PT treating inappropriate angiogenesis or for inhibiting bone resorption.

XX Claim 85; Page 80; 99pp; English.

XX
 CC The sequences given in AAR96301-417 are non-naturally occurring RGD-
 CC containing peptides which alter the alpha-v, beta-3 integrin receptor
 CC binding of a cell to a matrix, such as the binding of an osteoclast to a
 CC matrix such as bone. These peptides inhibit bone resorption and can
 CC inhibit or promote alpha-v, beta-3-mediated cell attachment depending on
 CC whether they are present in the cell in a soluble form or are bound to a
 CC solid substrate. These peptides can be used in the amelioration of the
 CC severity of a pathology involving alpha-v, beta-3 receptor-mediated
 CC binding of a cell, such as an osteoclast, endothelial cell or smooth
 CC muscle cell to a matrix. They are used for treating conditions associated
 CC with restenosis or inappropriate or insufficient angiogenesis, or for
 CC inhibiting osteoclast binding to the matrix

CC Revised record issued on 21-OCT-2004 : Correction to Feature Table Key

```
XX SQ Sequence 7 AA;
Query Match 90.6%; Score 29; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRGDD 5
Db 1 CKGDD 5

RESULT 33
AAW66822
ID AAW66822 standard; peptide; 7 AA.
XX AC AAW66822;
XX DT 25-MAR-2003 (revised)
DT 10-DEC-1998 (first entry)
DE Peptide useful for altering bone resorption.
XX bone resorption; pharmacore; angiogenesis; restenosis; integrin receptor;
KW alpha v beta 3 integrin receptor; osteoclast; cyclic.
XX Synthetic.
XX FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "N-terminal acetyl"
FT Modified-site 7
FT /note= "C-terminal amide"
XX US5807819-A.
XX PD 15-SEP-1998.
XX PF 12-APR-1995; 95US-00421698.
XX PR 15-APR-1994; 94US-00227316.
PR 08-SEP-1994; 94US-00303052.
XX (LJOL-) LA JOLLA CANCER RES CENT.
XX TSchoopp JF, Mullen D, Ingram R, Cheng S;
XX WPI; 1998-555601/47.
XX Use of peptide derivatives which can alter integrin receptor binding -
PT for altering bone resorption, treating angiogenesis or restenosis and
PT altering integrin receptor mediated interactions.
XX
XX Example 2; Fig 2D; 87pp; English.
XX A new method is claimed for altering bone resorption. It comprises
CC administration of a peptide of formula: X1X2X3X4GX5X6X7X8; where X1 =
CC R1R2N or 0-10 amino acids (optionally protected by acetylation at the N-
CC terminus); X2 = absent or 1 amino acid; X3 = absent or 1 or 2 amino acids
CC ; X4 = N-Me-Arg; X5 = residue which provides an ionic interaction with an
CC integrin receptor, or is Msa, Paa or Tfsa; X6 = residue which has an
CC aliphatic side chain; a non-natural amino acid that is hydrophobic; or
CC Thr; X7 = a residue capable of forming a bond (i) with a bridging amino
CC acid of X2, (ii) with X3 when X2 is absent, or (iii) with X4 when X2 and
CC X3 are absent, to conformationally restrain the peptide; X8 = NR3R4; OR5;
CC or 0-10 amino acids, optionally protected as an amide at the C- terminus;
CC R1, R3-R5 = H or alkyl; R2 = H, alkyl, alkyl-CO or phenyl-CO. The
CC peptides are useful for inhibiting bone resorption, angiogenesis or
CC restenosis, and for altering integrin receptor-mediated interactions,
CC especially alpha v beta 3 integrin receptor-mediated binding of cells to
CC a matrix. They may be used for reducing or inhibiting osteoclast binding
CC to a matrix. The present sequence represents an example of a circular
CC peptide disclosed in the specification. (Updated on 25-MAR-2003 to

CC correct PF field.)
XX SQ Sequence 7 AA;
Query Match 90.6%; Score 29; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRGDD 5
Db 1 CKGDD 5

RESULT 34
AAW97002
ID AAW97002 standard; peptide; 7 AA.
XX AC AAW97002;
XX DT 26-APR-1999 (first entry)
DE Peptide used to inhibit bone resorption, angiogenesis and restenosis.
XX RGD-peptide; bone resorption; angiogenesis; restenosis;
KW integrin receptor mediated interaction; binding; osteoclast; bone.
XX Synthetic.
XX FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "acetylated residue"
FT Modified-site 7
FT /note= "amidated residue"
XX US5849865-A.
XX PD 15-DEC-1998.
XX PF 12-APR-1995; 95US-00421695.
XX PR 13-APR-1994; 94US-00227316.
PR 08-SEP-1994; 94US-00303052.
XX (LJOL-) LA JOLLA CANCER RES FOUND.
XX TSchoopp JF, Mullen D, Ingram R, Cheng S;
XX WPI; 1999-179486/15.
XX RGD peptides - that modulate integrin-mediated cell-matrix binding.
XX Claim 6; Col 138; 90pp; English.
XX The present peptide represents a non-naturally occurring Arg-Gly-Asp
CC (RGD)-containing peptide. The peptide may be useful for reducing or
CC inhibiting bone resorption, angiogenesis or restenosis, and for altering
CC an integrin receptor mediated interaction. The peptide may also be used
CC to inhibit the binding of an osteoclast to bone
XX SQ Sequence 7 AA;
Query Match 90.6%; Score 29; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRGDD 5
Db 1 CKGDD 5

RESULT 35
AAW87384
ID AAW87384 standard; protein; 41 AA.
```

XX
AC AAM87384;
XX
XX 07-NOV-2001 (first entry)
XX
XX Human immune/haematopoietic antigen SEQ ID NO:14977.
XX
XX Human, immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis.
KW
XX Homo sapiens.
XX
XX WO200157182-A2.
PN
XX
XX 09-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001354.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 13-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226688P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234977P.
PR 25-SEP-2000; 2000US-0234988P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.

PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI; 2001-483426/52.
 DR N-PSDB; AAK60165.
 XX
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and metastasis.
 XX
 PS Claim 11; SEQ ID NO 14977; 3071pp + Sequence Listing; English.
 XX
 CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
 CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting the
 CC nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/haematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/haematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention
 XX
 SQ Sequence 41 AA;

 Query Match 90.6%; Score 29; DB 4; Length 41;
 Best Local Similarity 80.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 1 CRGDD 5
 Db |:|:
 1 CRGDD 5

 RESULT 36
 ABO67045
 ID ABO67045 standard; protein; 105 AA.
 AC ABO67045;
 XX
 XX 29-JUL-2004 (first entry)
 DT
 DE Klebsiella pneumoniae polypeptide seqid 13562.
 XX
 KW Recombinant expression vector; transcription regulatory element;
 KW Klebsiella pneumoniae protein; antibacterial; Vaccine.
 XX
 OS Klebsiella pneumoniae.
 XX
 FN US6610836-B1.
 XX
 PD 26-AUG-2003.
 XX
 PF 27-JAN-2000; 2000US-00489039.
 XX
 PR 29-JAN-1999; 99US-0117747P.
 XX

(GENO-) GENOME THERAPEUTICS CORP.
 Breton GL, Osborne M;
 WPI; 2003-895346/82.
 N-PSDB; ABD00616.
 New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
 preparing a vaccine composition against Klebsiella pneumoniae.
 Disclosure; SEQ ID NO 13562; 932pp; English.
 The invention describes a new isolated nucleic acid encoding a Klebsiella
 pneumoniae polypeptide. Also described are: a recombinant expression
 vector comprising the nucleic acid, operably linked to a transcription
 regulatory element; and a cell comprising the recombinant expression
 vector. The nucleic acid is useful for preparing a vaccine composition
 against Klebsiella pneumoniae. This is the amino acid sequence of a
 Klebsiella pneumoniae polypeptide of the invention
 Sequence 105 AA;

 Query Match 90.6%; Score 29; DB 7; Length 105;
 Best Local Similarity 80.0%; Pred. No. 8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 1 CRGDD 5
 Db |:|:
 46 CRGDD 50

 RESULT 37
 ADB08040
 ID ADB08040 standard; protein; 274 AA.
 AC ADB08040;
 XX
 XX 20-NOV-2003 (first entry)
 DT
 DE Alloicoccus otitis antigenic protein SEQ ID NO:1980.
 XX
 KW Alloicoccus otitis; antigenic protein; immunogenic; immunisation;
 KW gene therapy; Gram-positive bacterium; infection.
 XX
 OS Alloicoccus otitis.
 XX
 FN WO2003048304-A2.
 XX
 PD 12-JUN-2003.
 XX
 PF 25-NOV-2002; 2002WO-US036123.
 XX
 PR 29-NOV-2001; 2001US-0333777P.
 PR 19-NOV-2002; 2002US-0426742P.
 XX
 XX (AMHP) WYETH HOLDINGS CORP.
 XX
 XX Fletcher LD, McMichael JC, Russell DP, Zagursky RJ;
 PI
 XX WPI; 2003-505284/47.
 DR N-PSDB; ADB08039.
 XX
 PT New Alloicoccus otitis polynucleotides and polypeptides, useful for
 PT treating and diagnosing diseases, drug screening assays and monitoring of
 PT effects during drug clinical trials.
 XX
 PS Claim 33; SEQ ID NO 1980; 1019pp; English.
 XX
 CC The present invention describes an isolated polynucleotide (I) of
 CC Alloicoccus otitis genomic DNA, which encodes an antigenic protein.
 CC Alloicoccus otitis is a Gram-positive bacterium. Also described: (1)
 CC an isolated polypeptide that is encoded by the polynucleotide (I); (2) an
 CC expression vector comprising the novel isolated polynucleotide (I), its

CC complement, degenerate variant or fragment; (3) a genetically engineered
 CC host cell, transfected, transformed or infected with the vector of (2);
 CC (4) an antibody specific for the polypeptide of (1); (5) an immunogenic
 CC composition comprising the polypeptide, its complement, biological
 CC equivalent or fragment, or the polynucleotide that is comprised in the
 CC expression vector; (6) a pharmaceutical composition comprising the
 CC polypeptide of (1) and a carrier; (7) a protein chip comprising an array
 CC of the polypeptides of (1), their biological equivalent or fragment; (8)
 CC immunising against *Alloiooccus* otitidis by administering to a host the
 CC otitidis in the biological sample; (10) a kit comprising a container
 CC containing the novel polynucleotide, its degenerate variant or fragment,
 CC or the antibody of (4); and (11) producing a polypeptide by culturing the
 CC genetically engineered host cell under conditions suitable to produce the
 CC polypeptide from the culture. (1) can be used in gene therapy. The
 CC polynucleotides, polypeptides, antibodies and compositions of the present
 CC invention can be used for treating and diagnosing diseases, drug
 CC screening assays and monitoring of effects during drug clinical trials.
 CC The polynucleotides are useful for expressing and detecting *Alloiooccus*
 CC otitidis. The present sequence represents an *Alloiooccus* otitidis
 CC antigen protein from the present invention.

XX
 SQ Sequence 274 AA;

Query Match 90.6%; Score 29; DB 6; Length 274;
 Best Local Similarity 80.0%; Pred. No. 1.9e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 |:|
 Db 115 CKGDD 119

RESULT 38
 ADJ71969
 ID ADJ71969 standard; protein; 299 AA.
 AC ADJ71969;
 XX
 XX 06-MAY-2004 (first entry)
 XX Human PMMM protein amino acid sequence SeqID29.
 XX
 KW protein modification and maintenance molecule; PMMM; cytostatic;
 KW antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective;
 KW cerebroprotective; vasotropic; anti-HIV; antiallergic; antimicrobial;
 KW antiinflammatory; endocrine-Gen; thyromimetic;
 KW cell proliferative disorder; cancer; atherosclerosis;
 KW neurological disorder; epilepsy; Huntington's disease; stroke;
 KW immune disorder; inflammatory disorder; AIDS; allergy;
 KW developmental disorder; Hypothyroidism; Cushing's syndrome; infection;
 KW human.

OS Homo sapiens.
 XX
 XX WO2004009797-A2.
 XX
 XX 29-JAN-2004.
 XX
 XX 23-JUL-2003; 2003WO-US023249.
 XX
 XX 23-JUL-2002; 2002US-0398143P.
 PR 09-AUG-2002; 2002US-0402458P.
 PR 12-AUG-2002; 2002US-0403289P.
 PR 27-AUG-2002; 2002US-0406472P.
 PR 06-SEP-2002; 2002US-0409354P.
 XX
 XX (INCY-) INCYTE CORP.

XX Elliott VS, Swarnakar A, Griffin JA, Lee EA, Sprague WW;
 PI Hafalia AJA, Lee SV, Kable AE, Ison CH, Khare R, Chawla NK;
 PI Marquis JP, Jiang X, Jackson AA, Becha SD, Emerling BM, Jin P;
 PI Wilson AD, Richardson TW, Yang J, Baughn MR, Gandhi AR, Nguyen DB;

PI Ramkumar J, Kallick DA, Kearney L, Lu DAM, Gietzen KJ, Tribouley CM;
 PI Lal PG, Blake JJ, Lu Y, Arvizu CS;
 XX
 DR WPI; 2004-123392/12.
 DR N-PSDB; ADJ72031.
 XX
 PT New human protein modification and maintenance molecules (PMMM), useful
 PT for diagnosing, treating and preventing diseases or conditions associated
 PT with the aberrant PMMM expression e.g. cancer, AIDS, epilepsy, or
 PT infections.

XX Claim 1; SEQ ID NO 29; 387pp; English.
 XX
 CC This invention relates to novel protein modification and maintenance
 CC molecules (PMMM) and polynucleotides which identify and encode PMMM. The
 CC invention may be useful for the development of compositions with a
 CC cytostatic, antiarteriosclerotic, anticonvulsant, nootropic,
 CC neuroprotective, cerebroprotective, vasotropic, anti-HIV, antiallergic,
 CC antimicrobial, antiinflammatory, endocrine-Gen or thyromimetic activity.
 CC The polypeptides and polynucleotides are useful in diagnosing, treating
 CC and preventing diseases or conditions associated with the decreased
 CC expression or overexpression of PMMM, such as cell proliferative (for
 CC example cancer, atherosclerosis), neurological (for example epilepsy,
 CC Huntington's disease, stroke), immune/inflammatory (for example AIDS,
 CC allergies) and developmental (for example Hypothyroidism, Cushing's
 CC syndrome) disorders, or infections. These are also useful in assessing
 CC the effects of exogenous compounds on the expression of nucleic acid and
 CC amino acid sequences of PMMM. The present sequence is that of a human
 CC PMMM protein of the invention.

XX Sequence 299 AA;

Query Match 90.6%; Score 29; DB 8; Length 299;
 Best Local Similarity 80.0%; Pred. No. 2.1e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 |:|
 Db 261 CKGDD 265

RESULT 39
 ADA50457
 ID ADA50457 standard; protein; 357 AA.
 AC ADA50457;
 XX

DT 20-NOV-2003 (first entry)

XX Human protease SEQ ID NO:55.

DE enzyme; human; protease.

XX Homo sapiens.

XX WO2003040393-A2.

XX 15-MAY-2003.

XX 04-NOV-2002; 2002WO-IB004615.

XX 06-NOV-2001; 2001US-0332633P.

XX (DECO-) DECODE GENETICS EHF.

XX Martinez RAM, Sigurdson GT;

XX WPI; 2003-441582/41.

XX N-PSDB; ADA50504.

XX Novel isolated protease polypeptide and polynucleotide encoding the
 PT polypeptide useful for diagnosing and treating diseases or conditions
 PT associated with a protease.

XX Claim 1; Page 66; 160pp; English.

XX The invention relates to a novel isolated polypeptide comprising an amino

CC acid sequence that has greater than 95 % identity to any one of 47 150-

CC 350 residue protease polypeptide sequences, given in the specification.

CC The nucleic acids, probes, primers, polypeptides and antibodies of the

CC invention can be used in methods of diagnosis of a susceptibility to a

CC disease or condition associated with a protease. The present sequence

CC represents a protease of the invention.

XX SQ Sequence 357 AA;

Query Match 90.6%; Score 29; DB 6; Length 357;

Best Local Similarity 80.0%; Pred. No. 2.5e+03;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5

Db 113 CRGDD 117

RESULT 40

ABR40851

ID ABR40851 standard; protein; 412 AA.

XX AC ABR40851;

XX DT 16-MAY-2003 (first entry)

XX DE Glycine max oil trait related protein sequence SEQ ID NO:481.

XX Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;

KW receptor-like protein kinase; mitogen activated protein kinase; oil;

KW LIP15-like transcription factor caleosin; ATP citrate lyase; SNF1;

KW CKC-like transcription factor; antisense inhibition; co-suppression;

transgenic plant.

XX Glycine max.

OS Glycine max.

XX WO2003002751-A2.

XX 09-JAN-2003.

XX 27-JUN-2002; 2002WO-US020152.

XX 29-JUN-2001; 2001US-0301913P.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

PA (PION-) PIONEER HI-BRED INT INC.

XX Allen SM, Allen WB, Cahoon RE, Epelbaum S, Famodu OO, Harvell LT;

PI Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B;

PI Tarczyński MC;

XX WPI; 2003-201509/19.

DR N-PSDB; ACC00845.

XX Novel nucleotide fragment encoding polypeptides having receptor-like

PT protein kinase activity, caleosin-like activity, useful for altering oil

PT phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.

XX Claim 12; Page 497-498; 542pp; English.

XX The present invention describes an isolated nucleotide fragment (I)

CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a

CC polypeptide (PP) having receptor-like protein kinase activity, mitogen

CC activated protein (MAP)-kinase activity, LIP15-like transcription factor

CC activity, caleosin-like activity, ATP citrate lyase activity, SNF1-like

CC activity and CKC-like transcription factor activity. Also described: (1)

CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or

CC (II), operably linked to a regulatory sequence; (3) a plant (IV)

CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)

CC oil obtained from (V). (I) or its part can be used in antisense

CC inhibition or co-suppression in a transformed plant. (III) is useful for

CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,

CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for

CC creating transgenic plants having altered lipid profiles. (I) can also be

CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to

CC ABR40879 represent sequences used in the exemplification of the present

CC invention

XX SQ Sequence 412 AA;

Query Match 90.6%; Score 29; DB 6; Length 412;

Best Local Similarity 80.0%; Pred. No. 2.8e+03;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5

Db 325 CRGDD 329

RESULT 41

ADI16354

ID ADI16354 standard; protein; 435 AA.

XX AC ADI16354;

XX DT 22-APR-2004 (first entry)

XX DE Human protein modification and maintenance molecule (PMMM) protein #39.

XX human; protein modification and maintenance molecule; PMMM;

KW gastrointestinal disorders; peptic ulcer; Crohn's disease;

KW cardiovascular disorders; hypertension; congenital heart disease;

KW autoimmune disease; inflammatory disease; AIDS; anaemia;

KW developmental disorder; Cushing's syndrome; tubular acidosis;

KW epithelial disorder; eczema; scabies; neurological disorder;

KW Alzheimer's disease; multiple sclerosis; infection; cancer.

XX Homo sapiens.

OS Homo sapiens.

XX WO2003100016-A2.

XX 04-DEC-2003.

XX 22-MAY-2003; 2003WO-US016498.

XX 22-MAY-2002; 2002US-0383491P.

PR 24-JUN-2002; 2002US-0391378P.

PR 22-JUL-2002; 2002US-0397921P.

XX (INCY-) INCYTE CORP.

XX Khare R, Bulloch SA, Swarnakar A, Elliott VS, Marquis JP;

PI Mason PM, Chawla NK, Ramkumar J, Kable AE, Hafalia AJA, Lee SY;

PI Tran UK, Yue H, Becha SD, Griffin JA, Chang H, Jiang X, Jackson AA;

PI Richardson TW, Lal PG, Yao MG, Lu Y, Warren BA, Jin P, Wilson AD;

PI Gietzen KJ;

XX WPI; 2004-035124/03.

DR N-PSDB; ADI16406.

XX New protein modification and maintenance molecules, useful for diagnosing

PT or treating e.g. peptic ulcer, hypertension, rheumatic fever, AIDS,

PT Cushing's syndrome, Alzheimer's disease, multiple sclerosis, stroke or

PT cancers.

XX Claim 1; SEQ ID NO 39; 419pp; English.

XX The invention comprises the amino acid and coding sequences of human

CC protein modification and maintenance molecules (PMMM). The DNA and

CC protein sequences of the invention are useful for the diagnosis and

CC treatment of disorders associated with expression of PMMM, such as:

CC gastrointestinal disorders (e.g. peptic ulcer and Crohn's disease),

CC cardiovascular disorders (e.g. hypertension and congenital heart
 CC disease), autoimmune or inflammatory disease (e.g. AIDS and anaemia),
 CC developmental disorders (e.g. Cushing's syndrome and tubular acidosis),
 CC epithelial disorders (e.g. eczema and scabies), neurological disorders
 CC (e.g. Alzheimer's disease and multiple sclerosis), infections and cancer.
 CC The present amino acid sequence represents a human PMW protein of the
 CC invention.

XX
 SQ Sequence 435 AA;

Query Match 90.6%; Score 29; DB 8; Length 435;
 Best Local Similarity 80.0%; Pred. No. 3e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
 |:| | |
 Db 261 CRGDD 265

RESULT 42
 ABB98131
 ID ABB98131 standard; protein; 508 AA.
 AC ABB98131;
 DT 17-OCT-2002 (first entry)
 DE Human PMW Incyte ID 7485421CD1.

XX
 XX Human; PMW; protein modification and maintenance molecule;
 KW anticonvulsant; neuroprotective; nootropic; cytostatic; antipsoriatic;
 KW antiasthmatic; dermatological; antidiabetic; antiparkinsonian;
 KW antianaemic; antiinflammatory; antitumor; antidiabetic; cardiant;
 KW hepatotropic; osteopathic; antiemetic; antipyrretic; virucide;
 KW antibacterial; fungicide; gastrointestinal; antidiarrheic; laxative;
 KW haemostatic; anti-HIV; thrombolytic; anticoagulant; gynaecological;
 KW cardiovascular; antiarteriosclerotic; hypotensive; vasotropic;
 KW anticancer; antirheumatic; immunosuppressive; antiallergic; antithyroid;
 KW nephrotropic; antitumor; immunosuppressive; antiallergic; antithyroid;
 KW ophthalmological; antiparasitic; tranquiliser; vulnery; keratolytic;
 KW auditory; antiseborrheic; antidepressant; neuroleptic; antinfertility;
 KW anelminthic; protozoicidal; Crohn's disease; hypertension; autoimmune;
 KW inflammatory; anaemia; cell proliferative; developmental; epithelial;
 KW scabies; neurological; Alzheimer's disease; reproductive;
 KW ectopic pregnancy; gene therapy; vaccine; disorder;
 KW ubiquitin specific protease; chromosome 1.

XX
 OS Homo sapiens.

XX
 PN W0200246383-A2.

XX
 PD 13-JUN-2002.

XX
 PF 05-DEC-2001; 2001WO-US046964.

XX
 PR 08-DEC-2000; 2000US-0254399P.

XX
 PR 21-DEC-2000; 2000US-0257803P.

XX
 PR 05-JAN-2001; 2001US-0260110P.

XX
 PR 19-JAN-2001; 2001US-0262851P.

XX
 PR 25-JAN-2001; 2001US-0264623P.

XX
 PA (INCY-) INCYTE GENOMICS INC.

XX
 XX Yue H, Azimzai Y, Kallick DA, Baughn MR, Griffin JA, Swarnakar A;
 PI Lal PG, Wallia NK, Hafalia AJA, Gandhi AR, Au-Young J, Elliott VS;
 PI Ramkumar J, Thangavelu K, Lu Y, Warren BA, Lu DAM, Lee EA;
 PI Tribouley CM, Arvizu C, Deleage AM, Rao MG, Khan FA;
 PI Sanjanwala MM;

XX
 DR WPI; 2002-519664/55.

XX
 DR N-PSDB; ABQ75952.

XX
 PT New isolated Protein Modification and Maintenance polypeptides, useful

PT for diagnosis, and treatment of e.g. gastrointestinal disorders.

XX
 PS Claim 1 (a); Page 167-168; 200pp; English.

XX
 CC The invention relates to an isolated Protein Modification and Maintenance
 CC (PMW) polypeptide. Polypeptides of the invention may be used in the
 CC diagnosis, treatment and prevention of disorders associated with
 CC decreased expression or activity of PMW. These include gastrointestinal
 CC disorders (e.g. Crohn's disease), cardiovascular disorders (e.g.
 CC hypertension), autoimmune/inflammatory disorders (e.g. anaemia), cell
 CC proliferative disorders, developmental disorders, epithelial disorders
 CC (e.g. scabies), neurological disorders (e.g. Alzheimer's disease)
 CC reproductive disorders (e.g. ectopic pregnancy), and in gene therapy or a
 CC vaccine for such diseases. They may also be used in the assessment of the
 CC effects of exogenous compound on the expression of nucleic acid and amino
 CC acid sequences of protein modification and maintenance molecules. The
 CC current sequence represents a human PMW of the invention, which has been
 CC found to have homology with mouse ubiquitin specific protease. The gene
 CC encoding this polypeptide has been localised to chromosome 1

XX
 SQ Sequence 508 AA;

Query Match 90.6%; Score 29; DB 5; Length 508;
 Best Local Similarity 80.0%; Pred. No. 3.4e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
 |:| | |
 Db 261 CRGDD 265

RESULT 43
 ADF92397
 ID ADF92397 standard; protein; 514 AA.
 AC ADF92397;
 XX
 DT 26-FEB-2004 (first entry)
 DE Human ubiquitin-specific protease KIAA1063.

XX
 DE ubiquitin-specific protease; Ub; USP; de-ubiquitination;
 KW antiparkinsonian; nootropic; neuroprotective; neurodegenerative;
 KW Alzheimer's disease; Parkinson's; muscular atrophy; gene therapy; human;
 KW KIAA1063.

XX
 OS Homo sapiens.

XX
 PN JP2003189883-A.

XX
 PD 08-JUL-2003.

XX
 PF 30-SEP-2002; 2002JP-00287039.

XX
 PR 28-SEP-2001; 2001JP-00304709.

XX
 PA (DAUC) DAIICHI PHARM CO LTD.

XX
 DR WPI; 2003-856760/80.

XX
 DR N-PSDB; ADF92398.

XX
 PT Novel human ubiquitin specific protease having de-ubiquitination
 PT activity, useful in diagnosis and treatment of muscular atrophy and
 PT neurodegenerative diseases such as Alzheimer's disease, Parkinson's
 PT disease.

XX
 PS Claim 1; SEQ ID NO 11; 117pp; Japanese.

XX
 CC The invention relates to a novel ubiquitin (Ub)-specific protease (USP)
 CC polypeptide having de-ubiquitination activity. The polypeptide of the
 CC invention demonstrates antiparkinsonian, nootropic, neuroprotective and
 CC muscular activities and may be useful for treating neurodegenerative
 CC diseases such as Alzheimer's disease, Parkinson's disease and muscular

CC atrophy, as well as in gene therapy applications. The current sequence is
CC that of the human ubiquitin-specific protease of the invention.

XX Sequence 514 AA;

XX Query Match 90.6%; Score 29; DB 7; Length 514;
XX Best Local Similarity 80.0%; Pred. No. 3.5e+03;
XX Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5

|||

267 CKGDD 271

RESULT 44

ABG10994

ID ABG10994 standard; protein; 525 AA.

XX AC ABG10994;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #10985.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS75181.

XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.

XX PS Claim 20; SEQ ID NO 41353; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX CC sequences. (I) is useful as hybridisation probes, polymerase chain
XX CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX CC and in recombinant production of (II). The polynucleotides are also used
XX CC in diagnostics as expressed sequence tags for identifying expressed
XX CC genes. (I) is useful in gene therapy techniques to restore normal
XX CC activity of (II) or to treat disease states involving (II). (II) is
XX CC useful for generating antibodies against it, detecting or quantitating a
XX CC polypeptide in tissue, as molecular weight markers and as a food
XX CC supplement. (II) and its binding partners are useful in medical imaging
XX CC of sites expressing (II). (I) and (II) are useful for treating disorders
XX CC involving aberrant protein expression or biological activity. The
XX CC polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
XX CC amino acid sequences of the invention. Note: The sequence data for this
XX CC patent did not appear in the printed specification, but was obtained in
XX CC electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 525 AA;

XX Query Match 90.6%; Score 29; DB 4; Length 525;
XX Best Local Similarity 80.0%; Pred. No. 3.5e+03;
XX Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5

|||

278 CKGDD 282

RESULT 45

ADH54836

ID ADH54836 standard; protein; 525 AA.

XX AC ADH54836;

XX DT 25-MAR-2004 (first entry)

XX DE Human ubiquitin protease 8 (hUBP8/Ubp22), SEQ ID NO:1.

XX KW Human; hUBP8; ubiquitin protease 8; ubiquitin specific protease 22;
XX KW Ubp22; USP22; UbP8 homologue; deubiquitylation; histone H2B;
XX KW histone modification; transcriptional regulation; UB8 modulator;
XX KW drug screening; tumorigenic potential; cancer cell sensitivity; cancer;
XX KW tumour; inflammation; viral infection; fungal infection;

XX KW Alzheimer's disease; human immunodeficiency virus; HIV infection;

XX KW hypercholesterolaemia; cytostatic; antiinflammatory; virucide; fungicide;

XX KW nootropic; neuroprotective; anti-HIV; antilipaemic; enzyme.

XX OS Saccharomyces cerevisiae.

XX PN WO2004003004-A1.

XX PD 08-JAN-2004.

XX PF 27-JUN-2003; 2003WO-US016238.

XX PR 27-JUN-2002; 2002US-0392335P.

XX PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.

XX PI Berger SL, Henry KW, McMahon SB;

XX WPI; 2004-083014/08.

XX PT A composition altering the expression of human ubiquitin protease 8, for
XX PT treating or diagnosing a disease associated with the expression of a gene
XX PT that relies upon deubiquitylation for transcription, e.g. inflammation or
XX PT cancer.

XX PS Claim 2; SEQ ID NO 1; 78pp; English.

XX CC The invention relates to a composition that alters the expression of
XX CC human ubiquitin protease 8 (hUBP8; also known as ubiquitin specific
XX CC protease 22, Ubp22 or USP22; ADH54836) or its homologue, and reduces,
XX CC eliminates or enhances its deubiquitylating activity in a cell. The
XX CC composition is preferably a double-stranded RNA with a sense and
XX CC antisense regions, or a protein ligand of hUBP8 such as an antibody or
XX CC fragment thereof, which are capable of inhibiting hUBP8 expression. hUBP8
XX CC is required for chromatin development and regulation of genes in the
XX CC histone-modifying SAGA complex, particularly histone H2B. Overexpression
XX CC of hUBP8 can result in overproduction of certain genes such as oncogenes,
XX CC while reduced hUBP8 enzymatic activity may reduce the production of
XX CC tumour suppressor proteins. The invention also relates to an expression
XX CC construct encoding hUBP8; a method of identifying modulators of hUBP8
XX CC activity or expression; a method of determining the tumorigenic potential
XX CC in a cell; a method of assessing the sensitivity of a tumour cell to an
XX CC agent that disrupts deubiquitylation; regarding the growth of a cancer
XX CC cell; and a method of treating or diagnosing a disease associated with
XX CC the expression of a gene that relies upon deubiquitylation for
XX CC transcription. The hUBP8 modulatory compositions of the invention are

CC useful for treating or diagnosing a disease associated with the
CC expression of a gene that relies upon deubiquitylation for transcription,
CC e.g. inflammation, viral infection, fungal infection, cancer, Alzheimer's
CC disease, HIV infection or hypercholesterolaemia. The composition is also
CC useful in rendering a cancer cell more sensitive to additional anti-
CC tumour therapies, and in determining whether a cell is tumorigenic. The
CC present sequence represents hUBP8/UBp22 which is referred to in the
CC claims.
XX
SQ Sequence 525 AA;

Query Match 90.6%; Score 29; DB 8; Length 525;
Best Local Similarity 80.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
|:|:|
Db 278 CKGDD 282

RESULT 46
ABM81830
ID ABM81830 standard; protein; 525 AA.

XX AC ABM81830;

XX DT 18-NOV-2004 (first entry)

XX DE Tumour-associated antigenic target (TAT) polypeptide PRO82683, SEQ:4711.

XX KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic.

XX OS Homo sapiens.

XX PN WO2004030615-A2.

XX PD 15-APR-2004.

XX PF 29-SEP-2003; 2003WO-US028547.

XX PR 02-OCT-2002; 2002US-0414971P.

XX PA (GETH) GENENTECH INC.

XX PI Wu TD, Zhang Z, Zhou Y;

XX DR WPI; 2004-347921/32.

XX DR N-PSDB; ACN40124.

XX PT New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.

XX PS Claim 12; SEQ ID NO 4711; 7273pp; English.

XX CC The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,

CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
XX represents a TAT polypeptide of the invention

SQ Sequence 525 AA;

Query Match 90.6%; Score 29; DB 8; Length 525;
Best Local Similarity 80.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
|:|:|
Db 278 CKGDD 282

RESULT 47

AAU23205

ID AAU23205 standard; protein; 528 AA.

XX AC AAU23205;

XX DT 18-DEC-2001 (first entry)

XX DE Novel human enzyme polypeptide #291.

XX KW Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW ligase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; cytostatic; anti arthritic;
KW nephrotropic; anticoagulant.

XX OS Homo sapiens.

XX PN WO200155301-A2.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US001239.

XX PR 31-JAN-2000; 2000US-0179065P.

XX PR 04-FEB-2000; 2000US-0180628P.

XX PR 24-FEB-2000; 2000US-0184664P.

XX PR 02-MAR-2000; 2000US-0186350P.

XX PR 16-MAR-2000; 2000US-0189874P.

XX PR 17-MAR-2000; 2000US-0190076P.

XX PR 18-APR-2000; 2000US-0198123P.

XX PR 19-MAY-2000; 2000US-0205515P.

XX PR 07-JUN-2000; 2000US-0209467P.

XX PR 28-JUN-2000; 2000US-0214886P.

XX PR 30-JUN-2000; 2000US-0215135P.

XX PR 07-JUL-2000; 2000US-0216647P.

XX PR 11-JUL-2000; 2000US-0216880P.

XX PR 11-JUL-2000; 2000US-0217487P.

XX PR 14-JUL-2000; 2000US-0217496P.

XX PR 26-JUL-2000; 2000US-0218290P.

XX PR 26-JUL-2000; 2000US-0220963P.

XX PR 26-JUL-2000; 2000US-0220964P.

XX PR 14-AUG-2000; 2000US-0224518P.

XX PR 14-AUG-2000; 2000US-0224519P.

XX PR 14-AUG-2000; 2000US-0225213P.

XX PR 14-AUG-2000; 2000US-0225214P.

XX PR 14-AUG-2000; 2000US-0225266P.

XX PR 14-AUG-2000; 2000US-0225267P.

XX PR 14-AUG-2000; 2000US-0225268P.

XX PR 14-AUG-2000; 2000US-0225270P.

XX PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226686P.
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PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 08-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
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PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 23-SEP-2000; 2000US-0234997P.
PR 23-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
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PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
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PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-465566/50.
XX N-PSDB; AAS41075.
DR
XX Novel polypeptides and polynucleotides useful for diagnosing, preventing,
PT treating neural, immune system, muscular, reproductive, pulmonary,
PT cardiovascular, renal, proliferative disorders and cancerous diseases.
XX
PS Claim 11; SEQ ID NO 1201; 1180pp; English.
XX
XX The present invention relates to the isolation of novel human enzyme
CC polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences
CC encoding them. The enzyme polypeptides of the invention may comprise the
CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
CC isomerases or ligases. The sequences of the invention are useful in the
CC diagnosis, treatment, prevention and/or prognosis of a wide range of
CC disorders including hyperproliferative disorders (e.g. cancer),
CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.
CC arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic
CC disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),
CC cardiovascular disorders (e.g. atherosclerosis), blood-related disorders
CC (e.g. haemophilia), reproductive disorders (e.g. infertility) and
CC infectious disorders (e.g. Influenza). The polynucleotides of the
CC invention can also be used in gene therapy. AAU22915-AAU23814 represent
CC the novel human enzyme polypeptides of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 528 AA;
Query Match 90.6%; Score 29; DB 4; Length 528;
Best Local Similarity 80.0%; Pred. No. 3.5e+03;

```
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRGDD 5
Db 281 CKGDD 285

RESULT 48
ADCl0088
ID ADCl0088 standard; protein; 556 AA.
AC ADCl0088;
XX
XX
XX 18-DEC-2003 (first entry)
XX
XX Human NOVX polypeptide SEQ ID NO: 108.
DE
XX
XX cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective;
KW antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX;
KW pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder;
KW inflammatory disorder; chromosome mapping; tissue typing;
XX predictive medicine.
XX
XX Homo sapiens.
OS
XX
XX W02003000842-A2.
XX
XX 03-JAN-2003.
XX
XX 04-JUN-2002; 2002WO-US017443.
XX
XX 04-JUN-2001; 2001US-0295607P.
XX 04-JUN-2001; 2001US-0295661P.
XX 06-JUN-2001; 2001US-0296404P.
XX 06-JUN-2001; 2001US-0296418P.
XX 07-JUN-2001; 2001US-0296575P.
XX 11-JUN-2001; 2001US-0297414P.
XX 12-JUN-2001; 2001US-0295573P.
XX 12-JUN-2001; 2001US-0297567P.
XX 14-JUN-2001; 2001US-0298285P.
XX 15-JUN-2001; 2001US-0298285P.
XX 18-JUN-2001; 2001US-0299133P.
XX 19-JUN-2001; 2001US-0299230P.
XX 21-JUN-2001; 2001US-0299499P.
XX 22-JUN-2001; 2001US-0300177P.
XX 26-JUN-2001; 2001US-0300883P.
XX 28-JUN-2001; 2001US-0301530P.
XX 28-JUN-2001; 2001US-0301550P.
XX 03-JUL-2001; 2001US-0302951P.
XX 31-JUL-2001; 2001US-0308890P.
XX 14-SEP-2001; 2001US-0322297P.
XX 25-SEP-2001; 2001US-0324659P.
XX 03-DEC-2001; 2001US-0337477P.
XX 14-DEC-2001; 2001US-0341562P.
XX 21-FEB-2002; 2002US-0358566P.
XX 21-FEB-2002; 2002US-0359122P.
XX 22-FEB-2002; 2002US-0358978P.
XX 22-FEB-2002; 2002US-0359034P.
XX 22-FEB-2002; 2002US-0359352P.
XX 22-FEB-2002; 2002US-0359121P.
XX 27-FEB-2002; 2002US-0359964P.
XX 01-MAR-2002; 2002US-0360858P.
XX 12-MAR-2002; 2002US-0363430P.
XX 12-MAR-2002; 2002US-0363676P.
XX 10-APR-2002; 2002US-0371346P.
XX 10-MAY-2002; 2002US-0379444P.
XX 04-JUN-2002; 2002US-00379444.
XX (CURA-) CURAGEN CORP.
XX
XX Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
PI Dipippo VA, Edinger SR, Eigen A, Ellerman K, Gangolli EA;
PI Gerlach VL, Gorman L, Guo X, Herrmann JL, Hjalt I, Ji W, Kekuda R;
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PI Khramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;
PI Ort T, Padigar M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;
PI Rothenberg ME, Shenoy SG, Shinkets RA, Smithson G, Spaderna SK;
PI Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
PI Burgess CE, Lepley DM;
XX
XX WPI; 2003-210149/20.
DR N-PSDB; ADCl0087.
XX
XX New isolated NOVX polypeptides and nucleic acid molecules useful for
PT treating, preventing and diagnosing pathological conditions with NOVX-
PT associated disorders, such as cancer, obesity, diabetes and inflammatory
PT or CNS diseases.
XX
XX Claim 1; SEQ ID NO 108; 772pp; English.
XX
XX The invention relates to novel isolated polypeptides, mature form of the
CC polypeptide, a sequence that is 95% identical to the polypeptide or the
CC polypeptide comprising one or more conservative substitutions. The NOVX
CC polypeptide is useful for treating or preventing a pathology associated
CC with the polypeptide e.g. disorders associated with aberrant expression
CC or activity of the polypeptide, such as cancer, diabetes, obesity, and
CC endocrine, CNS and inflammatory disorders. They can also be used in
CC various detection and screening assays, chromosome mapping, tissue typing
CC and predictive medicine. This sequence corresponds to one of the
CC polypeptides of the invention.
XX
XX SQ Sequence 556 AA;
XX
XX Query Match 90.6%; Score 29; DB 7; Length 556;
XX Best Local Similarity 80.0%; Pred. No. 3.7e+03;
XX Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRGDD 5
Db 309 CKGDD 313

RESULT 49
ADCl0090
ID ADCl0090 standard; protein; 575 AA.
XX
XX ADCl0090;
AC
XX
XX 18-DEC-2003 (first entry)
DT
XX
XX Human NOVX polypeptide SEQ ID NO: 110.
XX
XX cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective;
KW antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX;
KW pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder;
KW inflammatory disorder; chromosome mapping; tissue typing;
XX predictive medicine.
XX
XX Homo sapiens.
OS
XX
XX W02003000842-A2.
XX
XX 03-JAN-2003.
XX
XX 04-JUN-2002; 2002WO-US017443.
XX
XX 04-JUN-2001; 2001US-0295607P.
XX 04-JUN-2001; 2001US-0295661P.
XX 06-JUN-2001; 2001US-0296404P.
XX 06-JUN-2001; 2001US-0296418P.
XX 07-JUN-2001; 2001US-0296575P.
XX 11-JUN-2001; 2001US-0297414P.
XX 12-JUN-2001; 2001US-0295573P.
XX 12-JUN-2001; 2001US-0297567P.
XX 14-JUN-2001; 2001US-0298285P.
XX 15-JUN-2001; 2001US-0298285P.
XX 18-JUN-2001; 2001US-0299133P.
```

PR 19-JUN-2001; 2001US-0299230P.
PR 21-JUN-2001; 2001US-0299949P.
PR 22-JUN-2001; 2001US-0300177P.
PR 26-JUN-2001; 2001US-0300883P.
PR 28-JUN-2001; 2001US-0301530P.
PR 28-JUN-2001; 2001US-0301550P.
PR 03-JUL-2001; 2001US-0302951P.
PR 14-JUL-2001; 2001US-0308890P.
PR 14-SEP-2001; 2001US-0322297P.
PR 25-SEP-2001; 2001US-0324669P.
PR 03-DEC-2001; 2001US-0337477P.
PR 14-DEC-2001; 2001US-0341562P.
PR 21-FEB-2002; 2002US-0358656P.
PR 21-FEB-2002; 2002US-0359122P.
PR 22-FEB-2002; 2002US-0358978P.
PR 22-FEB-2002; 2002US-0359034P.
PR 22-FEB-2002; 2002US-0359035P.
PR 22-FEB-2002; 2002US-0359121P.
PR 27-FEB-2002; 2002US-0359964P.
PR 01-MAR-2002; 2002US-0360858P.
PR 12-MAR-2002; 2002US-0363430P.
PR 12-MAR-2002; 2002US-0363676P.
PR 10-APR-2002; 2002US-0371346P.
PR 10-MAY-2002; 2002US-0379444P.
PR 04-JUN-2002; 2002US-00379444.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
PI Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
PI Gerlach VL, Gorman L, Guo X, Herrmann JM, Hjalte T, Ji W, Kekuda R;
PI Khramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;
PI Ort T, Padigar M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;
PI Rothenberg ME, Shenoy SG, Shinkets RA, Smithson G, Spaderna SK;
PI Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
PI Burgess CE, Lepley DM;
XX
XX WPI: 2003-210149/20.
DR N-PSDB; ADC10086.
XX
XX
PT New isolated NOVX polypeptides and nucleic acid molecules useful for
PT treating, preventing and diagnosing pathological conditions with NOVX-
PT associated disorders, such as cancer, obesity, diabetes and inflammatory
PT or CNS diseases.
XX
XX Claim 1; SEQ ID NO 110; 772pp; English.
XX
XX The invention relates to novel isolated polypeptides, mature form of the
XX polypeptide, a sequence that is 95% identical to the polypeptide or the
XX polypeptide comprising one or more conservative substitutions. The NOVX
XX polypeptide is useful for treating or preventing a pathology associated
XX with the polypeptide e.g. disorders associated with aberrant expression
XX or activity of the polypeptide, such as cancer, diabetes, obesity, and
XX endocrine, CNS and inflammatory disorders. They can also be used in
XX various detection and screening assays, chromosome mapping, tissue typing
XX and predictive medicine. This sequence corresponds to one of the
XX polypeptides of the invention.
XX
XX Sequence 575 AA;
SQ
Query Match 90.6%; Score 29; DB 7; Length 575;
Best Local Similarity 80.0%; Pred. No. 3.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRGDD 5
Db 328 CRGDD 332
RESULT 50
ADC10086
ID ADC10086 standard; protein; 581 AA.
XX
XX

AC ADC10086;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human NOVX polypeptide SEQ ID NO: 106.
XX
KW cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective;
KW antinflammatory; gene therapy; antisense therapy; thymomimetic; NOVX;
KW pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder;
KW inflammatory disorder; chromosome mapping; tissue typing;
KW predictive medicine.
XX
XX Homo sapiens.
XX
XX WO2003000842-A2.
XX
XX 03-JAN-2003.
XX
XX 04-JUN-2002; 2002WO-US017443.
XX
XX 04-JUN-2001; 2001US-0295607P.
XX 04-JUN-2001; 2001US-0295661P.
XX 06-JUN-2001; 2001US-0296404P.
XX 06-JUN-2001; 2001US-0296418P.
XX 07-JUN-2001; 2001US-0296575P.
XX 11-JUN-2001; 2001US-0297414P.
XX 12-JUN-2001; 2001US-0295573P.
XX 12-JUN-2001; 2001US-0297567P.
XX 14-JUN-2001; 2001US-0298285P.
XX 15-JUN-2001; 2001US-0298528P.
XX 18-JUN-2001; 2001US-0299133P.
XX 19-JUN-2001; 2001US-0299230P.
XX 21-JUN-2001; 2001US-0299949P.
XX 22-JUN-2001; 2001US-0300177P.
XX 26-JUN-2001; 2001US-0300883P.
XX 28-JUN-2001; 2001US-0301530P.
XX 28-JUN-2001; 2001US-0301550P.
XX 03-JUL-2001; 2001US-0302951P.
XX 31-JUL-2001; 2001US-0308890P.
XX 14-SEP-2001; 2001US-0322297P.
XX 25-SEP-2001; 2001US-0324669P.
XX 03-DEC-2001; 2001US-0337477P.
XX 14-DEC-2001; 2001US-0341562P.
XX 21-FEB-2002; 2002US-0358656P.
XX 21-FEB-2002; 2002US-0359122P.
XX 22-FEB-2002; 2002US-0358978P.
XX 22-FEB-2002; 2002US-0359034P.
XX 22-FEB-2002; 2002US-0359035P.
XX 22-FEB-2002; 2002US-0359121P.
XX 27-FEB-2002; 2002US-0359964P.
XX 01-MAR-2002; 2002US-0360858P.
XX 12-MAR-2002; 2002US-0363430P.
XX 12-MAR-2002; 2002US-0363676P.
XX 10-APR-2002; 2002US-0371346P.
XX 10-MAY-2002; 2002US-0379444P.
XX 04-JUN-2002; 2002US-00379444.
XX
XX (CURA-) CURAGEN CORP.
XX
XX
PI Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
PI Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
PI Gerlach VL, Gorman L, Guo X, Herrmann JM, Hjalte T, Ji W, Kekuda R;
PI Khramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;
PI Ort T, Padigar M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;
PI Rothenberg ME, Shenoy SG, Shinkets RA, Smithson G, Spaderna SK;
PI Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
PI Burgess CE, Lepley DM;
XX
XX WPI: 2003-210149/20.
DR N-PSDB; ADC10086.
XX
XX
PT New isolated NOVX polypeptides and nucleic acid molecules useful for
PT treating, preventing and diagnosing pathological conditions with NOVX-
PT associated disorders, such as cancer, obesity, diabetes and inflammatory
PT or CNS diseases.

PT associated disorders, such as cancer, obesity, diabetes and inflammatory
 FT or CNS diseases.

PS Claim 1; SEQ ID NO 106; 772pp; English.

XX The invention relates to novel isolated polypeptides, mature form of the
 CC polypeptide, a sequence that is 95% identical to the polypeptide or the
 CC polypeptide comprising one or more conservative substitutions. The NOVX
 CC polypeptide is useful for treating or preventing a pathology associated
 CC with the polypeptide e.g. disorders associated with aberrant expression
 CC or activity of the polypeptide, such as cancer, diabetes, obesity, and
 CC endocrine, CNS and inflammatory disorders. They can also be used in
 CC various detection and screening assays, chromosome mapping, tissue typing
 CC and predictive medicine. This sequence corresponds to one of the
 CC polypeptides of the invention.

XX Sequence 581 AA;

Query Match 90.6%; Score 29; DB 7; Length 581;
 Best Local Similarity 80.0%; Pred. No. 3.9e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 Db 334 CKGDD 338
 |:|:|

RESULT 51
 AAEE17560
 ID AAEE17560 standard; protein; 593 AA.

AC AAEE17560;

XX 22-APR-2002 (first entry)

XX Human pancreatic tumour protein, KIAA1063.

XX Human; pancreatic tumour protein; pancreatic cancer; gene therapy;
 KW vaccine.

XX Homo sapiens.

XX WO200194409-A2.

XX 13-DEC-2001.

XX 31-MAY-2001; 2001WO-US018003.

XX 07-JUN-2000; 2000US-0210329P.

XX 14-NOV-2000; 2000US-0248980P.

XX 15-MAY-2001; 2001US-0291197P.

XX (CORI-) CORIXA CORP.

XX First SK, Harlocker SL, Dillon DC, Kalos MD;

XX WPI; 2002-154565/20.

XX N-PSDB; AAD28257.

XX Pancreatic tumor polypeptide and polynucleotide useful in diagnosis,
 PT prevention and/or treatment of cancer, especially pancreatic cancer.

XX Claim 2a; Page 107-108; 115pp; English.

XX The invention relates to human pancreatic tumour polypeptides and nucleic
 CC acid molecules encoding such polypeptides. The invention also relates to
 CC compositions and methods for the diagnosis, prevention and therapy of
 CC cancer, particularly pancreatic cancer. Sequences of the invention are
 CC used in gene therapy and in vaccines. The present sequence is human
 CC pancreatic tumour protein

XX Sequence 593 AA;

Query Match 90.6%; Score 29; DB 5; Length 593;
 Best Local Similarity 80.0%; Pred. No. 3.9e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 Db 346 CKGDD 350
 |:|:|

RESULT 52

ADH54838

XX ADH54838 standard; protein; 593 AA.

XX ADH54838;

XX 25-MAR-2004 (first entry)

XX Human KIAA1063 protein related to hUBP8/Ubp22, SEQ ID NO:3.

XX Human; KIAA1063 protein; hUBP8; ubiquitin protease 8;
 KW ubiquitin specific protease 22; Ubp22; USP22; UbP8 homologue;
 KW deubiquitylation; histone H2B; histone modification;
 KW transcriptional regulation; UbP8 modulator; drug screening;
 KW tumorigenic potential; cancer cell sensitivity; cancer; tumour;
 KW inflammation; viral infection; fungal infection; Alzheimer's disease;
 KW human immunodeficiency virus; HIV infection; hypercholesterolemia;
 KW cytostatic; antiinflammatory; virucide; fungicide; neurotropic;
 KW neuroprotective; anti-HIV; antilipaemic; enzyme.

XX Saccharomyces cerevisiae.

XX Key Location/Qualifiers

FT Misc-difference 1. .68 /note= "This sequence is not present in SEQ ID NO:1"

FT Misc-difference 69. .593

FT /note= "identical to SEQ ID NO:1"

XX WO2004003004-A1.

XX 08-JAN-2004.

XX 27-JUN-2003; 2003WO-US016238.

XX 27-JUN-2002; 2002US-0392335P.

XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.

XX Berger SL, Henry KW, McMahon SB;

XX WPI; 2004-083014/08.

XX GENBANK; BAA83015.

XX A composition altering the expression of human ubiquitin protease 8, for
 PT treating or diagnosing a disease associated with the expression of a gene
 PT that relies upon deubiquitylation for transcription, e.g. inflammation or
 PT cancer.

XX Disclosure; SEQ ID NO 3; 78pp; English.

XX The invention relates to a composition that alters the expression of
 CC human ubiquitin protease 8 (hUBP8; also known as ubiquitin specific
 CC protease 22, Ubp22 or USP22; ADH54836) or its homologue, and reduces,
 CC eliminates or enhances its deubiquitylating activity in a cell. The
 CC composition is preferably a double-stranded RNA with a sense and
 CC antisense regions, or a protein ligand of hUBP8 such as an antibody or
 CC fragment thereof, which are capable of inhibiting hUBP8 expression. hUBP8
 CC is required for chromatin development and regulation of genes in the
 CC histone-modifying SAGA complex, particularly histone H2B. Overexpression
 CC of hUBP8 can result in overproduction of certain genes such as oncogenes,
 CC while reduced hUBP8 enzymatic activity may reduce the production of
 CC tumour suppressor proteins. The invention also relates to an expression
 CC construct encoding hUBP8; methods of identifying modulators of hUBP8
 CC activity or expression; a method of determining the tumorigenic potential

CC in a cell; a method of assessing the sensitivity of a tumour cell to an
 CC agent that disrupts deubiquitylation; retarding the growth of a cancer
 CC cell; and a method of treating or diagnosing a disease associated with
 CC the expression of a gene that relies upon deubiquitylation for
 CC transcription. The hUBP8 modulatory compositions of the invention are
 CC useful for treating or diagnosing a disease associated with the
 CC expression of a gene that relies upon deubiquitylation for transcription,
 CC e.g. inflammation, viral infection, fungal infection, cancer, Alzheimer's
 CC disease, HIV infection or hypercholesterolaemia. The composition is also
 CC useful in rendering a cancer cell more sensitive to additional anti-
 CC tumour therapies, and in determining whether a cell is tumorigenic. The
 CC present sequence represents human KIAA1063 protein, which consists of the
 CC hUBP8/UBP22 amino acid sequence (ADH54836), plus an additional 68 N-
 CC terminal region.

XX SQ Sequence 593 AA;

Query Match 90.6%; Score 29; DB 8; Length 593;
 Best Local Similarity 80.0%; Pred. No. 3.9e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 Db 346 CKGDD 350

RESULT 53

ADQ20907 ADQ20907 standard; protein; 593 AA.

XX AC ADQ20907;

XX DT 26-AUG-2004 (first entry)

XX DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3727.

XX KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.

XX OS Homo sapiens.

XX PN W02004048938-A2.

XX PD 10-JUN-2004.

XX PF 26-NOV-2003; 2003WO-US038193.

XX PR 26-NOV-2002; 2002US-0429739P.

XX PA (PROT-) PROTEIN DESIGN LABS INC.

XX PI Aziz N, Ginsburg WM, Zlotnik A;

XX DR WPI; 2004-441208/41.

XX PT Early detection of soft tissue sarcoma comprises determining expression
 CC of a gene in a first soft tissue sample and a normal soft tissue sample
 CC and comparing the gene expression, also useful in treating soft tissue
 CC sarcoma.

XX PS Example 2; SEQ ID NO 3727; 210pp; English.

XX CC The invention relates to a novel method for detecting soft tissue sarcoma
 CC which comprises obtaining a first soft tissue sample from an individual
 CC and a normal soft tissue sample from the same or different individual,
 CC determining the expression of a gene in both samples and comparing the
 CC of protein expression in the first soft tissue samples, where a higher level
 CC presence of soft tissue sarcoma. The method of the invention has
 CC cytostatic applications and may be useful for detecting soft tissue
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
 CC acid sequences may be useful in diagnostic and screening applications.
 CC The current sequence is that of a human soft tissue sarcoma-upregulated
 CC protein of the invention. The current sequence is not shown within the

CC specification per se but was submitted in CD format by the inventor.
 XX SQ Sequence 593 AA;

Query Match 90.6%; Score 29; DB 8; Length 593;
 Best Local Similarity 80.0%; Pred. No. 3.9e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 Db 346 CKGDD 350

RESULT 54

ABO70157 ABO70157 standard; protein; 639 AA.

XX AC ABO70157;

XX DT 29-JUL-2004 (first entry)

XX DE Pseudomonas aeruginosa polypeptide #2332.

XX KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

XX OS Pseudomonas aeruginosa.

XX PN US6551795-B1.

XX PD 22-APR-2003.

XX PF 18-FEB-1999; 99US-00252991.

XX PR 18-FEB-1998; 98US-0074788P.

XX PR 27-JUL-1998; 98US-0094150P.

XX PA (GENO-) GENOME THERAPEUTICS CORP.

XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;

XX DR WPI; 2003-615309/58.

XX DR N-PSDB; ABD03728.

XX PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
 CC useful as molecular targets for diagnostics, prophylaxis and treatment of
 CC pathological conditions resulting from bacterial infection.

XX PS Disclosure; SEQ ID NO 18903; 455pp; English.

XX CC The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences ABO67826-
 CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html

XX SQ Sequence 639 AA;

Query Match 90.6%; Score 29; DB 7; Length 639;
 Best Local Similarity 80.0%; Pred. No. 4.2e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5

Db 602 CKGDD 606

RESULT 55
ABU92027
ID ABU92027 standard; protein; 936 AA.
XX
AC ABU92027;
XX
DT 15-JUL-2003 (first entry)
XX
DE Human protein modification and maintenance molecule-7 (PMMM-7).
XX
KW Human; protein modification and maintenance molecule; PMMM; cancer;
KW cell proliferation disorder; atherosclerosis; neurological disorder;
KW epilepsy; Huntington's disease; stroke; immune disorder; allergy;
KW inflammatory disorder; AIDS; developmental disorder; hypothyroidism;
KW Cushing's syndrome; gastrointestinal disorder; epithelial disorder;
KW infection; cytostatic; antiarteriosclerotic; anticonvulsant; nootropic;
KW neuroprotective; cerebroprotective; anti-HIV; antiallergic; vulnerary;
KW antiinflammatory; thymimimetic.
XX
OS Homo sapiens.
XX
PN WO2003031939-A2.
XX
PD 17-APR-2003.
XX
XX 11-OCT-2002; 2002WO-US032850.
XX
PR 12-OCT-2001; 2001US-0329689P.
XX
PR 25-OCT-2001; 2001US-0335703P.
XX
PR 09-NOV-2001; 2001US-034887P.
XX
PR 28-NOV-2001; 2001US-0334145P.
XX
PR 06-DEC-2001; 2001US-0337451P.
XX
PR 14-DEC-2001; 2001US-0340584P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Ramkumar J, Gorvad AE, Baughn MR, Emerling BM, Yang J, Lee SY;
PI Tran UK, Becha SD, Duggan BM, Lee EA, Griffin JA, Li JX;
PI Sprague WW, Hafalia AJA, Chawla NK, Lehr-Mason PM, Kable AE, Yue H;
PI Marquis JP, Yao MG, Richardson RW, Tang TY, Jin P, Chien D;
PI Bhatia U, Burrill JD, Lee S, Blake JJ, Ho A, Zheng W;
XX
XX WPI; 2003-430274/40.
XX
DR N-PSDB; ACA92422.
XX
XX New human protein modification and maintenance molecules (PMMM), useful
PT for diagnosing, treating and preventing diseases or conditions associated
PT with the aberrant PMMM expression e.g. cancer, atherosclerosis, or
PT infections.
XX
XX Claim 1; Page 244-246; 311pp; English.
PS
XX The present invention relates to the isolation of human protein
CC modification and maintenance molecules (PMMM), and the polynucleotide
CC sequences encoding them. A total of 40 PMMM polypeptides (designated PMMM
CC -1 to PMMM-40) are disclosed. The sequences of the invention are useful
CC for diagnosing a condition or disease associated with the expression of
CC PMMM in a subject, preparing a polyclonal or monoclonal antibody, and
CC generating an expression profile of a sample containing the
CC polynucleotides. The diseases or conditions associated with decreased
CC expression or overexpression of PMMM are cell proliferation disorders
CC (e.g. cancer, atherosclerosis), neurological disorders (e.g. epilepsy,
CC Huntington's disease, stroke), immune/inflammatory disorders (e.g. AIDS,
CC allergies), developmental disorders (e.g. hypothyroidism, Cushing's
CC syndrome), gastrointestinal or epithelial disorders, and infections. The
CC PMMM polypeptides or their fragments are useful in screening compounds
CC for effectiveness as agonists or antagonists of the polypeptides, or in
CC altering the expression of the target polynucleotide and compounds that
CC specifically bind to, or modulate the activity of the polypeptide.

CC ABU92021-ABU92060 represent the human PMMM polypeptides of the invention
XX
SQ Sequence 936 AA;
Query Match 90.6%; Score 29; DB 6; Length 936;
Best Local Similarity 80.0%; Pred. No. 6e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRGDD 5
DB 678 CKGDD 682

RESULT 56
AAU82708
ID AAU82708 standard; protein; 953 AA.
XX
AC AAU82708;
XX
DT 23-APR-2002 (first entry)
XX
DE Amino acid sequence of novel human protease #7.
XX
KW Human; protease; cancer; immune-related disorder; cardiovascular disease;
KW neuronal-associated disease; metabolic disorder; inflammatory disorder;
KW nervous system disorder; sexual dysfunction; pain; mood disorder;
KW hypertension; psychotic disorder; neurological disorder; dyskinesia;
KW viral infection; human immunodeficiency virus; HIV; non-viral infection;
KW ocular disease; cytostatic; enzyme.
XX
OS Homo sapiens.
XX
PN WO200200860-A2.
XX
PD 03-JAN-2002.
XX
XX 26-JUN-2001; 2001WO-US020171.
XX
PR 26-JUN-2000; 2000US-0214047P.
XX
XX (SUGE-) SUGEN INC.
XX
PI Plowman G, Whyte D, Sudarsanam S, Manning G, Caenepeel S;
PI Charydczak G;
XX
XX WPI; 2002-139913/18.
XX
DR N-PSDB; ABK31750.
XX
XX Nucleic acids encoding novel human proteases, useful for useful for
PT treating diseases and disorders such as cancers, immune-related diseases
PT and disorders, cardiovascular disease (e.g. restenosis) and inflammatory
PT disorders.
XX
XX Claim 6; Fig 2C-D; 313pp; English.
PS
XX The present invention relates to the isolation of novel human proteases,
CC and the nucleic acids encoding them. The sequences of the invention are
CC useful for treating diseases and disorders such as cancers (e.g. breast,
CC colon, lung), immune-related diseases and disorders (e.g. inflammatory
CC diseases and asthma), cardiovascular diseases (e.g. restenosis and
CC coronary thrombosis), brain or neuronal-associated diseases, metabolic
CC disorders (e.g. diabetes, obesity), inflammatory disorders (e.g.
CC rheumatoid arthritis and psoriasis), central or peripheral nervous system
CC diseases, migraines, pain, sexual dysfunction, mood disorders, attention
CC disorders, cognitive disorders, hypotension, hypertension, psychotic
CC diseases and dyskinesias. The nucleic acids and polypeptides are also
CC useful for treating viral infections caused by human immunodeficiency
CC virus (HIV), and non-viral infections such as ocular disease (e.g.
CC glaucoma) and macular degeneration. AAU82702-AAU82760 represent the novel
CC human proteases of the invention
XX
SQ Sequence 953 AA;

Query Match 90.6%; Score 29; DB 5; Length 953;
Best Local Similarity 80.0%; Pred. No. 6.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
|:|:|
Db 695 CKGDD 699

RESULT 57
AAU74761
ID AAU74761 standard; protein; 953 AA.

AC AAU74761;

XX 09-APR-2002 (first entry)

DT Human protease PRYS-21 protein sequence.

DE Human; protease; PRYS; gastrointestinal; Crohn's disease; cancer;
KW cardiovascular; atherosclerosis; autoimmune deficiency disorder; dermatitis;
KW inflammatory disorder; acquired immunodeficiency syndrome; AIDS;
KW cell proliferative disorder; developmental disorder; epilepsy;
KW Duchenne muscular dystrophy; epithelial disorder; neurological disorder;
KW reproductive disorder; endometriosis.

XX Homo sapiens.

XX WO200198468-A2.

XX 27-DEC-2001.

XX 13-JUN-2001; 2001WO-US019178.

XX 16-JUN-2000; 2000US-0212336P.

XX 22-JUN-2000; 2000US-0213955P.

XX 29-JUN-2000; 2000US-0215396P.

XX 07-JUL-2000; 2000US-0216821P.

XX 14-JUL-2000; 2000US-0218946P.

XX (INCY-) INCYTE GENOMICS INC.

XX Yue H, Elliott VS, Gandhi AR, Lal P, Au-Young J, Tribouley CM;

XX Deleage AM, Baughn MR, Nguyen DB, Lee EA, Hafalia A, Khan FA;

XX Walia NK, Yao MG, Lu DAM, Patterson C, Tang YT, Walsh RT;

XX Azimzai Y, Lu Y, Ramkumar J, Xu Y, Reddy R, Das D, Kearney L;

XX Kallick DA;

XX WPI; 2002-090437/12.

XX N-PSDB; ABK12904.

XX Twenty one human proteases (referred to as PRYS-1 to PRYS-21), useful in
the diagnosis, treatment and prevention of gastrointestinal (e.g.
gastritis), cardiovascular (e.g. atherosclerosis) and cell proliferative
(e.g. cancer) disorders.

XX Claim 1; Page 158-160; 177pp; English.

XX The present invention relates to twenty one new human proteases, referred
to as PRYS-1 to PRYS-21. The PRYS polynucleotides and polypeptides of the
invention are useful in the diagnosis, treatment and prevention of
gastrointestinal e.g. gastritis, esophageal carcinoma and Crohn's
disease, cardiovascular e.g. atherosclerosis, hypertension and myocardial
infarction, autoimmune/inflammatory e.g. acquired immunodeficiency
syndrome (AIDS), allergies and osteoarthritis, cell proliferative e.g.
cancer, developmental e.g. Duchenne and Becker muscular dystrophy,
epithelial e.g. dermatitis, neurological e.g. epilepsy and Alzheimer's
disease and reproductive e.g. infertility and endometriosis disorders.
Numerous other examples of each disorder are given in the specification.

XX The present protein sequence represents the human protease PRYS-21
protein of the invention

SQ Sequence 953 AA;

Query Match 90.6%; Score 29; DB 5; Length 953;
Best Local Similarity 80.0%; Pred. No. 6.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
|:|:|
Db 695 CKGDD 699

RESULT 58
AAR96415

ID AAR96415 standard; peptide; 9 AA.

XX AAR96415;

XX 21-OCT-2004 (revised)

DT 05-JUL-1996 (first entry)

XX RGD cyclic peptide, TL#753, binds alpha-v, beta3 integrin receptor.

DE RGD-containing peptide; alpha-v, beta-3 integrin receptor; osteoclast;
KW matrix; bone; inhibition; bone resorption; promote; endothelial cell;
KW smooth muscle cell; restenosis; angiogenesis; cyclic.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1

FT Disulfide-bond 2..8

FT Modified-site 9

FT /note= "Amidated C-terminal"

XX WO9528426-A2.

XX 26-OCT-1995.

XX 12-APR-1995; 95WO-US004741.

XX 13-APR-1994; 94US-00227316.

XX 08-SEP-1994; 94US-00303052.

XX (LJOL-) LA JOLLA CANCER RES FOUND.

XX Cheng S, Ingram R, Mullen D, Tschopp J;

XX WPI; 1995-373767/48.

XX Altering alpha-v, beta-3 integrin receptor-mediated binding of cell to
matrix - using conformationally restrained peptide of RGD type, e.g. for
treating inappropriate angiogenesis or for inhibiting bone resorption.

XX Claim 85; Page 80; 99pp; English.

XX The sequences given in AAR96301-417 are non-naturally occurring RGD-
containing peptides which alter the alpha-v, beta-3 integrin receptor
binding of a cell to a matrix, such as the binding of an osteoclast to a
matrix such as bone. These peptides inhibit bone resorption and can
inhibit or promote alpha-v, beta-3-mediated cell attachment depending on
whether they are present in the cell in a soluble form or are bound to a
solid substrate. These peptides can be used in the amelioration of the
severity of a pathology involving alpha-v, beta-3 receptor-mediated
binding of a cell, such as an osteoclast, endothelial cell or smooth
muscle cell to a matrix. They are used for treating conditions associated
with restenosis or inappropriate or insufficient angiogenesis, or for
inhibiting osteoclast binding to the matrix

XX Revised record issued on 21-OCT-2004 : Correction to Feature Table Key

XX Sequence 9 AA;

SQ

Query Match 87.5%; Score 28; DB 2; Length 9;
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
 Db 2 CRGDE 6

RESULT 59

AAW66841
 ID AAW66841 standard; peptide; 9 AA.

XX AC AAW66841;

XX DT 25-MAR-2003 (revised)
 XX DT 10-DEC-1998 (first entry)

XX DE Peptide useful for altering bone resorption.

XX KW bone resorption; pharmacore; angiogenesis; restenosis; integrin receptor;
 KW alpha v beta 3 integrin receptor; osteoclast; cyclic.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 9

FT Modified-site 9 /note= "C-terminal amide"

XX US5807819-A.

XX PD 15-SEP-1998.

XX PF 12-APR-1995; 95US-00421698.

XX PR 15-APR-1994; 94US-00227316.

XX PR 08-SEP-1994; 94US-00303052.

XX (LJOL-) LA JOLLA CANCER RES CENT.

XX PI Tachopp JP, Mullen D, Ingram R, Cheng S;

XX WPI; 1998-555601/47.

XX Use of peptide derivatives which can alter integrin receptor binding -
 PT for altering bone resorption, treating angiogenesis or restenosis and
 PT altering integrin receptor mediated interactions.

XX Example 2; Fig 2E; 87pp; English.

XX A new method is claimed for altering bone resorption. It comprises
 CC administration of a peptide of formula: X1X2X3X4GX5X6X7X8 , where X1 =
 CC R1R2N or 0-10 amino acids (optionally protected by acetylation at the N-
 CC terminus); X2 = absent or 1 amino acid; X3 = absent or 1 or 2 amino acids
 CC ; X4 = N-Me-Arg; X5 = residue which provides an ionic interaction with an
 CC integrin receptor, or is Mea, Paa or Tfaa; X6 = residue which has an
 CC aliphatic side chain; a non-natural amino acid that is hydrophobic; or
 CC Thr; X7 = a residue capable of forming a bond (i) with a bridging amino
 CC acid of X2, (ii) with X3 when X2 is absent, or (iii) with X4 when X2 and
 CC X3 are absent, to conformationally restrain the peptide; X8 = NR3R4; OR5;
 CC R1, R3-R5 = H or alkyl; R2 = H, alkyl, alkyl-CO or phenyl-CO. The
 CC peptides are useful for inhibiting bone resorption, angiogenesis or
 CC restenosis, and for altering integrin receptor-mediated interactions,
 CC especially alpha v beta 3 integrin receptor-mediated binding of cells to
 CC a matrix. They may be used for reducing or inhibiting osteoclast binding
 CC to a matrix. The present sequence represents an example of a circular
 CC peptide disclosed in the specification. (Updated on 25-MAR-2003 to
 CC correct PF field.)

XX SQ Sequence 9 AA;

Query Match 87.5%; Score 28; DB 2; Length 9;
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
 Db 2 CRGDE 6

RESULT 60

AAV21792
 ID AAY21792 standard; peptide; 9 AA.

XX AC AAY21792;

XX DT 10-SEP-1999 (first entry)

XX DE Conserved peptide sequence of ICH-1 (caspase-2).

XX KW Rev-caspase; cysteine protease; zymogen; caspase; cancer; gene therapy;
 KW autoimmune disease; caspase-mediated apoptosis; neurodegenerative;
 KW tumour cell; myocardial infarction; human.

XX OS Homo sapiens.

XX PN W09935277-A2.

XX PD 15-JUL-1999.

XX PF 11-JAN-1999; 99WO-US000632.

XX PR 09-JAN-1998; 98US-0070987P.

XX PA (UYJE-) UNIV JEFFERSON THOMAS.

XX PI Alnemri ES;

XX DR WPI; 1999-419353/35.

XX New isolated nucleic acid molecule encoding a rev-caspase - used for
 PT screening and identifying inhibitors or enhancers for treating cancer or
 PT autoimmune disease.

XX Disclosure; Fig 6; 74pp; English.

XX The invention relates to nucleic acid molecules encoding rev-caspases.
 CC Rev-caspases are cysteine proteases that specifically cleave proteins
 CC after Asp residues and is expressed as a zymogen, in which the small
 CC subunit is N-terminal to a large subunit. A gene delivery vehicle
 CC comprising a rev-caspase coding sequence is internalised by tumour cells.
 CC cancer, where the gene delivery vehicle is used to treat autoimmune diseases.
 CC The gene delivery vehicle can also be used to treat autoimmune diseases.
 CC Cells transfected with a rev-caspase expressing vector can be used in
 CC identification of inhibitors or enhancers of caspase-mediated apoptosis.
 CC In vitro translated rev-caspase can be used to identify an inhibitor or
 CC enhancer of caspase processing activity. Caspase inhibitors are useful
 CC for treating neurodegenerative diseases as well as for inhibiting
 CC apoptosis in the heart following myocardial infarction. Sequences
 CC AAY21734 -AAY21795 represent conserved peptide sequences in various
 CC caspases

XX SQ Sequence 9 AA;

Query Match 87.5%; Score 28; DB 2; Length 9;
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
 Db 5 CRGDE 9

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RESULT 61
AAW97010
ID AAW97010 standard; peptide; 9 AA.
XX
XX
AC AAW97010;
XX
DT 26-APR-1999 (first entry)
XX
DE Peptide used to inhibit bone resorption, angiogenesis and restenosis.
XX
XX RGD-peptide; bone resorption; angiogenesis; restenosis;
KW integrin receptor mediated interaction; binding; osteoclast; bone.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Modified-site 1 /note= "acetylated residue"
FT Modified-site 10 /note= "amidated residue"
XX
XX US5849865-A.
XX
XX 15-DEC-1998.
XX
XX 12-APR-1995; 95US-00421695.
XX
XX 13-APR-1994; 94US-00227316.
XX 08-SEP-1994; 94US-00303052.
XX
XX (LJOL-) LA JOLLA CANCER RES FOUND.
XX
XX Techopp JF, Mullen D, Ingram R, Cheng S;
XX
XX WPI; 1999-179486/15.
XX
XX RGD peptides - that modulate integrin-mediated cell-matrix binding.
XX
XX Claim 6; Col 138; 90pp; English.
XX
XX The present peptide represents a non-naturally occurring Arg-Gly-Asp
CC (RGD)-containing peptide. The peptide may be useful for reducing or
CC inhibiting bone resorption, angiogenesis or restenosis, and for altering
CC an integrin receptor mediated interaction. The peptide may also be used
CC to inhibit the binding of an osteoclast to bone
XX
XX Sequence 9 AA;
SQ
Query Match 87.5%; Score 28; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 2 CRGDE 6

RESULT 62
AAE09007
ID AAE09007 standard; peptide; 9 AA.
XX
XX
AC AAE09007;
XX
DT 15-NOV-2001 (first entry)
XX
DE ICH-1 peptide fragment #3.
XX
XX Apoptotic protease; mammalian ced-3 homologue 6; Mch6; cancer; ICH-1;
KW aspartate-specific cysteine protease; ASCP; apoptosis; therapy;
KW autoimmune disease; cerebellar degeneration; Alzheimer's disease;
KW cytostatic; Parkinson's disease; immunomodulator; antimicrobial;
KW viral infection; cell death-mediated disease; neuroprotective.
XX
XX

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OS Unidentified.
XX
XX US6271361-B1.
XX
XX 07-AUG-2001.
XX
XX 25-FEB-1999; 99US-00257218.
XX
XX 29-MAY-1997; 97US-00865579.
XX
XX (UYJB-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES, Fernandes-Alnemri T, Litwack G;
XX
XX WPI; 2001-528686/58.
XX
XX New apoptotic genes and their apoptotic protease products, useful for
PT modulating apoptosis for the therapeutic treatment of human diseases,
PT e.g. cancers, autoimmune disease, Alzheimer's disease or Parkinson's
PT disease.
XX
XX Disclosure; Col 51; 36pp; English.
XX
XX The invention relates to an isolated gene encoding apoptotic protease,
CC mammalian ced-3 homologue 6 (Mch6). Mch6 is a member of the aspartate-
CC specific cysteine protease (ASCP) family. Mch6 DNA and protein sequences
CC are useful for modulating apoptosis for the therapeutic treatment of
CC human diseases. Mch6 sequences are useful for upregulating apoptosis
CC (e.g. for treating cancers, autoimmune disease or viral infections) or
CC downregulating apoptosis (e.g. for treating Alzheimer's disease,
CC Parkinson's disease or cerebellar degeneration). The Mch6 sequence is
CC useful for diagnosing, treating or reducing the severity of cell death-
CC mediated diseases, as well as other diseases mediated by either increased
CC or decreased programmed cell death. The present amino acid sequence is a
CC fragment of ICH-1 peptide which belongs to NEDD-like subfamily
XX
XX Sequence 9 AA;
SQ
Query Match 87.5%; Score 28; DB 4; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 5 CRGDE 9

RESULT 63
ABJ01296
ID ABJ01296 standard; peptide; 9 AA.
XX
XX
AC ABJ01296;
XX
XX 18-SEP-2002 (first entry)
XX
XX Human caspase conserved region SEQ ID NO: 112.
XX
XX Human; caspase; rev-caspase; gene therapy; protease; apoptosis; cancer;
KW autoimmune disease; cytostatic; immunosuppressive.
XX
XX Homo sapiens.
XX
XX US6376226-B1.
XX
XX 23-APR-2002.
XX
XX 26-APR-2000; 2000US-00561756.
XX
XX 09-JAN-1998; 98US-0070897P.
XX 08-JAN-1999; 99US-00227721.
XX
XX (UYJB-) UNIV JEFFERSON THOMAS.
XX
XX

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PI Alnemri ES;
XX WPI; 2002-453146/48.
XX
XX New rev-caspases engineered to contain the small subunit fused in frame N
PT -terminal to the large subunit, which is in reverse order to the wild
PT type caspases, are useful to treat cancer and autoimmune diseases.
XX
XX Disclosure; Fig 6; 81pp; English.
XX
XX The present invention provides the protein and coding sequences of human
CC rev-caspase-3, uncleavable rev-caspase-3 and rev-caspase-6. The sequences
CC can be used in the gene therapy of cancer and autoimmune diseases. The
CC present sequence is a peptide described in the exemplification of the
CC invention
XX
XX Sequence 9 AA;
SQ
Query Match 87.5%; Score 28; DB 5; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0;
Qy 1 CRGDD 5
Db 5 CRGDE 9
|||||
RESULT 64
ADM96249
ID ADM96249 standard; peptide; 21 AA.
XX
AC ADM96249;
XX
XX 15-JUL-2004 (first entry)
XX
XX Human caspase-2 peptide related to apoptosis modulation.
XX
XX apoptotic cell death; apoptotically active site; human alpha-fetoprotein;
KW human serum albumin; immunosuppressive; virucide;
KW apoptosis signaling modulator; apoptotic regulatory pathway;
KW organ preservation; cell preservation; transplantation;
XX autoimmune disorder; immunodeficiency syndrome; viral infection;
KW cytotoxicity; chemotherapy; radiotherapy; neuronal cell apoptosis;
KW non-specific drug-induced apoptosis; oxidative stress-mediated apoptosis;
KW cultured cell apoptosis; caspase-2; human.
XX
XX Homo sapiens.
XX
XX WO2004033500-A1.
XX
XX 22-APR-2004.
XX
XX 07-OCT-2003; 2003WO-FI000735.
XX
XX 09-OCT-2002; 2002FI-00001798.
XX
XX (DUDI/) DUDICH E I.
PA (SEME/) SEMENKOVA L N.
PA (DUDI/) DUDICH I V.
PA (TATU/) TATULOV E B.
PA (ZUBO/) ZUBOV D L.
PA (KORP/) KORPELA T K.
XX
XX Dudich EI, Semenkova LN, Dudich IV, Tatulov EB, Zubov DL;
PI KorpeLA TK;
PI
XX WPI; 2004-340893/31.
XX
XX New molecular structure of the recognition site of an anti-idiotypic
PT antibody against an apoptotically active site of human alpha-fetoprotein,
PT useful for preventing of autoimmune disorders and an immunodeficiency
PT syndrome.
XX

PS Example 2; Page 13; 36pp; English.
XX
XX This invention relates to novel peptides capable of modulating apoptotic
CC cell death. In particular, the invention relates to the molecular
CC structure of the apoptotically active site of human alpha-fetoprotein and
CC human serum albumin. The invention may be useful for the development of
CC compounds with an immunosuppressive or virucide activity acting as
CC apoptosis signaling modulators. The peptide structures are useful for
CC suppressing apoptotic regulatory pathways in human and animal cells, for
CC increasing preservation of organs or cells within their transplantation,
CC for preventing of autoimmune disorders and an immunodeficiency syndrome
CC induced by a viral infection, for lowering cytotoxic effects after chemo
CC or radiotherapy, for inhibiting neuronal cell apoptosis, non-specific
CC drug-induced apoptosis or oxidative stress-mediated apoptosis, and for
CC preventing apoptosis of cultured cells prepared for scientific or
CC technical purposes. The present sequence is that of a human caspase-2
CC peptide which was used in the exemplification of the invention.
XX
XX Sequence 21 AA;
SQ
Query Match 87.5%; Score 28; DB 8; Length 21;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRGDD 5
Db 12 CRGDE 16
|||||
RESULT 65
ABU61264
ID ABU61264 standard; peptide; 35 AA.
XX
AC ABU61264;
XX
XX 08-MAY-2003 (first entry)
XX
XX Human A domain from APOER2 #7.
XX
XX LDL-receptor class A domain; A domain; human; domain multimer;
KW multimer library; immuno-domain library.
XX
XX Homo sapiens.
XX
XX WO200288171-A2.
XX
XX 07-NOV-2002.
XX
XX 26-APR-2002; 2002WO-US013257.
XX
XX 26-APR-2001; 2001US-0286823P.
PR 19-NOV-2001; 2001US-0337209P.
PR 26-NOV-2001; 2001US-033359P.
PR 18-APR-2002; 2002US-0374107P.
XX
XX (MAXY-) MAXYGEN INC.
XX
XX Kolkman JA, Stemmer WPC;
XX
XX WPI; 2003-111869/10.
XX
XX Identifying a multimer that binds to a target molecule, comprises
PT identifying at least one monomer domain that bind to at least one target
PT molecule and linking the identified monomer domains to form a library of
PT multimers.
XX
XX Disclosure; Fig 10; 98pp; English.
XX
XX The invention relates to identifying a multimer that binds to a target
CC molecule, comprising identifying at least one monomer domain that binds
CC to at least one target molecule, linking the identified monomer domains
CC to form a library of multimers, each multimer comprising at least two
CC monomer domains, and screening the library of multimers for the ability

to bind to the first target molecule. Also included are: (1) a library of multimers formed by the method above (where each multimer comprises at least two monomer domains connected by a linker, and each monomer domain exhibits a binding specificity for a target molecule); (2) a polypeptide comprising: (a) the multimer selected from the novel method; or (b) at least two monomer domains separated by a heterologous linker, where each monomer domain specifically binds to a target molecule; (3) a polynucleotide encoding the multimer selected from the novel method; and (4) identifying hetero-immuno multimers that bind to a target molecule, comprising: (a) providing a library of immuno-domains; (b) screening the library of immuno-domains for affinity to a first target molecule; (c) providing a library of monomer domains; (d) screening the library of monomer domains for affinity to a first target molecule; (e) identifying at least one immuno-domain that binds to at least one target molecule; (f) identifying at least one monomer domain that binds to at least one target molecule; (g) linking the identified immuno-domain with the identified monomer domains to form a library of multimers, each multimer comprising at least two domains; (h) screening the library of multimers for the ability to bind to the first target molecule; and (i) identifying a multimer that binds to the first target molecule. The methods are useful for identifying multimers that bind to target molecules. The methods can also be used for selecting and optimising properties of discrete monomer domains and/or immuno-domains to create multimers. The multimers are useful for identifying the multimers with improved phenotype such as improved avidity or affinity or altered specificity for the target molecule. The polynucleotide, polypeptide and/or multimer are useful for preventing or treating a disease or disorder in a subject. The present sequence is a human LDL (low density lipoprotein) class A domain or simply an A domain used to design a library of A domain multimers of the invention

XX Sequence 35 AA;

Query Match 87.5%; Score 28; DB 6; Length 35;
Best Local Similarity 80.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
Db 1 CRGDE 5

RESULT 66
ADP21486
ID ADP21486 standard; peptide; 35 AA.
XX
AC ADP21486;
XX

12-AUG-2004 (first entry)
XX Human LDL receptor A domain peptide SeqID 62.
XX monomer; multimer; combinatorial library; LDL receptor A domain;
KW immunosuppressive; human; immunodomain; low density lipoprotein.
XX Homo sapiens.

OS WO2004044011-A2.

PN 27-MAY-2004.

XX 06-NOV-2003; 2003WO-US035664.
XX 06-NOV-2002; 2002US-00289660.

PR (AVID-) AVIDIA RES INST.

PA Kolkman JA, Stemmer WPC;

XX WPI; 2004-411701/38.

DR Identifying multimers binding to targets, by screening a library of

PT domains for affinity to the target, identifying domains binding to the

PT target, forming, screening a library of multimers and identifying

XX multimer binding to the target.

PS Disclosure; Fig 10; 161pp; English.

XX This invention relates to a novel method for identifying monomers and multimers that bind to a target molecule. Specifically, it refers to the generation of combinatorial libraries by screening a library of monomer and/or immunodomains to identify affinity for a target, and furthermore linking the identified monomer domains to a second monomer domain to form a library of multimers that still exhibit the ability to bind to the first target molecule. The present invention refers to monomer domains selected from the group consisting of EGF, EF, cadherin, C-type lectin, C2 and annexin domains, and in particular to a library of DNA sequences encoding the LDL receptor A domains. The generation of appropriate monomer/ multimer libraries is useful for creating antagonists to a target molecule, as well as for detection and other affinity based assays, such that the identified molecules can be used to increase the serum half-life of a molecule in the blood or for treating/ preventing a disease associated with the target molecule. In addition, they exhibit immunosuppressive activities and are useful for lowering the immune response in a mammal. This peptide sequence is a human low density lipoprotein (LDL) receptor class A-domain peptide of the invention.

XX Sequence 35 AA;

Query Match 87.5%; Score 28; DB 8; Length 35;
Best Local Similarity 80.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
Db 1 CRGDE 5

RESULT 67
AAR13677
ID AAR13677 standard; protein; 39 AA.
XX
AC AAR13677;
XX

13-NOV-1991 (first entry)
DT Decorsin.

XX Thrombin; factor Xa; cleavage site; receptor; GPIIb/IIIa; blood; clotting;
KW infarction; stroke; platelet aggregation; leech.
XX Macrobodella decora.

XX Key Location/Qualifiers
FH Peptide 23..37
FT /label= 2 /note= "claim 3, page 54"
FT 28..37
FT /label= 1
FT /note= "claim 1, page 54"

XX WO9112270-A.

XX 22-AUG-1991.

XX 14-FEB-1990; 90US-00479829.

XX 14-FEB-1990; 90US-00479829.

XX 26-OCT-1990; 90US-00602847.

XX (GETH) GENENTECH INC.

XX Lazarus RA, Seymour JL;

XX WPI; 1991-267097/36.

DR N-PSDB; AAQ13325.

XX New platelet aggregation inhibitors - derived from species of leech and
 PT used to treat conditions where blood has increased tendency to clot.
 XX
 XX
 PS Disclosure; Fig 7; 71pp; English.
 XX
 CC Decorsin has three disulfide bonds in its native (i.e. unreduced) form.
 CC Mol. wt. is less than 14.4 kD (SDS-PAGE) and 4384 D, calculated on the
 CC reduced protein. Decorsin is about 27 times more potent than the
 CC pentapeptide GRGDV. A peptide at least 70%, pref. 80%, homologous to
 CC indicated peptide 1 and pref. indicated peptide 2 is functional as
 CC inhibitor of platelet aggregation. The prod. binds to the GPIIb/IIIa
 CC receptors so prevent binding of fibrinogen to platelets. It can be
 CC administered therapeutically (esp. to provide a concn. of 1mM-50 microM)
 CC to prevent abnormal blood clotting (e.g. in phlebitis, infarction,
 CC stroke, etc.), opt. together with a fibrinolytic agent). See also
 CC AAQ13324-26, AAR13676-78, AAR13672-74 and AAR13761-63
 XX
 SQ Sequence 39 AA;

Query Match 87.5%; Score 28; DB 2; Length 39;
 Best Local Similarity 80.0%; Pred. No. 4.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
 Db 7 CQGDD 11

RESULT 68
 AAR95440
 ID AAR95440 standard; protein; 39 AA.

AC AAR95440;
 XX
 DT 17-SEP-1996 (first entry)
 XX

DE Decorsin platelet aggregation inhibitor.

XX Multifunctional protein; targeted hetero-association; protein assembly;
 KW decorsin; platelet aggregation inhibitor; antiaggregant; antithrombotic;
 KW leech.
 XX

OS Macrobodella decora.

XX WO9613583-A2.

XX 09-MAY-1996.

XX 20-OCT-1995; 95WO-EP004117.

XX 20-OCT-1994; 94EP-00116558.

XX (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.

XX Pack P, Lupas A;

XX WPI; 1996-239496/24.

XX Targetted hetero-association of recombinant proteins to multi-functional
 PT complexes - useful for therapeutic and diagnostic purposes.
 XX

PS Example 7; Fig 23; 34pp; English.

XX Decorsin (AAR95440), from the leech Macrobodella decora, acts as a potent
 CC antagonist of the platelet glycoprotein IIb-IIIa. 2 Gene cassettes
 CC (AAR15273 and AAR15274) respectively coding for the N-terminal (AAR95441)
 CC and C-terminal (AAR95442) portion of decorsin can be fused to an
 CC association segment used in a novel method for the targeted hetero-
 CC association of recombinant proteins to multi-functional complexes. A
 CC multivalent decorsin complex combined with an anti-fibrin antibody
 CC fragment can act as a powerful antithrombotic agent
 XX

SQ Sequence 39 AA;

Query Match 87.5%; Score 28; DB 2; Length 39;
 Best Local Similarity 80.0%; Pred. No. 4.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
 Db 7 CQGDD 11

RESULT 69

AAR92369
 ID AAR92369 standard; peptide; 39 AA.

XX AAR92369;

XX 22-JUN-2001 (first entry)

XX Miscellaneous peptide SEQ ID NO:1545.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX

OS Homo sapiens.

OS Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US013576.

XX 17-MAY-1999; 99US-0134406P.

XX 10-SEP-1999; 99US-0153406P.

XX 15-OCT-1999; 99US-0159783P.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents

XX peptidase degradation, useful for increasing length of in vivo activity.

XX Disclosure; Page 710; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAR90829 to AAR92441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX

SQ Sequence 39 AA;

Query Match 87.5%; Score 28; DB 4; Length 39;
 Best Local Similarity 80.0%; Pred. No. 4.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
|:|
Db 7 CQGGD 11

RESULT 70
AAR95442
ID AAR95442 standard; protein; 41 AA.
XX AC AAR95442;
XX 17-SEP-1996 (first entry)
XX Decorsin C-terminal portion.
XX Multifunctional protein; targetted hetero-association; protein assembly;
KW decorsin; platelet aggregation inhibitor; antiaggregant; antithrombotic;
KW leech; Macrobodella decora.
XX Synthetic.
XX WO9613583-A2.
XX 09-MAY-1996.
XX 20-OCT-1995; 95WO-EP004117.
XX 20-OCT-1994; 94EP-00116558.
XX (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.
XX Pack P, Lupas A;
XX MPI; 1996-239496/24.
XX N-PSDB; AAT15274.
XX Targetted hetero-association of recombinant proteins to multi-functional
PT complexes - useful for therapeutic and diagnostic purposes.
XX Example 7; Fig 25; 34pp; English.
XX Decorsin (AAR95440), from the leech Macrobodella decora, acts as a potent
CC antagonist of the platelet glycoprotein IIB-IIIa. 2 Gene cassettes
CC (AAT15273 and AAT15274) respectively coding for the N-terminal (AAR95441)
CC and C-terminal (AAR95442) portion of decorsin can be fused to an
CC association segment used in a novel method for the targetted hetero-
CC association of recombinant proteins to multi-functional complexes. A
CC multivalent decorsin complex combined with an anti-fibrin antibody
CC fragment can act as a powerful antithrombotic agent
XX Sequence 41 AA;
SQ

Query Match 87.5%; Score 28; DB 2; Length 41;
Best Local Similarity 80.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
|:|
Db 9 CQGGD 13

RESULT 71
AAW20043
ID AAW20043 standard; protein; 41 AA.
XX AAW20043;
XX 04-SEP-1997 (first entry)
XX Decorsin platelet aggregation inhibitor with flanking linker residues.
DE Multimerisation; self assembly; functional domain; linker; folding;
XX KW multimerisation domain; post-translational modification; secretion;
KW

KW interleukin-2; TAFII131; TAFII180; TATA box binding associated factor; p53;
KW histone; H3; H4; thrombospondin; TSP-4; platelet factor; PF4;
KW cartilage oligomeric protein; COMP.
XX Synthetic.
XX Key Location/Qualifiers
FT Misc-difference 3. .41 /note= "decorsin"
FT
XX
XX WO9637621-A2.
XX 28-NOV-1996.
XX 23-MAY-1996; 96WO-EP002230.
XX 23-MAY-1995; 95EP-00107914.
XX (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.
XX Pack P, Hoess A;
XX MPI; 1997-021226/02.
XX N-PSDB; AAT71291.
XX Multimerisation devices for self assembly of multifunctional proteins -
PT used to express recombinant multivalent poly:peptide(s) by incorporation
PT in a cistron encoding the protein.
XX Example 5; Fig 15; 64pp; English.
XX AAW20043 shows human decorsin, a platelet aggregation inhibitor, flanked
CC by residues of surrounding linker peptides. The sequence is the product
CC of an expression cassette that was incorporated into a larger DNA
CC cassette as a C-terminal functional domain. The larger cassette
CC comprises, in 5' to 3' direction, a 1st functional domain; a 1st linker
CC sequence; a multimerisation device; a 2nd linker sequence; and a 2nd
CC functional domain. The multimerisation device allows the combination of self-
CC two or more functional domains in a structure which is capable of self-
CC multimerisation (at least trimerisation). Functional domains may, for
CC example, bind to a defined target, catalyse a reaction, block a receptor
CC binding site, inhibit the action of another protein or bind to a metal
CC ion. Multimerisation domains from p53, platelet factor 4, thrombospondin,
CC TSP-4, TATA box binding associated factors and cartilage oligomeric
CC protein may be used. The multifunctional proteins can be prepared using
CC standard recombinant micro-organisms, even though the molecular weight of
CC the assembled protein exceeds that of the proteins commonly expressed in
CC bacteria. They have low immunogenicity in humans and carry two or more
CC functions in a single multimeric structure. Use of a combination of in
CC vivo expression and in vitro synthesis overcomes prior art problems due
CC to the differences in folding, secretion and post-translational
CC modifications for different polypeptides in different hosts
XX Sequence 41 AA;
SQ

Query Match 87.5%; Score 28; DB 2; Length 41;
Best Local Similarity 80.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
|:|
Db 9 CQGGD 13

RESULT 72
AAR95441
ID AAR95441 standard; protein; 42 AA.
XX AAR95441;
XX 17-SEP-1996 (first entry)
XX Decorsin N-terminal portion.
XX

XX Multifunctional protein; targeted hetero-association; protein assembly;
 KW decorsin; platelet aggregation inhibitor; antiaggregant; antithrombotic;
 KW leech; Macrobodella decora.
 XX Synthetic.
 OS
 XX WO9613583-A2.
 PN
 XX 09-MAY-1996.
 PD
 XX 20-OCT-1995; 95WO-EP004117.
 PF
 XX 20-OCT-1994; 94EP-00116558.
 PR
 XX (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.
 PA
 XX Pack P, Lupas A;
 PI
 XX WPI; 1996-239496/24.
 DR
 XX N-PSDB; AAT15273.
 DR
 XX Targetted hetero-association of recombinant proteins to multi-functional
 PT complexes - useful for therapeutic and diagnostic purposes.
 PT
 XX Example 7; Fig 24; 34pp; English.
 PS
 XX Decorsin (AAR95440), from the leech Macrobodella decora, acts as a potent
 CC antagonist of the platelet glycoprotein IIb-IIIa. 2 Gene cassettes
 CC (AAT15273 and AAT15274) respectively coding for the N-terminal (AAR95441)
 CC and C-terminal (AAR95442) portion of decorsin can be fused to an
 CC association segment used in a novel method for the targetted hetero-
 CC association of recombinant proteins to multi-functional complexes. A
 CC multivalent decorsin complex combined with an anti-fibrin antibody
 CC fragment can act as a powerful antithrombotic agent
 XX
 SQ Sequence 42 AA;
 Query Match 87.5%; Score 28; DB 2; Length 42;
 Best Local Similarity 80.0%; Pred. No. 5.2e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRGDD 5
 Db |::|||
 9 CQGGD 13
 RESULT 73
 AAW20042
 ID AAW20042 standard; protein; 42 AA.
 AC AAW20042;
 XX
 DT 04-SEP-1997 (first entry)
 XX
 DE Decorsin platelet aggregation inhibitor with flanking linker residues.
 XX
 KW Multimerisation; self assembly; functional domain; linker; folding;
 KW multimerisation domain; post-translational modification; secretion;
 KW interleukin-2; TAFI131; TAFI180; TATA box binding associated factor; p53;
 KW histone; H3; H4; thrombospondin; TSP-4; platelet factor; PF4;
 KW cartilage oligomeric protein; COMP; ss.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 3..41
 FT /note= "decorsin"
 XX
 XX WO9637621-A2.
 PN
 XX 28-NOV-1996.
 PD
 XX

PF 23-MAY-1996; 96WO-EP002230.
 XX
 PR 23-MAY-1995; 95EP-00107914.
 XX
 PA (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.
 XX
 XX Pack P, Hoess A;
 PI
 XX WPI; 1997-021236/02.
 DR
 XX N-PSDB; AAT71290.
 DR
 XX Multimerisation devices for self assembly of multifunctional proteins -
 PT used to express recombinant multivalent poly-peptide(s) by incorporation
 PT in a cistron encoding the protein.
 XX
 XX Example 5; Fig 14; 64pp; English.
 PS
 XX AAW20042 shows human decorsin, a platelet aggregation inhibitor, flanked
 CC by residues of surrounding linker peptides. The sequence is the product
 CC of an expression cassette that was incorporated into a larger DNA
 CC cassette as an N-terminal functional domain. The larger cassette
 CC comprises, in 5' to 3' direction, a 1st functional domain; a 1st linker
 CC sequence; a multimerisation device; a 2nd linker sequence; and a 2nd
 CC functional domain. The multimerisation device allows the combination of
 CC two or more functional domains in a structure which is capable of self-
 CC multimerisation (at least trimerisation). Functional domains may, for
 CC example, bind to a defined target, catalyse a reaction, block a receptor
 CC binding site, inhibit the action of another protein or bind to a metal
 CC ion. Multimerisation domains from p53, platelet factor 4, thrombospondin,
 CC TSP-4, TATA box binding associated factors and cartilage oligomeric
 CC protein may be used. The multifunctional proteins can be prepared using
 CC standard recombinant micro-organisms, even though the molecular weight of
 CC the assembled protein exceeds that of the proteins commonly expressed in
 CC bacteria. They have low immunogenicity in humans and carry two or more
 CC functions in a single multimeric structure. Use of a combination of in
 CC vivo expression and in vitro synthesis overcomes prior art problems due
 CC to the differences in folding, secretion and post-translational
 CC modifications for different polypeptides in different hosts
 XX
 SQ Sequence 42 AA;
 Query Match 87.5%; Score 28; DB 2; Length 42;
 Best Local Similarity 80.0%; Pred. No. 5.2e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRGDD 5
 Db |::|||
 9 CQGGD 13
 RESULT 74
 AAR13676
 ID AAR13676 standard; protein; 45 AA.
 AC AAR13676;
 XX
 DT 13-NOV-1991 (first entry)
 XX
 DE Decorsin fusion protein.
 XX
 KW Thrombin; factor Xa; cleavage site; receptor; GRP113a; blood; clotting;
 KW infarction; stroke; platelet aggregation; leech.
 XX
 OS Macrobodella decora.
 XX
 XX Key Location/Qualifiers
 FH Cleavage-site 1..6
 FT /note= "cleavable by thrombin and factor Xa"
 FT Protein 7..45
 FT /label= decorsin
 FT Peptide 29..43
 FT /label= 2
 FT /note= "claim 3, page 54"

FT Peptide 34..43
FT /label= 1
FT /note= "claim 1, page 54"
XX
PN WO9112270-A.
XX
PD 22-AUG-1991.
XX
XX 14-FEB-1990; 90US-00479829.
XX
XX 14-FEB-1990; 90US-00479829.
PR 26-OCT-1990; 90US-00602847.
XX
XX (GETH) GENENTECH INC.
PA
XX Lazarus RA, Seymour JL;
XX WPI; 1991-267097/36.
DR N-PSDB; AAQ13324.
XX
XX New platelet aggregation inhibitors - derived from species of leech and
PT used to treat conditions where blood has increased tendency to clot.
XX
XX Disclosure; Fig 6; 71pp; English.
XX
XX The sequence comprises decorin and a 6 amino acid cleavage site amenable
CC to cleavage by thrombin and factor Xa. This cleavage site is used to
CC generate decorin from a fusion protein (constructed e.g. for secretion
CC into the periplasmic space or for intracellular expression). A peptide at
CC least 70%, pref. 80%, homologous to indicated peptide 1 and pref.
CC indicated peptide 2 is functional as inhibitor of platelet aggregation.
CC The prod. binds to the GPIIb/IIIa receptors so prevent binding of
CC fibrinogen to platelets. It can be administered therapeutically (esp. to
CC provide a concn. of 1m-50 microm) to prevent abnormal blood clotting
CC (e.g. in phlebitis, infarction, stroke, etc.), opt. together with a
CC fibrinolytic agent). See also AAQ13324-26, AAR13676-78, AAR13672-74 and
CC AAR13761-63
XX
SQ Sequence 45 AA;
Query Match 87.5%; Score 28; DB 2; Length 45;
Best Local Similarity 80.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRGDD 5
Db 13 CQGDD 17
RESULT 75
AAE08949
ID AAE08949 standard; peptide; 46 AA.
AC
AAE08949;
XX
DT 15-NOV-2001 (first entry)
XX
DE ICH-1 peptide of NEDD-like ASCP subfamily.
XX
KW Apoptotic protease; mammalian ced-3 homologue 6; Mch6; cancer; ICH-1;
KW aspartate-specific cysteine protease; ASCP; apoptosis; therapy;
KW autoimmune disease; cerebellar degeneration; Alzheimer's disease;
KW cytostatic; Parkinson's disease; immunomodulator; antimicrobial;
KW viral infection; cell death-mediated disease; neuroprotective.
XX
OS Unidentified.
XX
XX US6271361-B1.
PN
XX
PD 07-AUG-2001.
XX
XX 25-FEB-1999; 99US-00257218.
PF
XX

PR 29-MAY-1997; 97US-00865579.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Alnemri ES, Fernandes-Alnemri T, Litwack G;
XX WPI; 2001-528686/58.
XX
XX New apoptotic genes and their apoptotic protease products, useful for
PT modulating apoptosis for the therapeutic treatment of human diseases,
PT e.g. cancers, autoimmune disease, Alzheimer's disease or Parkinson's
PT disease.
XX
XX Example 1; Fig 2; 36pp; English.
XX
XX The invention relates to an isolated gene encoding apoptotic protease,
CC mammalian ced-3 homologue 6 (Mch6). Mch6 is a member of the aspartate-
CC specific cysteine protease (ASCP) family. Mch6 DNA and protein sequences
CC are useful for modulating apoptosis for the therapeutic treatment of
CC human diseases. Mch6 sequences are useful for upregulating apoptosis
CC (e.g. for treating cancers, autoimmune disease or viral infections) or
CC downregulating apoptosis (e.g. for treating Alzheimer's disease,
CC Parkinson's disease or cerebellar degeneration). The Mch6 sequence is
CC useful for diagnosing, treating or reducing the severity of cell death-
CC mediated diseases, as well as other diseases mediated by either increased
CC or decreased programmed cell death. The present amino acid sequence is
CC ICH-1 peptide which belongs to NEDD-like ASCP subfamily
XX
SQ Sequence 46 AA;
Query Match 87.5%; Score 28; DB 4; Length 46;
Best Local Similarity 80.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRGDD 5
Db 17 CRGDE 21
Search completed: September 7, 2005, 20:09:43
Job time : 196 secs

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OM protein - protein search, using sw model

Run on: September 7, 2005, 19:58:16 ; Search time 39 Seconds

(without alignments)
12.335 Million cell updates/sec

Title: US-10-812-238B-41

Perfect score: 32

Sequence: 1 CRGDD 5

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	255	2	hypothetical prote
2	32	100.0	289	2	oligopeptide trans
3	32	100.0	357	2	conserved hypotet
4	32	100.0	363	2	probable mureinpep
5	32	100.0	400	1	nicotinate phospho
6	32	100.0	400	1	nicotinate phospho
7	32	100.0	400	2	nicotinate phospho
8	32	100.0	400	2	nicotinate phospho
9	32	100.0	400	2	nicotinate phospho
10	32	100.0	430	2	serine-tRNA ligase
11	32	100.0	1116	2	serine/threonine-p
12	29	90.6	264	2	hypothetical prote
13	29	90.6	296	2	hypothetical prote
14	29	90.6	413	2	probable C2H2-type
15	29	90.6	732	2	hypothetical prote
16	29	90.6	761	2	topoisomerase IV,
17	28	87.5	39	2	decorain - leech (
18	28	87.5	66	1	DNPBP
19	28	87.5	74	1	DNPBP
20	28	87.5	182	2	DNA-binding protei
21	28	87.5	234	2	interleukin-1-beta
22	28	87.5	416	2	hypothetical prote
23	28	87.5	423	2	TNFR-associated pr
24	28	87.5	427	2	conserved hypotet
25	28	87.5	431	2	hypothetical prote
26	28	87.5	435	2	apoptosis regulato
27	28	87.5	452	2	capase-2 - rat
28	28	87.5	470	2	hypothetical prote
29	28	87.5	490	2	hypothetical prote

30	28	87.5	521	2	Tl8896	glypican 1 precurs
31	28	87.5	548	2	T22137	hypothetical prote
32	28	87.5	572	2	T51525	hypothetical prote
33	28	87.5	632	2	E81684	1-deoxyxylulose-5-
34	28	87.5	635	2	T00602	hypothetical prote
35	28	87.5	636	2	D84823	hypothetical prote
36	28	87.5	640	2	F71527	probable transketo
37	28	87.5	657	2	T00859	hypothetical prote
38	28	87.5	664	2	JH0770	probable atp-depen
39	28	87.5	730	2	JH0798	fasciclin IV precu
40	28	87.5	842	2	C83177	probable phosphotr
41	28	87.5	1267	1	MWXR31	lambda 3 protein -
42	28	87.5	1267	1	MWXR32	lambda 3 protein -
43	28	87.5	1267	1	MWXR33	lambda 3 protein -
44	28	87.5	1323	2	T37533	coronin-like prote
45	28	87.5	1806	2	T23298	hypothetical prote
46	28	87.5	2043	2	T18524	scavenger receptor
47	28	87.5	2098	2	T18397	protein CTRP - mal
48	28	87.5	3036	2	T18995	hypothetical prote
49	27	84.4	57	1	TIFHBP	proteinase inhibit
50	27	84.4	130	2	A13045	hypothetical prote
51	27	84.4	138	2	E95330	HmrR heavy metal d
52	27	84.4	147	2	C95969	probable transcrip
53	27	84.4	153	2	A60585	thyroglobulin - gl
54	27	84.4	164	2	H64803	ybfp protein - Bsc
55	27	84.4	219	2	A70734	probable cutinase
56	27	84.4	220	2	A44805	eggshell protein p
57	27	84.4	224	2	F64859	Putative lambdoid
58	27	84.4	255	2	T15553	hypothetical prote
59	27	84.4	263	2	C56084	interleukin-lbeta
60	27	84.4	276	2	AF0402	transketolase (EC
61	27	84.4	299	2	F85835	hypothetical prote
62	27	84.4	299	2	D90990	hypothetical prote
63	27	84.4	299	2	E64975	hypothetical prote
64	27	84.4	323	2	G83892	hypothetical prote
65	27	84.4	326	1	GOVZML	T2 protein - myxom
66	27	84.4	333	2	B42476	hypothetical prote
67	27	84.4	333	2	S15309	hypothetical prote
68	27	84.4	333	2	AC0766	probable glycosylt
69	27	84.4	343	2	H70517	probable lppb prot
70	27	84.4	346	2	H70722	probable transfera
71	27	84.4	370	2	F84550	hypothetical prote
72	27	84.4	399	2	A84972	hypothetical prote
73	27	84.4	504	2	C64398	hypothetical prote
74	27	84.4	507	2	AD3382	ABC transporter-as
75	27	84.4	553	2	E27793	methyl coenzyme M
76	27	84.4	602	1	S46676	probable phosphoe
77	27	84.4	603	2	JC6128	insulin-like growt
78	27	84.4	603	2	JC1282	insulin-like growt
79	27	84.4	605	2	JCS239	insulin-like growt
80	27	84.4	605	2	A41915	insulin-like growt
81	27	84.4	671	2	JC2029	annexin - chicken
82	27	84.4	684	2	T48357	hypothetical prote
83	27	84.4	721	2	H82528	L-ascorbate oxidas
84	27	84.4	914	2	B96592	hypothetical prote
85	27	84.4	940	2	T01854	hypothetical prote
86	27	84.4	996	2	T25512	hypothetical prote
87	27	84.4	1041	2	PQ0442	polyprotein - barl
88	27	84.4	1058	2	A48195	ubiquitin-protein
89	27	84.4	1202	2	PQ0440	polyprotein - barl
90	27	84.4	1283	2	T13799	neurxin IV - frui
91	27	84.4	1470	2	S45323	genome polyprotein
92	27	84.4	1475	2	T29809	hypothetical prote
93	27	84.4	1820	2	S71853	genome polyprotein
94	27	84.4	1847	2	T30558	resistance protein
95	27	84.4	2042	2	T18399	variant-specific s
96	27	84.4	2212	2	T28157	erythrocyte membra
97	27	84.4	2410	1	JQ1948	genome polyprotein
98	27	84.4	2412	1	JQ1537	genome polyprotein
99	27	84.4	2647	2	T28161	hypothetical prote
100	26	81.2	45	2	T05477	hypothetical prote
101	26	81.2	57	2	B38180	hypothetical prote
102	26	81.2	64	1	WM1HB2	3b protein - avian

103	26	81.2	64	1	WMIB85	3b protein - avian	176	26	81.2	295	2	S05006	calcium channel al
104	26	81.2	64	1	WMIB88	3b protein - avian	177	26	81.2	302	2	A96661	unknown protein, 8
105	26	81.2	87	2	Q01693	U49A protein - hu	178	26	81.2	303	2	B84744	hypothetical prote
106	26	81.2	88	2	G84393	hypothetical prote	179	26	81.2	304	2	T42554	tegument protein -
107	26	81.2	102	2	A72518	hypothetical prote	180	26	81.2	308	2	K89950	porphobilinogen de
108	26	81.2	103	2	S62052	hypothetical prote	181	26	81.2	309	1	KIECRB	ribokinase (EC 2.7
109	26	81.2	104	2	T46246	hypothetical prote	182	26	81.2	309	2	AB0952	ribokinase (import
110	26	81.2	125	2	D97478	lipA protein [limpo	183	26	81.2	309	2	F91215	ribokinase (import
111	26	81.2	127	2	S01286	wheny acidic protei	184	26	81.2	309	2	G86061	ribokinase (import
112	26	81.2	137	2	T33210	hypothetical prote	185	26	81.2	311	2	F84030	porphobilinogen de
113	26	81.2	139	2	S58234	lipA protein - Rhi	186	26	81.2	311	2	B56084	interleukin-1beta
114	26	81.2	142	2	T41313	hypothetical prote	187	26	81.2	312	2	A61183	hypothetical prote
115	26	81.2	142	2	AD2696	lipA protein [limpo	188	26	81.2	313	2	T18092	hypothetical prote
116	26	81.2	145	2	F82133	hypothetical prote	189	26	81.2	315	2	T10613	hypothetical prote
117	26	81.2	149	2	S12913	cystatin - fruit f	190	26	81.2	321	2	H87683	transcription regu
118	26	81.2	152	2	T41310	hypothetical prote	191	26	81.2	323	2	T27640	hypothetical prote
119	26	81.2	152	2	D89753	protein Fl1C7.2 [i	192	26	81.2	325	2	C95952	hypothetical prote
120	26	81.2	156	2	B23863	tissue kallikrein	193	26	81.2	326	2	A97751	hypothetical prote
121	26	81.2	158	2	T04875	hypothetical prote	194	26	81.2	336	2	AH2040	porphobilinogen de
122	26	81.2	161	2	AC0893	conserved hypotet	195	26	81.2	336	2	E69845	thiamin biosynthes
123	26	81.2	163	2	S43240	troponin C - commo	196	26	81.2	337	2	T49627	probable DNA-direc
124	26	81.2	164	2	WM0061	troponin C - Flori	197	26	81.2	338	2	H83228	hypothetical prote
125	26	81.2	164	2	JM0060	troponin C - commo	198	26	81.2	342	2	T22167	hypothetical prote
126	26	81.2	168	2	T75542	hypothetical prote	199	26	81.2	349	2	T36944	haptoglobin - chim
127	26	81.2	173	2	T19469	hypothetical prote	200	26	81.2	350	2	AD3560	methylated-DNA-lpr
128	26	81.2	174	2	T15658	hypothetical prote	201	26	81.2	350	2	T25451	transforming growt
129	26	81.2	176	2	E96754	Similar to downy m	202	26	81.2	352	2	C96643	hypothetical prote
130	26	81.2	182	2	T20533	hypothetical prote	203	26	81.2	356	2	AH2431	oxidoreductase all
131	26	81.2	182	2	H69026	ribosomal protein	204	26	81.2	360	2	F69342	DNA primase homolo
132	26	81.2	187	2	B82857	pre-pilin like lea	205	26	81.2	360	2	A56066	basic helix-loop-h
133	26	81.2	188	2	B32340	tissue kallikrein	206	26	81.2	362	2	H69958	aminomethyltransfe
134	26	81.2	188	2	G86226	hypothetical prote	207	26	81.2	367	2	JE0104	testicular serine
135	26	81.2	193	2	E95340	hypothetical prote	208	26	81.2	371	2	F86546	hypothetical prote
136	26	81.2	196	2	T29016	hypothetical prote	209	26	81.2	371	2	C72077	conserved hypotet
137	26	81.2	205	2	T37940	hypothetical prote	210	26	81.2	371	2	D84186	hypothetical prote
138	26	81.2	208	2	T04796	hypothetical prote	211	26	81.2	373	2	FW0042	activin - fruit fl
139	26	81.2	209	2	H86259	protein T12C24.14	212	26	81.2	374	1	S35669	alcohol dehydrogen
140	26	81.2	213	2	S43723	lactase (EC 3.2.1.	213	26	81.2	374	1	DEHOAS	alcohol dehydrogen
141	26	81.2	213	2	S43722	lactase (EC 3.2.1.	214	26	81.2	374	1	S48157	alcohol dehydrogen
142	26	81.2	214	2	S65052	plastil-specific pr	215	26	81.2	375	1	A35837	alcohol dehydrogen
143	26	81.2	219	2	A53305	pentose-5-phosphat	216	26	81.2	375	1	A38405	alcohol dehydrogen
144	26	81.2	220	2	S70766	cathepsin D inhibi	217	26	81.2	375	1	A48257	alcohol dehydrogen
145	26	81.2	221	2	E96591	hypothetical prote	218	26	81.2	375	1	A49107	alcohol dehydrogen
146	26	81.2	222	2	S26994	cellulose 1,4-beta	219	26	81.2	375	1	DECHA1	alcohol dehydrogen
147	26	81.2	223	2	C59215	conserved hypotet	220	26	81.2	375	1	DEHOAL	alcohol dehydrogen
148	26	81.2	224	2	E90908	probable tail asse	221	26	81.2	375	1	DEMSAA	alcohol dehydrogen
149	26	81.2	226	2	H84237	hypothetical prote	222	26	81.2	375	1	I60970	alcohol dehydrogen
150	26	81.2	227	2	S77594	probable trehalose	223	26	81.2	375	1	I60973	alcohol dehydrogen
151	26	81.2	228	2	S26995	cellulose 1,4-beta	224	26	81.2	375	1	S29343	alcohol dehydrogen
152	26	81.2	228	2	G70902	probable lprH prot	225	26	81.2	375	1	S62638	alcohol dehydrogen
153	26	81.2	228	2	T47425	NAC domain-like pr	226	26	81.2	375	1	S62639	alcohol dehydrogen
154	26	81.2	236	2	S26993	cellulose 1,4-beta	227	26	81.2	375	1	S66272	alcohol dehydrogen
155	26	81.2	240	2	A46587	extracellular hemo	228	26	81.2	376	1	A26468	occlusion-derived
156	26	81.2	243	2	B87631	enoyl-CoA hydratase	229	26	81.2	376	2	F72868	hypothetical prote
157	26	81.2	255	2	A84723	hypothetical prote	230	26	81.2	376	2	AD2697	3beta-hydroxy-belt
158	26	81.2	258	2	C70968	probable ribD - My	231	26	81.2	377	2	I50147	Wnt inhibitory fac
159	26	81.2	258	2	T45931	hypothetical prote	232	26	81.2	378	2	B59180	phosphonate metabo
160	26	81.2	259	2	WMMS28	complement factor	233	26	81.2	378	2	AB2083	Similar to part of
161	26	81.2	259	2	T01008	ribonuclease (EC 3	234	26	81.2	380	2	C96754	hypothetical prote
162	26	81.2	259	2	E84427	hypothetical prote	235	26	81.2	380	2	T32163	hypothetical prote
163	26	81.2	262	1	JC4803	venombin A (EC 3.4	236	26	81.2	382	2	G85234	hypothetical prote
164	26	81.2	263	1	I55608	complement factor	237	26	81.2	383	2	A56084	interleukin-1beta
165	26	81.2	265	2	T04834	hypothetical prote	238	26	81.2	384	2	E75587	probable oxidoredu
166	26	81.2	266	2	T10609	hypothetical prote	239	26	81.2	384	2	AI1843	hypothetical prote
167	26	81.2	268	2	T31699	hypothetical prote	240	26	81.2	389	2	T04006	libeta-hydroxyster
168	26	81.2	268	2	F87076	probable reductase	241	26	81.2	389	2	T27085	hypothetical prote
169	26	81.2	270	2	C96731	unknown protein F5	242	26	81.2	390	2	AD1035	probable major tai
170	26	81.2	270	2	F86177	protein Fl9P19.1 [243	26	81.2	390	2	AG0929	probable major tai
171	26	81.2	273	2	T10610	hypothetical prote	244	26	81.2	390	2	AI0816	probable bacteriop
172	26	81.2	274	2	T31943	hypothetical prote	245	26	81.2	392	1	A30100	serine proteinase
173	26	81.2	284	2	G96660	protein F2K11.8 [i	246	26	81.2	401	2	E88613	protein T2B29.9 [i
174	26	81.2	285	2	S72787	hypothetical prote	247	26	81.2	402	2	A42677	interleukin-1 beta
175	26	81.2	288	2	D83184	conserved hypotet	248	26	81.2	407	2	C97234	probable glycosyl

249	26	81.2	408	2	T25376	hypothetical prote	322	26	81.2	661	1	KPHU13	coagulation factor
250	26	81.2	408	2	G97194	ornithine acetyltr	323	26	81.2	663	2	G81384	succinate dehydrog
251	26	81.2	410	2	AF1974	hypothetical prote	324	26	81.2	665	2	T06082	protein kinase hom
252	26	81.2	417	2	B69254	3-ketoacyl-CoA thi	325	26	81.2	675	2	D85065	receptor protein k
253	26	81.2	423	2	T14526	S-locus-specific g	326	26	81.2	676	2	T47526	protein kinase-lik
254	26	81.2	423	2	AH0053	conserved hypothet	327	26	81.2	678	2	T04832	probable serine/th
255	26	81.2	424	2	F84729	hypothetical prote	328	26	81.2	686	1	A59271	Ra-reactive factor
256	26	81.2	426	2	T14527	S-locus-specific g	329	26	81.2	688	2	T05353	hypothetical prote
257	26	81.2	428	2	S35215	sodium channel pro	330	26	81.2	689	1	JW0107	very-long-chain ac
258	26	81.2	429	2	S48172	variable surface g	331	26	81.2	703	2	H86349	protein F8K7.9 (im
259	26	81.2	430	2	E86188	hypothetical prote	332	26	81.2	705	2	A70669	probable acid-CoA
260	26	81.2	430	2	B84212	hypothetical prote	333	26	81.2	706	2	A86350	F8K7.10 protein -
261	26	81.2	433	2	T14392	S-locus glycoprote	334	26	81.2	707	2	T35196	probable DNA gyras
262	26	81.2	441	2	T149819	hypothetical prote	335	26	81.2	707	2	F86925	probable acyl-CoA
263	26	81.2	447	2	C82958	probable two-compo	336	26	81.2	708	1	TFBOL	lactotransferrin p
264	26	81.2	450	2	A34169	alpha-2A-adrenergic	337	26	81.2	708	2	JC2323	lactoferrin - goat
265	26	81.2	450	2	A38316	alpha-2-adrenergic	338	26	81.2	710	1	C43497	early transcriptio
266	26	81.2	450	2	I49481	alpha-2-adrenergic	339	26	81.2	710	1	I42517	early transcriptio
267	26	81.2	450	2	B40392	alpha-2-adrenergic	340	26	81.2	710	2	T37394	VEGF, 82k subunit
268	26	81.2	457	2	T35443	aminotransferase -	341	26	81.2	714	2	G71963	fumarate reductase
269	26	81.2	457	2	S03961	Ig mu chain C regi	342	26	81.2	714	2	H64543	arginine decarboxy
270	26	81.2	459	2	G86212	hypothetical prote	343	26	81.2	728	1	S59553	transcription regu
271	26	81.2	460	2	JC5137	beta-glucosidase (344	26	81.2	729	2	C69038	melanotransferrin
272	26	81.2	460	2	F88085	protein Tf1p1.6 [i	345	26	81.2	738	1	TFHUM	hypothetical prote
273	26	81.2	462	2	AH1130	glutamate decarbox	346	26	81.2	738	2	T27289	hypothetical prote
274	26	81.2	463	2	T32111	hypothetical prote	347	26	81.2	740	2	T12223	NADH2 dehydrogenas
275	26	81.2	468	2	T10595	hypothetical prote	348	26	81.2	753	2	S48261	hypothetical prote
276	26	81.2	469	2	E70076	arabinan endo-1,5-	349	26	81.2	763	2	I50807	complement factor
277	26	81.2	475	2	T184077	hypothetical prote	350	26	81.2	764	1	BBHU	complement factor
278	26	81.2	475	2	A48948	aspartate carbamoy	351	26	81.2	778	2	R70667	hypothetical prote
279	26	81.2	476	2	E97631	probable membrane	352	26	81.2	783	2	A41627	hypothetical prote
280	26	81.2	485	2	T04840	hypothetical prote	353	26	81.2	794	2	T23048	furin (EC 3.4.21.7
281	26	81.2	488	2	D82991	conserved hypothet	354	26	81.2	849	2	T38728	hypothetical prote
282	26	81.2	489	2	C87480	conserved hypothet	355	26	81.2	861	2	T15903	trehalose-phosphat
283	26	81.2	489	2	C94725	probable protein k	356	26	81.2	822	2	S77112	DNA mismatch repai
284	26	81.2	489	2	F65125	probable general s	357	26	81.2	826	2	T43638	casepase-related pr
285	26	81.2	490	2	S28355	hypothetical prote	358	26	81.2	830	2	T04848	protein kinase hom
286	26	81.2	501	2	T37747	hypothetical prote	359	26	81.2	841	2	T14398	S-receptor kinase
287	26	81.2	510	2	S41943	hypothetical prote	360	26	81.2	849	2	T38728	probable trehalose
288	26	81.2	511	2	S44716	cellulose 1,4-beta	361	26	81.2	861	2	T15903	protein kinase C h
289	26	81.2	513	2	B87481	cellulose 1,4-beta	362	26	81.2	878	2	H83184	phosphoenolpyruvat
290	26	81.2	514	1	S21125	anthranilate synth	363	26	81.2	888	2	H88085	protein Tf1p1.8 [i
291	26	81.2	514	2	D84723	steroid 17alpha-mo	364	26	81.2	938	2	A56731	chromatin assembly
292	26	81.2	522	2	S33029	hypothetical prote	365	26	81.2	957	2	F69729	excinuclease ABC c
293	26	81.2	540	2	S41942	cellulose 1,4-beta	366	26	81.2	957	2	B84099	excinuclease ABC (
294	26	81.2	548	2	T28910	hypothetical prote	367	26	81.2	1004	2	S51133	transposase Tn4652
295	26	81.2	550	2	G70768	hypothetical prote	368	26	81.2	1023	2	T30257	IGG FC binding pro
296	26	81.2	558	2	S68981	aminonucleoside an	369	26	81.2	1076	2	T26044	hypothetical prote
297	26	81.2	566	2	F84903	probable ubiquitin	370	26	81.2	1088	2	D82246	probable chitinase
298	26	81.2	569	2	T50711	urease (EC 3.5.1.5	371	26	81.2	1137	2	T02097	glutamate synthase
299	26	81.2	574	2	B29677	complement C9 prec	372	26	81.2	1166	1	S06142	protein-tyrosine k
300	26	81.2	576	2	T41587	probable carbon ca	373	26	81.2	1185	2	S15809	gene ERCC5 protein
301	26	81.2	583	2	S46265	cysteine proteinas	374	26	81.2	1186	2	S35993	DNA repair protein
302	26	81.2	586	2	I37202	B-CAM protein - hu	375	26	81.2	1192	2	S69000	laminin gamma 2 ch
303	26	81.2	596	2	B41627	furin (EC 3.4.21.7	376	26	81.2	1240	2	T04833	hypothetical prote
304	26	81.2	597	2	E85090	probable transposo	377	26	81.2	1260	2	T01334	hypothetical prote
305	26	81.2	597	2	T04954	hypothetical prote	378	26	81.2	1270	2	T21269	hypothetical prote
306	26	81.2	598	1	QBEG7	HHLF7 protein - hu	379	26	81.2	1275	2	T18556	O-antigen biosynth
307	26	81.2	609	1	FPGO	alpha-fetoprotein	380	26	81.2	1318	2	T21368	hypothetical prote
308	26	81.2	609	1	FPHU	alpha-fetoprotein	381	26	81.2	1327	2	T21368	hypothetical prote
309	26	81.2	609	2	JC4258	alpha-fetoprotein	382	26	81.2	1331	2	S05011	calcium channel al
310	26	81.2	612	2	T02414	probable protein k	383	26	81.2	1381	2	S55619	capsid protein 25
311	26	81.2	619	2	G84489	probable TNP2-like	384	26	81.2	1465	2	S31262	tyb protein - years
312	26	81.2	628	2	I38000	Lutheran blood gro	385	26	81.2	1467	2	FC1253	tyb protein - years
313	26	81.2	631	2	C96768	hypothetical prote	386	26	81.2	1482	2	S67496	glutamate synthase
314	26	81.2	633	2	T04835	probable serine/th	387	26	81.2	1531	2	T42218	glut-1 protein hom
315	26	81.2	635	2	T72215	hypothetical prote	388	26	81.2	1538	2	S73296	glutamate synthase
316	26	81.2	640	2	T06419	gag-proteinase pol	389	26	81.2	1549	2	T11974	glutamate synthase
317	26	81.2	650	2	A69390	3-hydroxyacyl-CoA	390	26	81.2	1556	2	S76781	glutamate synthase
318	26	81.2	656	1	B44954	fumarate reductase	391	26	81.2	1559	2	A12348	ferredoxin-glutama
319	26	81.2	658	2	D96656	hypothetical prote	392	26	81.2	1580	2	T26204	hypothetical prote
320	26	81.2	658	2	T04831	probable serine/th	393	26	81.2	1616	2	A38596	glutamate synthase
321	26	81.2	659	2	A64139	ribonuclease T2 ho	394	26	81.2	1629	2	C84839	ferredoxin-depende
										1802	2	S52611	tyb protein - years

395	26	81.2	1803	2	S56894	TYB protein - Yeas	468	25	78.1	276	2	F89826	hypothetical prote
396	26	81.2	1918	2	S43719	lactase (EC 3.2.1.1	469	25	78.1	278	2	T35146	glutamate-binding
397	26	81.2	1920	2	S43721	lactase (EC 3.2.1.1	470	25	78.1	281	2	T52470	cytochrome-b5 redu
398	26	81.2	1926	2	S01159	beta-glycosidase c	471	25	78.1	293	2	D96605	unknown protein F1
399	26	81.2	2051	2	T30938	receptor tyrosine	472	25	78.1	300	2	D95971	conserved hypochet
400	26	81.2	2108	2	S72458	sodium channel pro	473	25	78.1	300	2	AF3092	conserved hypochet
401	26	81.2	2166	2	S11339	calcium channel pr	474	25	78.1	300	2	D98194	hypothetical prote
402	26	81.2	2171	2	S05054	calcium channel al	475	25	78.1	303	2	A84831	probable protein k
403	26	81.2	2204	1	RRNZNV	genome polypeptin	476	25	78.1	304	2	E95342	NosF copper ABC tr
404	26	81.2	2657	2	T18497	hypothetical prote	477	25	78.1	308	2	B83403	ribokinase PA1950
405	26	81.2	2796	2	JC4743	fatty-acid synthas	478	25	78.1	318	1	LUP84	annexin IV - pig
406	26	81.2	2911	2	T20566	hypothetical prote	479	25	78.1	319	1	LUBO4	annexin IV - bovin
407	26	81.2	2924	2	T18378	variant-specific s	480	25	78.1	319	2	AC0942	annexin IV - human
408	26	81.2	3026	2	T28431	variant surface pr	481	25	78.1	321	1	A42077	annexin V - chicke
409	26	81.2	3328	2	T30835	breast cancer tumo	482	25	78.1	321	1	LUCH5	annexin V - chicke
410	26	81.2	3329	2	T42205	breast cancer susc	483	25	78.1	323	1	LUDU3	annexin III - huma
411	26	81.2	3329	2	T30904	breast cancer tumo	484	25	78.1	323	2	A70404	acetyl-CoA carboxy
412	26	81.2	3430	1	GNWVU	genome polypeptin	485	25	78.1	323	1	LUR73	annexin III - rat
413	26	81.2	3432	1	GNWVUS	genome polypeptin	486	25	78.1	325	2	T04677	hypothetical prote
414	26	81.2	3432	1	GNWVUS	genome polypeptin	487	25	78.1	325	2	AE2466	acetyl-CoA carboxy
415	26	81.2	3433	1	GNWVKV	genome polypeptin	488	25	78.1	326	2	S40818	hypothetical 36.9K
416	26	81.2	3434	1	GNWVNV	genome polypeptin	489	25	78.1	326	2	S40242	homeotic protein E
417	26	81.2	4131	2	T21085	hypothetical prote	490	25	78.1	335	2	G01448	homeobox protein H
418	26	81.2	5147	1	IJFFFM	cadherin-related t	491	25	78.1	339	1	LUBO36	annexin II - bovin
419	25	78.1	36	2	A60602	annexin II - golde	492	25	78.1	339	1	LUDU36	annexin II - human
420	25	78.1	85	2	T10571	hypothetical prote	493	25	78.1	339	1	LUMS36	annexin II - mouse
421	25	78.1	89	2	B91173	phosphotransferase	494	25	78.1	339	2	S33700	annexin II - rat
422	25	78.1	89	2	B86019	probable phosphoca	495	25	78.1	340	1	JQ1297	annexin II type 1
423	25	78.1	109	2	B72763	hypothetical prote	496	25	78.1	340	1	JQ1298	annexin II type 2
424	25	78.1	110	2	B85547	probable transcript	497	25	78.1	341	2	S55277	annexin II - rat
425	25	78.1	113	2	B86934	probable membrane	498	25	78.1	352	2	AI2884	hypothetical prote
426	25	78.1	120	1	PSKF3U	phospholipase A2 (499	25	78.1	352	2	F97660	probable ABC trans
427	25	78.1	122	1	PSABA	phospholipase A2 (500	25	78.1	353	2	S33322	(S)-2-hydroxy-acid
428	25	78.1	122	1	PSRSAE	phospholipase A2 (501	25	78.1	353	2	T42517	bromodomain protei
429	25	78.1	122	1	PSRSAE	phospholipase A2 (502	25	78.1	353	2	T06726	cysteine proteinas
430	25	78.1	122	2	A33317	phospholipase A2 (503	25	78.1	368	2	T46607	3-isopropylmalate
431	25	78.1	122	2	A39557	phospholipase A2 (504	25	78.1	387	2	JL0101	methane monooxygen
432	25	78.1	122	2	B37478	phospholipase A2 (505	25	78.1	396	2	E96911	glutamil-tRNA redu
433	25	78.1	122	2	A37478	phospholipase A2 (506	25	78.1	397	2	E69173	protoporphyrin IX
434	25	78.1	122	2	A44179	phospholipase A2 (507	25	78.1	401	2	E96570	hypothetical prote
435	25	78.1	124	2	A26535	phospholipase A2 (508	25	78.1	403	2	T25556	hypothetical prote
436	25	78.1	124	2	A59420	phospholipase A2 (509	25	78.1	407	2	C36786	hypothetical prote
437	25	78.1	125	2	A45660	lysozyme (EC 3.2.1	510	25	78.1	412	2	C38104	LFY floral meriste
438	25	78.1	129	2	S07290	lysozyme (EC 3.2.1	511	25	78.1	420	2	B38104	LFY floral meriste
439	25	78.1	129	2	G35558	lysozyme (EC 3.2.1	512	25	78.1	423	2	E84751	hypothetical protine
440	25	78.1	132	2	I39193	gene HOXA1 protein	513	25	78.1	424	2	AI3606	adenosylmethionine
441	25	78.1	133	2	B30242	stem cell protein	514	25	78.1	424	2	A38104	LFY floral meriste
442	25	78.1	135	2	F64779	probable transcript	515	25	78.1	424	2	T35535	probable secreted
443	25	78.1	135	2	A90697	probable transcript	516	25	78.1	429	2	S72829	trehalose-6-phosph
444	25	78.1	137	1	JC4877	phospholipase A2 h	517	25	78.1	435	2	D81272	hypothetical prote
445	25	78.1	137	2	S22388	phospholipase A2 (518	25	78.1	435	2	S55661	hypothetical prote
446	25	78.1	138	1	I51380	phospholipase A2 h	519	25	78.1	456	2	T00090	glycosyltransferas
447	25	78.1	138	2	JC1342	phospholipase A2 (520	25	78.1	465	2	S54089	hypothetical prote
448	25	78.1	138	2	AF0564	copper efflux regu	521	25	78.1	470	2	T04738	hypothetical prote
449	25	78.1	147	1	LZDK	lysozyme (EC 3.2.1	522	25	78.1	476	2	T35528	probable aminotran
450	25	78.1	155	2	C64314	conserved hypochet	523	25	78.1	478	2	F89651	protein T04F8.2 li
451	25	78.1	155	2	C69002	conserved hypochet	524	25	78.1	484	2	T50909	hypothetical prote
452	25	78.1	167	2	T47385	hypothetical prote	525	25	78.1	484	2	T21421	hypothetical prote
453	25	78.1	185	2	H87107	ribosome recycling	526	25	78.1	491	2	T21421	probable cobQ prot
454	25	78.1	186	2	S65723	extracellular hemo	527	25	78.1	499	2	T49064	cytochrome P450-li
455	25	78.1	201	2	S52833	probable heme bind	528	25	78.1	502	2	T24471	hypothetical prote
456	25	78.1	204	2	B84173	hypothetical prote	529	25	78.1	503	2	E70853	probable Zn finger
457	25	78.1	211	2	G84202	hypothetical prote	530	25	78.1	509	2	T02864	probable acid-CoA
458	25	78.1	217	2	T48642	hypothetical prote	531	25	78.1	541	2	S56653	thioglucoisidase (E
459	25	78.1	218	2	G98291	hypothetical prote	532	25	78.1	550	1	KJHUID	iduronate-2-sulfat
460	25	78.1	219	2	JQ1692	aspartic proteinas	533	25	78.1	550	1	KJHUID	hypothetical prote
461	25	78.1	221	2	T07411	proteinase inhibit	534	25	78.1	607	2	F86230	low density lipopr
462	25	78.1	221	2	T07413	proteinase inhibit	535	25	78.1	621	2	I38467	hypothetical prote
463	25	78.1	222	2	I39192	gene HOXA1 protein	536	25	78.1	632	2	T32454	probable beta-gluc
464	25	78.1	231	2	H84535	hypothetical prote	537	25	78.1	636	2	T37843	H-protein promoter
465	25	78.1	264	1	A53239	aminoglycoside-O-p	538	25	78.1	640	2	T51231	B west mating prot
466	25	78.1	271	2	AF1157	phosphomethylpyrim	539	25	78.1	666	2	JQ2150	conserved hypochet
467	25	78.1	271	2	AC1516	phosphomethylpyrim	540	25	78.1	673	1	S01786	annexin VI - mouse

541	25	78.1	673	1	S52844	annexin VI - rat	614	24	75.0	182	2	F97201	hypothetical prote
542	25	78.1	694	2	D87330	sensory box/GGDEF	615	24	75.0	183	2	S05569	signaling protein
543	25	78.1	712	2	T02479	potassium transpor	616	24	75.0	183	2	B90643	Ampl protein limpo
544	25	78.1	743	2	E71432	hypothetical prote	617	24	75.0	183	2	B85494	regulates ampc (im
545	25	78.1	754	2	T45910	hypothetical prote	618	24	75.0	183	2	F69049	conserved ampc (im
546	25	78.1	768	2	T17462	disease resistance	619	24	75.0	184	2	A82371	carbonic anhydrase
547	25	78.1	782	2	I48746	senaphorin C - mou	620	24	75.0	187	2	A10520	Ampl protein (anhy
548	25	78.1	784	2	T65855	hypothetical prote	621	24	75.0	191	2	AC3285	leucine-, isoleuci
549	25	78.1	792	2	G84830	probable potassium	622	24	75.0	206	2	D70628	hypothetical prote
550	25	78.1	797	2	T22294	hypothetical prote	623	24	75.0	210	2	AC0259	hypothetical phage
551	25	78.1	843	1	T01438	hypothetical prote	624	24	75.0	224	2	B96925	hypothetical prote
552	25	78.1	854	1	ORHYLD	LDL receptor precu	625	24	75.0	229	2	T09215	H ₂ -exporting ATPas
553	25	78.1	855	2	T17460	disease resistance	626	24	75.0	230	2	I48685	mast cell proteina
554	25	78.1	855	2	T07015	Cf-4A protein - to	627	24	75.0	242	2	T40458	hypothetical prote
555	25	78.1	860	2	T16892	hypothetical prote	628	24	75.0	244	2	S75653	hypothetical prote
556	25	78.1	881	2	F84404	valyl-tRNA synthet	629	24	75.0	245	2	G82175	hypothetical prote
557	25	78.1	896	2	S48761	trehalose-phosphat	630	24	75.0	252	2	E69034	hypothetical prote
558	25	78.1	931	2	AP3276	ATP-dependent clip	631	24	75.0	256	2	T21238	hypothetical prote
559	25	78.1	956	1	A46016	thrombospondin 3 -	632	24	75.0	262	2	T51409	MADS box protein A
560	25	78.1	956	2	A57121	thrombospondin 3 p	633	24	75.0	272	2	T36770	probable expressio
561	25	78.1	969	2	H69425	modification methy	634	24	75.0	284	2	F82666	phage-related prot
562	25	78.1	996	2	J80237	apolipoprotein E r	635	24	75.0	293	2	S75355	probable lacyl-car
563	25	78.1	1027	2	A56533	chromatin remodel	636	24	75.0	296	2	D36788	hypothetical prote
564	25	78.1	1046	2	F71432	hypothetical prote	637	24	75.0	298	2	A49630	ubiquitin conjugat
565	25	78.1	1049	2	JC4783	sucrose-phosphate	638	24	75.0	301	2	E71482	phosphatidylserine
566	25	78.1	1084	2	T04103	sucrose-phosphate	639	24	75.0	305	2	T27930	hypothetical prote
567	25	78.1	1160	2	F88369	protein unc-52 [im	640	24	75.0	306	2	D82497	ribokinase VCA0131
568	25	78.1	1237	2	E86457	probable RNA helic	641	24	75.0	308	2	A10001	ribokinase [EC 2.7
569	25	78.1	1254	1	A32686	DNA-directed DNA p	642	24	75.0	308	2	T26716	hypothetical prote
570	25	78.1	1268	2	T31420	C-terminal domain-	643	24	75.0	310	2	T30152	hypothetical prote
571	25	78.1	1347	2	F84531	probable retroelem	644	24	75.0	310	2	T43147	hypothetical prote
572	25	78.1	1358	2	A03905	genome polyprotein	645	24	75.0	312	2	S75932	hypothetical prote
573	25	78.1	1444	2	T18856	angiogenesis inhib	646	24	75.0	317	2	C97245	probable phosphohy
574	25	78.1	1451	1	J01719	E2 glycoprotein pr	647	24	75.0	318	2	T39594	ribokinase - fisci
575	25	78.1	1453	2	S41453	spike protein - ca	648	24	75.0	324	2	E82741	thiamin monophosph
576	25	78.1	1460	1	EDBEIP	immediate-early pr	649	24	75.0	326	2	T51941	homocysteine S-met
577	25	78.1	1468	2	S11515	formin - mouse	650	24	75.0	332	2	S44743	C02D5.1 protein -
578	25	78.1	1694	2	JQ1896	hypothetical 191.1	651	24	75.0	343	2	C85020	hypothetical prote
579	25	78.1	2165	2	T21371	hypothetical prote	652	24	75.0	343	2	T03960	r40g2 protein - ri
580	25	78.1	2227	1	GNNYHB	genome polyprotein	653	24	75.0	349	2	AF2967	trehalose utilizat
581	25	78.1	2227	1	GNNYHM	genome polyprotein	654	24	75.0	349	2	E98315	thub protein (AP17
582	25	78.1	2227	1	GNNYHR	genome polyprotein	655	24	75.0	351	2	T22861	hypothetical vpi -
583	25	78.1	2227	1	GNNYK	genome polyprotein	656	24	75.0	354	1	VWVPLJ	coat protein vpi -
584	25	78.1	2228	2	T14029	variant-specific s	657	24	75.0	357	2	S56601	hypothetical 39.8K
585	25	78.1	2230	1	GNNYSA	genome polyprotein	658	24	75.0	357	2	B86137	hypothetical prote
586	25	78.1	2295	2	C88369	protein unc-52 [im	659	24	75.0	357	2	G91295	hypothetical prote
587	25	78.1	2643	2	T29149	hypothetical prote	660	24	75.0	359	2	AH3465	oxidoreductase (EC
588	25	78.1	2764	2	T13949	neurofibromin - fr	661	24	75.0	361	2	T48014	serine/threonine p
589	25	78.1	2802	2	T13945	neurofibromin - fr	662	24	75.0	362	2	E95972	probable sugar upt
590	25	78.1	2802	2	T13947	neurofibromin - fr	663	24	75.0	363	2	C87336	serine proteinase
591	25	78.1	2895	2	H85362	hypothetical prote	664	24	75.0	374	1	A56436	alcohol dehydrogen
592	25	78.1	3078	2	T28432	variant-specific s	665	24	75.0	374	1	DEHUAS	alcohol dehydrogen
593	25	78.1	3375	2	T19821	hypothetical prote	666	24	75.0	375	1	A33909	alcohol dehydrogen
594	25	78.1	3573	2	S23070	erythronolide synt	667	24	75.0	375	1	DEHUAB	hypothetical prote
595	25	78.1	4660	2	T42737	gp330 protein prec	668	24	75.0	380	2	T19096	hypothetical prote
596	25	78.1	4753	1	A47437	LDL-receptor-relat	669	24	75.0	382	2	S50762	hydroxymethylbilan
597	24	75.0	54	2	H81814	probable small sec	670	24	75.0	412	1	G69965	ATP/GTP-binding pr
598	24	75.0	60	2	A54369	fibrinogen recepto	671	24	75.0	425	2	A31026	probable membrane
599	24	75.0	62	2	S01803	chymotrypsin inhib	672	24	75.0	427	1	XUECVS	3-phosphoshikimate
600	24	75.0	73	2	T31219	hypothetical prote	673	24	75.0	427	2	E85616	5-enolpyruvylshiki
601	24	75.0	112	2	A47130	neurotoxin Txi pre	674	24	75.0	427	2	G90752	5-enolpyruvylshiki
602	24	75.0	119	2	JN0403	phospholipase A2 (675	24	75.0	428	2	S41485	sp2 protein - mous
603	24	75.0	119	2	S07528	phospholipase A2 (676	24	75.0	428	2	AD0085	probable type II s
604	24	75.0	149	2	C95917	hypothetical prote	677	24	75.0	432	2	T43476	hypothetical prote
605	24	75.0	150	2	G93840	ferric uptake regu	678	24	75.0	434	2	T01938	hypothetical prote
606	24	75.0	160	2	F82664	hypothetical proté	679	24	75.0	438	2	H70844	probable aminoran
607	24	75.0	164	2	B84766	conserved hypothet	680	24	75.0	442	2	AG2325	hypothetical prote
608	24	75.0	164	2	G71802	hypothetical prote	681	24	75.0	443	2	S56609	yjfy protein - Esc
609	24	75.0	170	2	AG2479	aminoglycoside N6'	682	24	75.0	446	2	S69051	hypothetical prote
610	24	75.0	171	1	B64671	serine O-acetyltra	683	24	75.0	462	2	G69220	sensory transducti
611	24	75.0	171	2	B71845	o-serine acetyltra	684	24	75.0	462	2	A57120	small nuclear ribo
612	24	75.0	172	2	F81439	translation initia	685	24	75.0	462	2	F96842	hypothetical prote
613	24	75.0	173	2	D84644	hypothetical prote	686	24	75.0	481	2	B64585	cag pathogenicity

687	24	75.0	483	2	I40031	uoporphyrin-III C	760	24	75.0	1429	2	S16233	nitric-oxide synth
688	24	75.0	486	2	S43274	gag-like protein -	761	24	75.0	1433	2	G01946	nitric-oxide synth
689	24	75.0	497	2	B97555	hypothetical prote	762	24	75.0	1436	2	A46496	antigen WCl.1 prec
690	24	75.0	497	2	AD2775	fumarate hydratase	763	24	75.0	1484	2	C97196	probable membrane
691	24	75.0	502	2	T02306	probable protein k	764	24	75.0	1584	2	T22674	hypothetical prote
692	24	75.0	510	2	F96649	hypothetical prote	765	24	75.0	2214	2	T16305	hypothetical prote
693	24	75.0	533	2	T49061	hypothetical prote	766	24	75.0	2254	2	T09053	low voltage-activa
694	24	75.0	541	2	A54841	DFT1 protein - Ara	767	24	75.0	4574	2	G02520	plectin - human
695	24	75.0	552	2	C96171	hypothetical prote	768	24	75.0	4684	2	A59404	plectin [imported]
696	24	75.0	557	2	T16656	hypothetical prote	769	24	75.0	4687	1	A39638	plectin - rat
697	24	75.0	557	2	A48434	variant-specific s	770	23	71.9	36	2	C82694	hypothetical prote
698	24	75.0	581	2	B87678	hypothetical prote	771	23	71.9	41	2	S19566	ornatin A3 - leech
699	24	75.0	594	2	A86309	F20D23.3 protein -	772	23	71.9	41	2	S19621	ornatin A2 - leech
700	24	75.0	597	2	T16006	protein kinase C3	773	23	71.9	47	2	A35982	echistatin alpha-2
701	24	75.0	599	2	G71481	probable phosphoen	774	23	71.9	49	2	S53432	echistatin gamma-2
702	24	75.0	600	2	E72027	phosphoenolpyruvat	775	23	71.9	49	2	A32029	echistatin alpha-1
703	24	75.0	600	2	A86537	phosphoenolpyruvat	776	23	71.9	50	2	A69055	hypothetical prote
704	24	75.0	607	2	T45969	mRNA capping enzym	777	23	71.9	55	1	BGHS	spermatid transiti
705	24	75.0	608	2	QJ1462	phosphoenolpyruvat	778	23	71.9	55	1	BGMT	spermatid transiti
706	24	75.0	619	2	A45625	phosphoenolpyruvat	779	23	71.9	55	1	T6BP3D	short toxin 3 - bl
707	24	75.0	622	1	QYCHGC	phosphoenolpyruvat	780	23	71.9	60	1	A39165	calciseptine - bla
708	24	75.0	622	1	QYRTCP	phosphoenolpyruvat	781	23	71.9	60	1	DNVEP4	DNA-binding protei
709	24	75.0	622	2	A45746	phosphoenolpyruvat	782	23	71.9	62	1	S01802	chymotrypsin inhib
710	24	75.0	631	2	T38167	electron transfer	783	23	71.9	62	2	TIIMTC3	chymotrypsin inhib
711	24	75.0	634	2	T17232	hypothetical prote	784	23	71.9	63	1	T36227	hypothetical prote
712	24	75.0	640	2	QYCHQM	phosphoenolpyruvat	785	23	71.9	66	2	A59409	platelet-aggregati
713	24	75.0	640	2	S69546	phosphoenolpyruvat	786	23	71.9	71	2	A59411	platelet-aggregati
714	24	75.0	640	2	T08758	hypothetical prote	787	23	71.9	71	2	A33990	aplaggin - easter
715	24	75.0	647	1	QIFFQM	phosphoenolpyruvat	788	23	71.9	71	2	A59410	platelet aggregati
716	24	75.0	653	2	H97777	DNA helicase II (E	789	23	71.9	73	2	A23731	alloblabin - green
717	24	75.0	654	2	T24168	hypothetical prote	790	23	71.9	73	2	E35982	trigramin gamma -
718	24	75.0	656	2	JC2005	integrin beta-5 ch	791	23	71.9	73	2	D35982	trigramin beta-2 -
719	24	75.0	656	2	B84547	hypothetical prote	792	23	71.9	73	2	B45206	metallothionein 2
720	24	75.0	658	2	F71703	DNA helicase II (u	793	23	71.9	75	2	T16742	hypothetical prote
721	24	75.0	659	2	F70175	rep helicase, sing	794	23	71.9	75	2	G72214	hypothetical prote
722	24	75.0	660	2	T20569	hypothetical prote	795	23	71.9	77	2	AG0590	hypothetical prote
723	24	75.0	680	2	G82526	ATP-dependent DNA	796	23	71.9	81	2	B82599	hypothetical prote
724	24	75.0	713	2	B38992	cadherin 13 precu	797	23	71.9	84	2	IMECE8	colicin E8 immunit
725	24	75.0	727	2	A56879	diacylglycerol kin	798	23	71.9	85	1	I40591	immunity protein 8
726	24	75.0	735	2	AC1946	adenylate cyclase	799	23	71.9	85	2	JQ0327	colicin E8 immunit
727	24	75.0	759	2	D69846	ATP-dependent DNA	800	23	71.9	85	2	C87181	hypothetical prote
728	24	75.0	775	2	C81594	hypothetical prote	801	23	71.9	86	2	A46461	T-cell receptor et
729	24	75.0	775	2	D86549	hypothetical prote	802	23	71.9	86	2	S38920	hypothetical prote
730	24	75.0	775	2	B72074	hypothetical prote	803	23	71.9	86	2	T06986	hypothetical prote
731	24	75.0	792	2	S32244	x-pro dipeptidyl-p	804	23	71.9	88	2	T43992	hypothetical prote
732	24	75.0	795	2	B97294	stage II sporulati	805	23	71.9	93	2	T35660	probable acylphosp
733	24	75.0	796	2	T34805	hypothetical prote	806	23	71.9	93	2	C81102	conserved hypotnet
734	24	75.0	799	2	A38308	integrin beta-5 ch	807	23	71.9	97	2	H72868	AcOrf-150 protein
735	24	75.0	805	2	G87438	DNA helicase II [i	808	23	71.9	99	2	S72839	probable transcrip
736	24	75.0	824	2	AB2829	DNA helicase II [i	809	23	71.9	102	2	E70737	probable whiB3 pro
737	24	75.0	826	2	T01494	trehalose-6-phosph	810	23	71.9	102	2	S15395	tissue kallikrein-
738	24	75.0	827	2	H97606	probable DNA helic	811	23	71.9	104	2	T49850	hypothetical prote
739	24	75.0	827	2	AF3326	DNA helicase II (E	812	23	71.9	105	2	S60590	Ig heavy chain var
740	24	75.0	847	2	C96703	hypothetical prote	813	23	71.9	107	2	PVLAB	parvalbumin beta -
741	24	75.0	851	2	A86200	hypothetical prote	814	23	71.9	108	1	S58825	hypothetical prote
742	24	75.0	853	2	S49876	gamma-adaptin - sm	815	23	71.9	109	2	B69468	nitrogen regulator
743	24	75.0	861	2	T02267	trehalose-6-phosph	816	23	71.9	112	2	H70232	hypothetical prote
744	24	75.0	862	2	E84567	probable trehalose	817	23	71.9	112	2	T35596	probable regulator
745	24	75.0	865	2	H71447	trehalose-6-phosph	818	23	71.9	112	2	H75064	tetracenomycin pol
746	24	75.0	870	2	T31795	hypothetical prote	819	23	71.9	112	2	I84765	brain-derived neur
747	24	75.0	884	2	S53396	telomerase catalyt	820	23	71.9	114	2	B75060	hypothetical prote
748	24	75.0	919	2	T32541	unc-5 protein - Ca	821	23	71.9	114	2	C86412	protein Flk23.7 [i
749	24	75.0	943	2	G84402	dipeptide ABC tran	822	23	71.9	114	2	NGNXXI	nerve growth facto
750	24	75.0	943	2	S59317	DIP2 protein - yea	823	23	71.9	115	1	A58566	hypothetical prote
751	24	75.0	947	1	B44234	unc-5 protein, lon	824	23	71.9	116	2	D84285	nerve growth facto
752	24	75.0	966	1	PIBVBH	RNA Ia protein - b	825	23	71.9	116	2	S28161	hypothetical prote
753	24	75.0	980	2	T05414	protein kinase hom	826	23	71.9	116	2	G84322	50S ribosomal prot
754	24	75.0	983	2	T19874	hypothetical prote	827	23	71.9	117	2	A39426	saxiphilin - bullf
755	24	75.0	1032	2	T20342	pyruvate carboxyla	828	23	71.9	118	2	A37331	secretory protein
756	24	75.0	1127	2	D70671	hypothetical prote	829	23	71.9	121	1	H72507	hypothetical prote
757	24	75.0	1142	2	T30272	hypothetical prote	830	23	71.9	121	2	A81657	conserved hypotnet
758	24	75.0	1250	2	T00454	nitric-oxide synth	831	23	71.9	124	2		
759	24	75.0	1429	2	JN0609	nitric-oxide synth	832	23	71.9	124	2		

833	23	71.9	125	2	A26312	nerve growth facto	906	23	71.9	180	2	C81664	ribosomal protein
834	23	71.9	127	2	B84172	hypothetical prote	907	23	71.9	180	2	B71506	ribosomal protein
835	23	71.9	128	1	I64059	mercuric resistanc	908	23	71.9	180	2	T07702	hypothetical prote
836	23	71.9	128	2	T06028	hypothetical prote	909	23	71.9	180	2	AC3270	hypothetical expor
837	23	71.9	128	2	AB2682	carboxymuconolacto	910	23	71.9	180	2	D87474	conserved hypothet
838	23	71.9	130	2	S66474	cytochrome P450 (C	911	23	71.9	181	2	A64393	hypothetical prote
839	23	71.9	131	2	S66475	cytochrome P450 (C	912	23	71.9	181	2	S77302	hypothetical prote
840	23	71.9	131	2	S23511	thionin type V pre	913	23	71.9	181	2	D69129	conserved hypothet
841	23	71.9	131	2	B53350	hypothetical prote	914	23	71.9	183	2	S36038	bHLH m8 protein -
842	23	71.9	131	2	F70880	hypothetical prote	915	23	71.9	183	2	C83913	hypothetical prote
843	23	71.9	132	2	T48370	hypothetical prote	916	23	71.9	184	2	T13186	hypothetical prote
844	23	71.9	132	2	E82518	hypothetical prote	917	23	71.9	184	2	B87708	hypothetical prote
845	23	71.9	132	2	D83003	hypothetical prote	918	23	71.9	185	1	HLMS2	MHC class I histoc
846	23	71.9	134	2	S66694	histone H2A.HTA3 -	919	23	71.9	186	2	E69537	conserved hypothet
847	23	71.9	135	2	C70890	hypothetical prote	920	23	71.9	187	2	D72501	hypothetical prote
848	23	71.9	136	2	F64416	hypothetical prote	921	23	71.9	187	2	H75606	hypothetical prote
849	23	71.9	137	2	S76936	conserved hypothet	922	23	71.9	190	2	JC4514	TATA-binding prote
850	23	71.9	138	2	B90665	hypothetical prote	923	23	71.9	190	2	H71245	hypothetical prote
851	23	71.9	138	2	E85515	unknown protein en	924	23	71.9	191	2	S54115	complement factor
852	23	71.9	138	2	AI1214	hypothetical prote	925	23	71.9	191	2	E75072	transcription init
853	23	71.9	139	2	E71110	hypothetical prote	926	23	71.9	191	2	S56012	XS-2 protein (homo
854	23	71.9	140	2	F69010	hypothetical prote	927	23	71.9	191	2	A81870	hypothetical prote
855	23	71.9	141	2	G87702	conserved hypothet	928	23	71.9	191	2	D72711	hypothetical prote
856	23	71.9	146	2	A25233	replication protei	929	23	71.9	191	2	D71093	probable TATA-bind
857	23	71.9	146	2	H84259	hypothetical prote	930	23	71.9	193	2	T35847	probable carbonic
858	23	71.9	147	2	C84338	hypothetical prote	931	23	71.9	193	2	PQ0503	surface protein -
859	23	71.9	148	2	B70964	hypothetical prote	932	23	71.9	193	2	PQ0504	hypothetical prote
860	23	71.9	149	2	AG1991	hypothetical prote	933	23	71.9	193	2	H64174	hypothetical prote
861	23	71.9	150	2	C82994	conserved hypothet	934	23	71.9	193	2	B64435	hypothetical prote
862	23	71.9	150	2	S15914	hypothetical prote	935	23	71.9	193	2	AI2628	hypothetical prote
863	23	71.9	153	2	H81413	hypothetical prote	936	23	71.9	195	2	E27733	nifQ protein - Azo
864	23	71.9	154	2	A60998	replication protei	937	23	71.9	195	2	T32819	hypothetical prote
865	23	71.9	154	2	B81810	hypothetical prote	938	23	71.9	195	2	A85364	hypothetical prote
866	23	71.9	156	2	T49921	ribosomal protein-1	939	23	71.9	197	2	S25825	polygalacturonase
867	23	71.9	156	2	S70970	bfgu protein - Esc	940	23	71.9	197	2	C83003	imidazoleglycerol-
868	23	71.9	156	2	A70968	hypothetical prote	941	23	71.9	200	2	F95985	conserved hypothet
869	23	71.9	157	1	EDXP3	immediate-early pr	942	23	71.9	201	2	S12789	GTP-binding protei
870	23	71.9	157	2	S77122	hypothetical prote	943	23	71.9	203	2	G84284	hypothetical prote
871	23	71.9	157	2	H89967	hypothetical prote	944	23	71.9	203	2	AI0367	probable lipoprote
872	23	71.9	158	1	T05710	2S albumin precurs	945	23	71.9	205	2	E84334	hypothetical prote
873	23	71.9	158	1	YQBZN	fimbrial protein p	946	23	71.9	205	2	T08272	probable thioredox
874	23	71.9	158	2	A29827	replication protei	947	23	71.9	206	2	T08285	hypothetical prote
875	23	71.9	158	2	A61069	replication protei	948	23	71.9	206	2	T20376	hypothetical prote
876	23	71.9	158	2	T30791	hypothetical prote	949	23	71.9	206	2	E83047	hypothetical prote
877	23	71.9	158	2	B42508	F15L protein - vac	950	23	71.9	206	2	T33097	hypothetical prote
878	23	71.9	158	2	D82782	hypothetical prote	951	23	71.9	206	2	C82588	conserved hypothet
879	23	71.9	159	2	I94615	coagulation factor	952	23	71.9	207	2	A48608	E1 glycoprotein -
880	23	71.9	160	2	PL0105	anti-PR2 erythrocy	953	23	71.9	208	1	S26196	imidazoleglycerol-
881	23	71.9	160	2	F81844	hypothetical prote	954	23	71.9	208	2	A82077	MutT/nudix family
882	23	71.9	161	2	T28477	hypothetical prote	955	23	71.9	209	2	A83524	hypothetical prote
883	23	71.9	161	2	E72155	E15L protein - var	956	23	71.9	209	2	B42687	neurotrophin-4 pre
884	23	71.9	161	2	A36841	C19L protein - var	957	23	71.9	210	2	A42687	neurotrophin-4 pre
885	23	71.9	162	2	B87655	conserved hypothet	958	23	71.9	210	2	D85098	hypothetical prote
886	23	71.9	162	2	B24497	replication protei	959	23	71.9	210	2	T15105	hypothetical prote
887	23	71.9	162	2	E69011	3-isopropylmalate	960	23	71.9	212	2	A25856	ubiquitin thiolest
888	23	71.9	164	2	B84283	hypothetical prote	961	23	71.9	212	2	E86561	glycerol-3-P acylt
889	23	71.9	164	2	G84290	hypothetical prote	962	23	71.9	212	2	B72063	probable 1-acylgly
890	23	71.9	164	2	AC3046	hypothetical prote	963	23	71.9	212	2	H81344	hypothetical prote
891	23	71.9	164	2	S57074	HTT1 protein - yea	964	23	71.9	213	2	T03911	DNA binding protei
892	23	71.9	167	2	T43621	hypothetical prote	965	23	71.9	213	2	S50799	probable membrane
893	23	71.9	168	2	B64333	formate hydrogenly	966	23	71.9	214	2	H82314	conserved hypothet
894	23	71.9	168	2	B69059	acetylactate synth	967	23	71.9	214	2	A70593	probable tmk prote
895	23	71.9	169	2	AC0556	conserved hypothet	968	23	71.9	214	2	T19247	hypothetical prote
896	23	71.9	169	2	T15611	hypothetical proté	969	23	71.9	215	1	C69015	probable uracil ph
897	23	71.9	172	2	T39026	conserved hypothet	970	23	71.9	216	2	S49483	somatotropin precu
898	23	71.9	172	2	F84393	hypothetical prote	971	23	71.9	217	2	T31449	dheme cytochrome-
899	23	71.9	174	2	H97463	gamma-carboxymucon	972	23	71.9	219	2	F83160	two-component resp
900	23	71.9	175	2	T51077	hypothetical prote	973	23	71.9	219	2	F70779	hypothetical prote
901	23	71.9	175	2	D86699	hypothetical prote	974	23	71.9	221	2	T04238	hypothetical prote
902	23	71.9	177	2	T32766	hypothetical prote	975	23	71.9	222	2	E84283	TRK potassium upta
903	23	71.9	178	2	E81151	conserved hypothet	976	23	71.9	223	2	JX0222	ubiquitin thiolest
904	23	71.9	179	2	S03627	neurogenic gene co	977	23	71.9	223	2	A81068	hypothetical prote
905	23	71.9	179	2	T22521	hypothetical prote	978	23	71.9	225	2	AH0839	probable transcrip

979 23 71.9 225 2 T20325 hypothetical prote
980 23 71.9 226 2 D70540 probable decthiobio
981 23 71.9 226 2 T14675 hypothetical prote
982 23 71.9 227 2 T10510 cbbY protein - Rho
983 23 71.9 227 2 B71358 hypothetical prote
984 23 71.9 228 2 S28019 gene iofap protein
985 23 71.9 229 2 T46614 nerve growth facto
986 23 71.9 230 2 T51265 probable HLH DNA b
987 23 71.9 230 2 AH1864 hypothetical prote
988 23 71.9 231 2 A60468 venombin A (EC 3.4
989 23 71.9 231 2 A10372 hypothetical prote
990 23 71.9 232 2 A87363 dnaj family protei
991 23 71.9 232 2 T14939 hypothetical prote
992 23 71.9 233 2 D69181 hypothetical prote
993 23 71.9 234 2 T30427 probable apoptosis
994 23 71.9 235 1 B41326 nitrite hydratase
995 23 71.9 235 2 S14481 nerve growth facto
996 23 71.9 235 2 JC4603 conserved hypothet
997 23 71.9 236 2 JH0400 neurotrophin-4 pre
998 23 71.9 237 2 C95370 probable oxidoredu
999 23 71.9 238 2 AF3608 two component resp
1000 23 71.9 238 2 T11718 hypothetical prote

ALIGNMENTS

RESULT 1
G64320
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: G64320
R;Bult, C.O.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Frazer, C.M.; Smith, H.O.; Woese, C
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: G64320
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-255 <BUL>
A:Cross-references: UNIPROT:Q57630; GB:U67473; GB:L77117; NID:g2826256; PIDN:AAB98148.1;
C:Genetics:
A:Map position: REV170194-169427
C:Superfamily: Pyrococcus horikoshii hypothetical protein PH0006

Query Match 100.0%; Score 32; DB 2; Length 255;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRGDD 5
Db 233 CRGDD 237

RESULT 2
T44599
C:Species: Rhizobium meliloti
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T44599
R;Kroll, E.A.; Soberon, M.; Yurgel, S.N.; Miranda Rios, J.; Simarov, B.V.
submitted to the EMBL Data Library, May 1999
A:Accession: T44599
A:Reference number: Z22806
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-289 <KRO>
A:Cross-references: UNIPROT:Q9X6W2; EMBL:AF148072; PIDN:AAD39993.1
A:Experimental source: strain CXM1-188

C:Genetics:
A:Gene: oppC
A:Map position: megaplasmid 2
A:Genome: plasmid
C:Superfamily: oligopeptide permease protein oppB
Query Match 100.0%; Score 32; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRGDD 5
Db 36 CRGDD 40
RESULT 3
AG1072
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AG1072
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
; S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AG1072
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD03398.1; PID:g16505667; GSPDB:GN00176
C:Genetics:
A:Gene: STY4914
Query Match 100.0%; Score 32; DB 2; Length 357;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRGDD 5
Db 139 CRGDD 143
RESULT 4
G95937
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: G95937
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernanc
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: G95937
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-363 <PAR>
A:Cross-references: UNIPROT:Q92VE0; GB:AL591985; PIDN:CAC49167.1; PID:g15140652; GSPDB:G
C:Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: SMB21263

A:Genome: plasmid
C:Superfamily: oligopeptide permease protein oppB

Query Match 100.0%; Score 32; DB 2; Length 363;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRGDD 5
Db 110 CRGDD 114

RESULT 5

AB0617
nicotinate phosphoribosyltransferase (EC 2.4.2.11) - Salmonella typhimurium
C:Species: Salmonella typhimurium
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A39130
R:Vinitsky, A.; Teng, H.; Grubmeyer, C.T.
J. Bacteriol. 173, 536-540, 1991
A:Title: Cloning and nucleic acid sequence of the Salmonella typhimurium pncB gene and
A:Reference number: A39130; MUID:91100340; PMID:1987148
A:Accession: A39130
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-400 <VIN>
A:Cross-references: UNIPROT:P22253; GB:M55986; NID:gl54268; PIDN:AAA27190.1; PID:gl54268
C:Genetics:
A:Gene: pncB
C:Function:
A:Pathway: nicotinate and nicotinamide metabolism
C:Superfamily: nicotinate phosphoribosyltransferase
C:Keywords: glycosyltransferase; pentosyltransferase

Query Match 100.0%; Score 32; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRGDD 5
Db 41 CRGDD 45

RESULT 6

JQ0756
nicotinate phosphoribosyltransferase (EC 2.4.2.11) - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: JQ0756; B64833
R:Wubbolds, M.G.; Terpstra, P.; van Beilen, J.B.; Kingma, J.; Meesters, H.A.R.; Witholt,
J. Biol. Chem. 265, 17665-17672, 1990
A:Title: Variation of cofactor levels in Escherichia coli; sequence analysis and express
A:Reference number: JQ0756; MUID:91009224; PMID:2211655
A:Accession: JQ0756
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-400 <WUB>
A:Cross-references: UNIPROT:P18133; GB:J05569; NID:gl47306; PIDN:AAA24400.1; PID:gl47307
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: B64833
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-400 <BLAT>
A:Cross-references: GB:AB000195; GB:U00096; NID:gl787156; PIDN:AAC74017.1; PID:gl787162;
A:Experimental source: strain K-12, substrain MGL655
C:Genetics:
A:Gene: pncB
C:Function:

A:Pathway: nicotinate and nicotinamide metabolism
C:Superfamily: nicotinate phosphoribosyltransferase
C:Keywords: glycosyltransferase; pentosyltransferase

Query Match 100.0%; Score 32; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRGDD 5
Db 41 CRGDD 45

RESULT 7

AB0617
nicotinate phosphoribosyltransferase [imported] - Salmonella enterica subsp. enterica ser
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AB0617
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AB0617
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-400 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD05404.1; PID:gl6502165; GSPDB:GN00176
C:Genetics:
A:Gene: STY1010
C:Superfamily: nicotinate phosphoribosyltransferase

Query Match 100.0%; Score 32; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRGDD 5
Db 41 CRGDD 45

RESULT 8

F90755
nicotinate phosphoribosyltransferase [imported] - Escherichia coli (strain O157:H7, subst
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: F90755
R:Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F90755
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-400 <HAY>
A:Cross-references: UNIPROT:Q8XDE8; GB:BA000007; PIDN:BA834437.1; PID:gl13360473; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECa1014
C:Superfamily: nicotinate phosphoribosyltransferase

Query Match 100.0%; Score 32; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRGDD 5
Db 41 CRGDD 45

```

RESULT 9
D85619
nicotinate phosphoribosyltransferase [imported] - Escherichia coli (strain O157:H7, sub
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: D85619
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: D85619
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-400 <STO>
A;Cross-references: UNIPROT:Q8XDE8; GB:AB005174; NID:G12514106; PIDN:AAG55416.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: pncB
C;Superfamily: nicotinate phosphoribosyltransferase

Query Match 100.0%; Score 32; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 41 CRGDD 45

RESULT 10
S75313
serine-tRNA ligase (EC 6.1.1.11) - Synechocystis sp. (strain PCC 6803)
N;Alternate names: protein slr703; seryl-tRNA synthetase
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S75313
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
S.
A;Reference number: S74322; MUID:97061203; PMID:8905231
A;Accession: S75313
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-430 <KAN>
A;Cross-references: UNIPROT:P73201; EMBL:D90904; GB:AB001339; NID:G1652225; PIDN:BAAL722
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Gene: serS
A;Start codon: GTG
C;Function:
A;Description: charges tRNA(Ser) with serine
A;Pathway: protein biosynthesis
C;Superfamily: serine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ATP; ligase; protein biosynthesis

Query Match 100.0%; Score 32; DB 2; Length 430;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 228 CRGDD 232

RESULT 11
T38073
serine/threonine-protein kinase mhk1 - fission yeast (Schizosaccharomyces pombe)

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C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38073
R;Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, April 1996
A;Reference number: Z21767
A;Accession: T38073
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1116 <CON>
A;Cross-references: UNIPROT:Q10407; EMBL:Z70630; PIDN:CAA94620.1; GSPDB:GNO0066; SPDB:SP
A;Experimental source: strain 972h-; cosmid c1F3
C;Genetics:
A;Gene: pmk1; SPDB:SPAC1F3.02c
A;Map position: 1

Query Match 100.0%; Score 32; DB 2; Length 1116;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 677 CRGDD 681

RESULT 12
T47183
hypothetical protein DKFZp434K1822.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47183
R;Blum, H.; Bauersachs, S.; Mewes, H.W.; Weil, B.; Wiemann, S.
submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24379
A;Accession: T47183
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-264 <AAA>
A;Cross-references: UNIPROT:Q9NSJ7; EMBL:AL162082
A;Experimental source: adult testis; clone DKFZp434K1822
C;Genetics:
A;Note: DKFZp434K1822.1
C;Superfamily: deubiquinating enzyme SSV7

Query Match 90.6%; Score 29; DB 2; Length 264;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 17 CRGDD 21

RESULT 13
A95408
hypothetical protein SMA2147 [imported] - Sinorhizobium meliloti (strain 1021) magaplasmi
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: A95408
R;Barnett, M.J.; Fisher, R.P.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yen, K.C.;
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: A95408
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-296 <KUR>
A;Cross-references: UNIPROT:Q92XS2; GB:AB006469; PIDN:AAK65827.1; PID:G14524331; GSPDB:G
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.

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Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, heault, P.; Vandenbol, M.; Vorholter, F.U.; Weidner, S.; Wells, D.H.; Wong, K.; Yen, K.

A;Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.

A;Reference number: A96039; MUID:21368234; PMID:11474104

C;Genetics:

A;Gene: Sma2147

A;Genome: plasmid

Query Match 90.6%; Score 29; DB 2; Length 296;

Best Local Similarity 80.0%; Pred. No. 1.3e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5

Db 5 CKGDD 9

RESULT 14

F96743 probable C2H2-type zinc finger protein F28P5.6 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: F96743

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: F96743

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-413 <STO>

A;Cross-references: UNIPROT:Q9C7G8; GB:AE005173; NID:g11054410; PIDN:AAG27797.1; GSPDB:G

C;Genetics:

A;Gene: F28P5.6

A;Map position: 1

Query Match 90.6%; Score 29; DB 2; Length 413;

Best Local Similarity 80.0%; Pred. No. 1.7e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5

Db 191 CKGDD 195

RESULT 15

T16422

hypothetical protein F52C9.3 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C;Accession: T16422

R;Favell, T.

submitted to the EMBL Data Library, November 1995

A;Description: The sequence of *C. elegans* cosmid F52C9.

A;Reference number: 218511

A;Accession: T16422

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-732 <FAV>

A;Cross-references: EMBL:U39850; NID:g1055052; PID:g1055058; PIDN:AAA81060.1; CESP:F52C9

C;Genetics:

A;Gene: CESP:F52C9.3

A;Introns: 63/1; 106/3; 148/2; 303/1; 347/1; 408/2; 650/2

Query Match 90.6%; Score 29; DB 2; Length 732;

Best Local Similarity 80.0%; Pred. No. 2.9e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5

Db 643 CKGDD 647

RESULT 16

F82078

topoisomerase IV, chain A VC2430 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1

C;Species: *Vibrio cholerae*

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: F82078

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: F82078

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-761 <HEI>

A;Cross-references: UNIPROT:Q9KPE0; GB:AE004312; GB:AE003852; NID:g9656995; PIDN:AAF9557;

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC2430

A;Map position: 1

C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomerase (I

Query Match 90.6%; Score 29; DB 2; Length 761;

Best Local Similarity 80.0%; Pred. No. 3e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5

Db 611 CKGDD 615

RESULT 17

A36453

decorsin - leech (*Macrobdella decora*)

C;Species: *Macrobdella decora*

C;Date: 08-Mar-1991 #sequence_revision 08-Mar-1991 #text_change 09-Jul-2004

C;Accession: A36453

R;Seymour J.L.; Henzel, W.J.; Nevins, B.; Stults, J.T.; Lazarus, R.A.

J. Biol. Chem. 265, 10143-10147, 1990

A;Title: Decorsin. A potent glycoprotein IIB-IIIa antagonist and platelet aggregation in

A;Reference number: A36453; MUID:90277628; PMID:2351655

A;Accession: A36453

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-39 <SEY>

A;Cross-references: UNIPROT:PI7350

Query Match 87.5%; Score 28; DB 2; Length 39;

Best Local Similarity 80.0%; Pred. No. 35;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5

Db 7 CQGDD 11

RESULT 18

DNVPE

DNA-binding protein - polyomavirus BK

N;Alternate names: agnoprotein

C;Species: Polyomavirus hominis 1 (polyomavirus BK)

C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004

C;Accession: B03632; B36762; JQ0627; A03632

R;Self, I.; Khoury, G.; Dhar, R.
Cell 18, 963-977, 1979
A;Title: The genome of human papovavirus BKV
A;Reference number: A03632; MUID:80090082; PMID:229976
A;Accession: B03632
A;Molecule type: DNA
A;Residues: 1-66 <SEI>
A;Cross-references: UNIPROT:P03085; GB:V01108; GB:J02038; NID:G60844; PIDN:CAA24296.1; R
A;Experimental source: strain Dunlop
R;Yang, R.C.A.; Wu, R.
Science 206, 456-462, 1979
A;Title: BK virus DNA: complete nucleotide sequence of a human tumor virus.
A;Reference number: A36762; MUID:80058557; PMID:228391
A;Accession: B36762
A;Molecule type: DNA
A;Residues: 1-66 <YAN>
A;Cross-references: GB:V01109; GB:J02039; NID:G60851; PIDN:CAA24304.1; PID:G60854
A;Experimental source: strain MM
R;Moens, U.; Sundsfjord, A.; Flegstad, T.; Traavik, T.
J. Gen. Virol. 71, 1461-1471, 1990
A;Title: BK virus early RNA transcripts in stably transformed cells: Enhanced levels ind
A;Reference number: JQ0627; MUID:90324932; PMID:2165132
A;Accession: JQ0627
A;Molecule type: Genomic RNA
A;Residues: 1-66 <MOE>
A;Cross-references: DBJ:D00678; NID:G222309; PIDN:BAA00584.1; PID:G222311
A;Experimental source: strain BKT-1B
R;Jay, G.; Nomura, S.; Anderson, C.W.; Khoury, G.
Nature 291, 346-349, 1981
A;Title: Identification of the SV40 agnogene product: a DNA binding protein.
A;Reference number: A93257; MUID:81197675; PMID:6262654
A;Contents: annotation; identification of the protein
C;Comment: This protein, encoded by the agnogene, is also called agnoprotein. It may hav
C;Superfamily: polyomavirus DNA-binding protein
C;Keywords: DNA binding

Query Match 87.5%; Score 28; DB 1; Length 66;
Best Local Similarity 80.0%; Pred. No. 56;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
|||:
Db 40 CRGED 44

RESULT 19
DNVPAS
DNA-binding protein - polyomavirus BK (strain AS)
N;Alternate names: agnoprotein
C;Species: Polyomavirus hominis 1 (polyomavirus BK)
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
C;Accession: C33278
R;Tavie, J.E.; Walker, D.L.; Gardner, S.D.; Friesque, R.J.
J. Virol. 63, 901-911, 1989
A;Title: Nucleotide sequence of the human polyomavirus AS virus, an antigenic variant of
A;Reference number: A33278; MUID:89095020; PMID:2536111
A;Accession: C33278
A;Molecule type: DNA
A;Residues: 1-74 <TAV>
A;Cross-references: UNIPROT:P14998; GB:M23122; NID:G332774; PIDN:AAA46879.1; PID:G332776
C;Comment: The DNA sequence was obtained from Genbank, release 61.0.
C;Superfamily: polyomavirus DNA-binding protein
C;Keywords: DNA binding

Query Match 87.5%; Score 28; DB 1; Length 74;
Best Local Similarity 80.0%; Pred. No. 62;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
|||:
Db 48 CRGED 52

RESULT 20
I67436
interleukin-1-beta-converting enzyme and ced-3 homolog-1, long isoform - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I67436
R;Flaws, J.A.; Kugu, K.; Trbovich, A.M.; DeSanti, A.; Tilly, K.I.; Hirschfield, A.N.; Tili
Endocrinology 136, 5042-5053, 1995
A;Title: interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian cell
nucosa cells of the ovarian follicle.
A;Reference number: I53300; MUID:96042508; PMID:7588240
A;Accession: I67436
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-182 <RES>
A;Cross-references: UNIPROT:P55215; EMBL:U34684; NID:G1004368; PIDN:AAC52260.1; PID:G1004

Query Match 87.5%; Score 28; DB 2; Length 182;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
|||:
Db 123 CRGDE 127

RESULT 21
S76342
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S76342
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76342
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-234 <KAN>
A;Cross-references: UNIPROT:Q57208; EMBL:D64000; GB:AB001339; NID:G1001484; PIDN:BAA10194
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Mg2+-transporting ATPase

Query Match 87.5%; Score 28; DB 2; Length 234;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
|||:
Db 153 CRGDE 157

RESULT 22
B55649
TNFR-associated protein EBI6 - human
C;Species: Homo sapiens (man)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Accession: B55649
R;Mosialos, G.; Birkenbach, M.; Yalamanchili, R.; VanArsdale, T.; Ware, C.; Kieff, E.
Cell 80, 389-399, 1995
A;Title: The Epstein-Barr virus transforming protein LMP1 engages signaling proteins for
A;Reference number: A55649; MUID:95163092; PMID:7859281
A;Accession: B55649
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-416 <MOS>
A;Cross-references: UNIPROT:Q13077; GB:U19261; NID:G675461; PIDN:AAA62309.1; PID:G675462

Query Match 87.5%; Score 28; DB 2; Length 416;
 Best Local Similarity 80.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
 |||||
 Db 57 CRGED 61

RESULT 23
 B82611
 conserved hypothetical protein XF1995 [imported] - Xylella fastidiosa (strain 9a5c)
 C/Species: Xylella fastidiosa
 C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C/Accession: B82611
 R/Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
 Nature 406, 151-157, 2000
 A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A/Reference number: A82515; MUID:20365717; PMID:10910347
 A/Note: for a complete list of authors see reference number A59328 below
 A/Accession: B82611
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-423 <STM>
 A/Cross-references: UNIPROT:Q9PBZ0; GB:AE004019; GB:AE003849; NID:g9107105; PIDN:AAF8479
 A/Experimental source: strain 9a5c
 R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
 as-Neto, E.; Docena, C.; El-Dokry, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
 A/Authors: Martins, E.M.P.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
 , F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A/Authors: da Silva, A.C.R.; da Silva, P.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Tshunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A/Reference number: A59328
 A/Contents: annotation
 C/Genetics:
 A/Gene: XF1995

Query Match 87.5%; Score 28; DB 2; Length 423;
 Best Local Similarity 80.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
 |||||
 Db 313 CRGDE 317

RESULT 24
 T14237
 hypothetical protein ORF427 - Synechococcus sp. (strain PCC 7002)
 C/Species: Synechococcus sp.
 A/Variety: strain PCC 7002
 C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C/Accession: T14237
 R/Klughammer, B.; Sultemeyer, D.; Badger, M.R.; Price, G.D.
 submitted to the EMBL Data Library, April 1997
 A/Description: Involvement of ndhF3, ndhD3 and ORF427 genes in high affinity CO2 uptake
 A/Reference number: Z17936
 A/Accession: T14237
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-427 <KLJ>
 A/Cross-references: UNIPROT:O33751; EMBL:U97516; NID:g2232044; PID:g2232048; PIDN:AA8621
 A/Experimental source: strain PCC 7002
 C/Supfamily: uncharacterized conserved protein alr4158

Query Match 87.5%; Score 28; DB 2; Length 427;
 Best Local Similarity 80.0%; Pred. No. 2.9e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
 |||||
 Db 352 CRGED 356

RESULT 25
 S77330
 hypothetical protein sll1734 - Synechocystis sp. (strain PCC 6803)
 C/Species: Synechocystis sp.
 A/Variety: PCC 6803
 C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C/Accession: S77330
 R/Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O, K.; Okumura, S.; Shingo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,
 DNA Res. 3, 109-136, 1996
 A/Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
 S.
 A/Reference number: S74322; MUID:97061201; PMID:8905231
 A/Accession: S77330
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-431 <KAN>
 A/Cross-references: UNIPROT:P73393; EMBL:D90906; GB:AB001339; NID:gl652492; PIDN:BAAL743;
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C/Supfamily: uncharacterized conserved protein alr4158

Query Match 87.5%; Score 28; DB 2; Length 431;
 Best Local Similarity 80.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
 |||||
 Db 356 CRGED 360

RESULT 26
 A54821
 apoptosis regulator ICH-1, stimulatory form L - human
 C/Species: Homo sapiens (man)
 C/Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 09-Jul-2004
 C/Accession: A54821
 R/Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
 Cell 76, 739-750, 1994
 A/Title: Ich-1, an I κ B/c κ B-3-related gene, encodes both positive and negative regulators
 A/Reference number: A54821; MUID:94373811; PMID:8087842
 A/Accession: A54821
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-435 <WAN>
 A/Cross-references: UNIPROT:P42575; GB:U13021; NID:g537291; PID:g537292
 C/Keywords: alternative splicing; apoptosis

Query Match 87.5%; Score 28; DB 2; Length 435;
 Best Local Similarity 80.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
 |||||
 Db 303 CRGDE 307

RESULT 27
 JC6507
 caspase-2 - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C/Accession: JC6507
 R/Sato, N.; Milligan, C.E.; Uchiyama, Y.; Oppenheim, R.W.
 Gene 202, 127-132, 1997
 A/Title: cloning and expression of the cDNA encoding rat caspase-2.
 A/Reference number: JC6507; MUID:98087427; PMID:9427555

A/Accession: JC6507
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-452 <SAT>
A/Cross-references: UNIPROT:O55194; GB:U77933; NID:g2769705; PIDN:AAB96379.1; PID:g27697

Query Match 87.5%; Score 28; DB 2; Length 452;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
Db 320 CRGDE 324
|||||

RESULT 28
E72376
hypothetical protein TM0434 - Thermotoga maritima (strain MSB8)
C/Species: Thermotoga maritima
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C/Accession: E72376; F72298
R/Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.N.
Nature 399, 323-329, 1999
A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A/Reference number: A72200; MUID:99287316; PMID:10360571
A/Accession: E72376
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-470 <ARN>
A/Cross-references: UNIPROT:Q9WVR5; GB:AE001722; NID:g4980938; PIDN:AAD3551
A/Experimental source: strain MSB8
A/Accession: F72298
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-415, 'A', 417-464, 'GS', <AR2>
A/Cross-references: GB:AE001767; GB:AE000512; NID:g4981611; PIDN:AAD36145.1; PID:g498161
C/Genetics:
A/Gene: TM0434; TM1068
C/Superfamily: melibiose-specific alpha-galactosidase

Query Match 87.5%; Score 28; DB 2; Length 470;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
Db 216 CRGED 220
|||||

RESULT 29
T24497
hypothetical protein T05A6.4 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T24497
R/Thomas, K.
submitted to the EMBL Data Library, August 1995
A/Reference number: Z19899
A/Accession: T24497
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-490 <WIL>
A/Cross-references: UNIPROT:Q22200; EMBL:Z50796; PIDN:CAA90668.1; GSPDB:GN00020; CESP:T0
A/Experimental source: clone T05A6
C/Genetics:
A/Gene: CESP:T05A6.4
A/Map position: 2
A/Introns: 39/1; 125/1; 189/1; 286/3; 432/3; 474/1
C/Superfamily: Caenorhabditis elegans hypothetical protein T05A6.4

Query Match 87.5%; Score 28; DB 2; Length 452;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
Db 320 CRGDE 324
|||||

RESULT 28
E72376
hypothetical protein TM0434 - Thermotoga maritima (strain MSB8)
C/Species: Thermotoga maritima
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C/Accession: E72376; F72298
R/Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.N.
Nature 399, 323-329, 1999
A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A/Reference number: A72200; MUID:99287316; PMID:10360571
A/Accession: E72376
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-470 <ARN>
A/Cross-references: UNIPROT:Q9WVR5; GB:AE001722; NID:g4980938; PIDN:AAD3551
A/Experimental source: strain MSB8
A/Accession: F72298
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-415, 'A', 417-464, 'GS', <AR2>
A/Cross-references: GB:AE001767; GB:AE000512; NID:g4981611; PIDN:AAD36145.1; PID:g498161
C/Genetics:
A/Gene: TM0434; TM1068
C/Superfamily: melibiose-specific alpha-galactosidase

Query Match 87.5%; Score 28; DB 2; Length 470;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
Db 216 CRGED 220
|||||

RESULT 29
T24497
hypothetical protein T05A6.4 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T24497
R/Thomas, K.
submitted to the EMBL Data Library, August 1995
A/Reference number: Z19899
A/Accession: T24497
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-490 <WIL>
A/Cross-references: UNIPROT:Q22200; EMBL:Z50796; PIDN:CAA90668.1; GSPDB:GN00020; CESP:T0
A/Experimental source: clone T05A6
C/Genetics:
A/Gene: CESP:T05A6.4
A/Map position: 2
A/Introns: 39/1; 125/1; 189/1; 286/3; 432/3; 474/1
C/Superfamily: Caenorhabditis elegans hypothetical protein T05A6.4

Query Match 87.5%; Score 28; DB 2; Length 490;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
Db 190 CRGDE 194
|||||

RESULT 30
T18896
glypican 1 precursor - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T18896; T22999
R/Lloyd, C.
submitted to the EMBL Data Library, November 1996
A/Reference number: Z19040
A/Accession: T18896
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-521 <WIL>
A/Cross-references: UNIPROT:O17900; EMBL:Z81459; PIDN:CAB03828.1; GSPDB:GN00028; CESP:F5;
A/Experimental source: clone C03H12
R/Lloyd, C.
submitted to the EMBL Data Library, November 1996
A/Reference number: Z19649
A/Accession: T22999
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-521 <WI2>
A/Cross-references: EMBL:Z81558; PIDN:CAB04542.1; GSPDB:GN00028; CESP:F59D12.4
A/Experimental source: clone F59D12
C/Genetics:
A/Gene: CESP:F59D12.4
A/Map position: X
A/Introns: 74/1; 134/3; 192/3; 247/1; 290/3; 339/3; 403/1; 450/3
C/Keywords: glycoprotein; lipoprotein; membrane protein; phosphoprotein

Query Match 87.5%; Score 28; DB 2; Length 521;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
Db 355 CRGED 359
|||||

RESULT 31
T22137
hypothetical protein F43G6.6 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T22137
R/Swinburne, J.
submitted to the EMBL Data Library, July 1995
A/Reference number: Z19522
A/Accession: T22137
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-548 <WIL>
A/Cross-references: UNIPROT:Q20367; EMBL:Z50070; NID:e1519046; PIDN:CAA90395.1; GSPDB:GN0;
A/Experimental source: clone F43G6
C/Genetics:
A/Gene: CESP:F43G6.6
A/Map position: 2
A/Introns: 78/1; 120/2; 228/2; 296/3; 421/1; 547/1

Query Match 87.5%; Score 28; DB 2; Length 548;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5

```

Db          |||||:
           503 CRGDE 507

RESULT 32
T51525
hypothetical protein T20K14_80 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C:Accession: T51525
R:Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, H.; Kotani, H.; Tabata, S.; Mew
submitted to the Protein Sequence Database, August 2000
A:Reference number: 225394
A:Accession: T51525
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-572 <SAT>
A:Cross-references: UNIPROT:Q9LFP35; EMBL:AL391143
A:Experimental source: cultivar Columbia; BAC clone T20K14
C:Genetics:
A:Map position: 5
A:Introns: 43/2; 114/1; 129/3; 181/3; 378/3; 479/3
A:Note: T20K14_80

Query Match      87.5%; Score 28; DB 2; Length 572;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDD 5
      |||||:
Db      418 CRGED 422

RESULT 33
E81684
1-deoxyxylulose-5-phosphate synthase TC0608 [imported] - Chlamydia muridarum (strain Nig
C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: E81684
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: E81684
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-632 <TET>
A:Cross-references: UNIPROT:Q9PK62; GB:AE002329; GB:AE002160; NID:g7190640; PIDN:AAF3943
A:Experimental source: strain Nigg (MoPn)
C:Genetics:
A:Gene: TC0608
C:Superfamily: deoxyxylulose-5-phosphate synthase

Query Match      87.5%; Score 28; DB 2; Length 632;
Best Local Similarity 80.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDD 5
      |||||:
Db      501 CQGGD 505

RESULT 34
T00602
hypothetical protein At2g02620 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein T8K22.8
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C:Accession: T00602; G84438
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, June 1998
A:Description: Arabidopsis thaliana chromosome II BAC T8K22 genomic sequence.

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A:Reference number: Z14192
A:Accession: T00602
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-635 <ROU>
A:Cross-references: UNIPROT:O64715; EMBL:AC004136; NID:g3184270; PID:g3184278
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: G84438
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-635 <STO>
A:Cross-references: GB:AE002093; NID:g3184278; PIDN:AAC18925.1; GSPDB:GN00139
C:Genetics:
A:Gene: T8K22.8; At2g02620
A:Map position: 2
A:Introns: 18/3

Query Match      87.5%; Score 28; DB 2; Length 635;
Best Local Similarity 80.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDD 5
      |||||:
Db      532 CRGDE 536

RESULT 35
D84823
hypothetical protein At2g39950 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: D84823
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.
euss, D.; Nierman, W.C.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: D84823
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-635 <STO>
A:Cross-references: UNIPROT:O04198; GB:AE002093; NID:g2088648; PIDN:AAB95280.1; GSPDB:GNC
C:Genetics:
A:Gene: At2g39950
A:Map position: 2

Query Match      87.5%; Score 28; DB 2; Length 636;
Best Local Similarity 80.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CRGDD 5
      |||||:
Db      88 CRGDE 92

RESULT 36
F71527
probable transketolase - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C>Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C:Accession: F71527
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trach
A:Reference number: A71570; MUID:9900809; PMID:9784136
A:Accession: F71527

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-640 <ARN>
A;Cross-references: UNIPROT:O84335; GB:AE001306; NID:G3328748; PIDN:AA06752
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: dxa
C;Superfamily: deoxyxylulose-5-phosphate synthase

Query Match 87.5%; Score 28; DB 2; Length 640;
Best Local Similarity 80.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
|:|:|
Db 503 CQGGD 507

RESULT 37

T00859
Hypothetical protein At2g02690 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein T2086.17; hypothetical protein T8K22.1
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: T00859; T00595; F84439
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, March 1998
A;Description: Arabidopsis thaliana chromosome II BAC T20P6 genomic sequence.
A;Reference number: Z14206
A;Accession: T00859
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-657 <ROU>
A;Cross-references: UNIPROT:Q858R7; EMBL:AC002521; NID:g2947056; PID:g2947072
A;Experimental source: cultivar Columbia
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, June 1998
A;Description: Arabidopsis thaliana chromosome II BAC T8K22 genomic sequence.
A;Reference number: Z14192
A;Accession: T00595
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-613 <ROW>
A;Cross-references: EMBL:AC004136; NID:g3184270; PID:g3184271
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: F84439

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-657 <STO>
A;Cross-references: GB:AE002093; NID:g2947072; PIDN:AA05353.1; GSPDB:GN00139
C;Genetics:
A;Gene: T20P6.17; T8K22.1; At2g02690
A;Map position: 2
A;Introns: 471/3; 489/2; 560/3; 583/3

Query Match 87.5%; Score 28; DB 2; Length 657;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
|:|:|
Db 500 CRGDE 504

RESULT 38

E70770
probable atp-dependent helicase ding - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: E70770
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: E70770
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-664 <COL>
A;Cross-references: UNIPROT:Q10640; GB:Z73902; GB:AL123456; NID:g3261576; PIDN:CAA98093.1
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: ding

Query Match 87.5%; Score 28; DB 2; Length 664;
Best Local Similarity 80.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
|:|:|
Db 517 CQGGD 521

RESULT 39

JH0798
fasciclin IV precursor - American bird grasshopper
C;Species: Schistocerca americana (American bird grasshopper)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JH0798
R;Kolodkin, A.; Matthes, D.J.; O'Connor, T.P.; Patel, N.H.; Admon, A.; Bentley, D.; Good
Neuron 9, 831-845, 1992
A;Title: Fasciclin IV: sequence, expression, and function during growth cone guidance in
A;Reference number: JH0798; MUID:93040225; PMID:1418998
A;Accession: JH0798
A;Molecule type: mRNA
A;Residues: 1-730 <KOL>
A;Cross-references: UNIPROT:Q26473; GB:L00709; NID:g160844; PID:g160845
A;Experimental source: embryo
C;Comment: This protein plays a role in growth cone guidance in the developing central ne
C;Keywords: glycoprotein; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-730/Product: fasciclin IV #status predicted <MAT>
F;23-627/Domain: extracellular #status predicted <EXT>
F;628-652/Domain: transmembrane #status predicted <TM>
F;653-730/Domain: intracellular #status predicted <INT>
F;44,71,163,267,360,539/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 87.5%; Score 28; DB 2; Length 730;
Best Local Similarity 80.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
|:|:|
Db 655 CRGED 659

RESULT 40

C83177
probable phosphotransferase protein PA3760 [imported] - Pseudomonas aeruginosa (strain P
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: C83177
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bri
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Loty, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: CB31177
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-842 <STO>
 A:Cross-references: UNIPROT:Q9HXN5; GB:AE004794; GB:AE004091; NID:g9949917; PIDN:AAG0714
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA3760

Query Match 87.5%; Score 28; DB 2; Length 842;
 Best Local Similarity 80.0%; Pred. No. 5.2e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
 Db 237 CRGDD 241

RESULT 41

MWXR31

lambda 3 protein - reovirus type 1 (strain Lang)

N:Alternate names: minor core protein

C:Species: reovirus type 1

C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004

C:Accession: A30121

R:Wiener, J.R.; Joklik, W.K.

Virology 169, 194-203, 1989

A:Title: The sequences of the reovirus serotype 1, 2, and 3 L1 genome segments and analysis

A:Reference number: A94390; MUID:89163254; PMID:2922925

A:Accession: A30121

A:Molecule type: genomic RNA

A:Residues: 1-1267 <NIE>

A:Cross-references: UNIPROT:P17376; GB:M24734; NID:g499863

A:Note: This sequence, which matches the sequence attributed to type 1 in Fig. 2, matches the translations in entries REOLAM3P and REO3LAM3P now differ only by the sequence correction.

C:Genetics:

A:Map position: segment L1

C:Superfamily: reovirus lambda 3 protein

C:Keywords: core protein

Query Match 87.5%; Score 28; DB 1; Length 1267;

Best Local Similarity 80.0%; Pred. No. 7.5e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
 Db 731 CQGGD 735

RESULT 42

MWXR32

lambda 3 protein - reovirus type 2 (strain D5/Jones)

N:Alternate names: minor core protein

C:Species: reovirus type 2

C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004

C:Accession: B30121

R:Wiener, J.R.; Joklik, W.K.

Virology 169, 194-203, 1989

A:Title: The sequences of the reovirus serotype 1, 2, and 3 L1 genome segments and analysis

A:Reference number: A94390; MUID:89163254; PMID:2922925

A:Accession: B30121

A:Molecule type: genomic RNA

A:Residues: 1-1267 <NIE>

A:Cross-references: UNIPROT:P17377; GB:M31057; NID:g499865; PIDN:AAA47245.1; PID:g499866

C:Genetics:

A:Map position: segment L1

C:Superfamily: reovirus lambda 3 protein

C:Keywords: core protein

Query Match 87.5%; Score 28; DB 1; Length 1267;

Best Local Similarity 80.0%; Pred. No. 7.5e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5

Db 731 CQGGD 735

RESULT 43

MWXR33

lambda 3 protein - reovirus type 3 (strain Dearing)

N:Alternate names: minor core protein

C:Species: reovirus type 3

C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004

C:Accession: C30121

R:Wiener, J.R.; Joklik, W.K.

Virology 169, 194-203, 1989

A:Title: The sequences of the reovirus serotype 1, 2, and 3 L1 genome segments and analysis

A:Reference number: A94390; MUID:89163254; PMID:2922925

A:Accession: C30121

A:Molecule type: genomic RNA

A:Residues: 1-1267 <NIE>

A:Cross-references: UNIPROT:P17378; GB:M31058; NID:g499867; GB:M24734; NID:g499863; PIDN:

A:Note: This sequence, which matches the sequence attributed to type 3 in Fig. 2, matches the translations in entries REOLAM3P and REO3LAM3P now differ only by the sequence correction apparently made.

C:Comment: See also PIR:MWXR31.

C:Genetics:

A:Map position: segment L1

C:Superfamily: reovirus lambda 3 protein

C:Keywords: core protein

Query Match 87.5%; Score 28; DB 1; Length 1267;

Best Local Similarity 80.0%; Pred. No. 7.5e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
 Db 731 CQGGD 735

RESULT 44

T37533

coronin-like protein - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T37533

R:Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.

submitted to the EMBL Data Library, August 1997

A:Reference number: Z21721

A:Accession: T37533

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-1323 <MUR>

A:Cross-references: UNIPROT:O13686; EMBL:Z98595; PIDN:CAB11184.1; GSPDB:GN00066; SPDB:SP/

A:Experimental source: strain 972h-; cosmid c11E3

C:Genetics:

A:Gene: SPDB:SPAC11E3.05

A:Map position: 1

Query Match 87.5%; Score 28; DB 2; Length 1323;

Best Local Similarity 80.0%; Pred. No. 7.8e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
 Db 514 CRGED 518

RESULT 45

T23298

hypothetical protein K04B12.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T23298

R;Steward, C.
submitted to the EMBL Data Library, December 1996
A;Reference number: Z19723
A;Accession: T23298
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1806 <WIL>
A;Cross-references: UNIPROT:O45657; EMBL:Z83232; PIDN:CA805755.1; GSPDB:GN00020; CESP:K04B12
A;Experimental source: clone K04B12
C;Genetics:
A;Gene: CESP:K04B12.1
A;Map position: 2
A;Introns: 24/2; 77/3; 294/2; 378/3; 433/3; 478/3; 523/3; 743/1; 794/3; 1049/3; 1414/3;

Query Match 87.5%; Score 28; DB 2; Length 1806;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
| | | | |
Db 305 CRGED 309

RESULT 46
T18524
scavenger receptor cysteine-rich protein homolog srcrm2 - Geodia cydonium
C;Species: Geodia cydonium
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18524
R;Blumbach, B.; Pancer, Z.; Diehl-Seifert, B.; Steffen, R.; Muenkner, J.; Mueller, I.; M
J. Cell Sci. 111, 2635-2644, 1998
A;Title: The putative sponge aggregation receptor: Isolation and characterization of a m
A;Reference number: Z18947; MUID:98369060; PMID:9701562
A;Accession: T18524
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-2043 <BLU>
A;Cross-references: UNIPROT:O96943; EMBL:Y14953; NID:e1364818; PID:e1364819; PIDN:CAA751
C;Genetics:
A;Gene: SRCRM2

Query Match 87.5%; Score 28; DB 2; Length 2043;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
| | | | |
Db 1440 CRGDE 1444

RESULT 47
T18397
protein CTRP - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18397
R;Trottein, F.; Trigilia, T.; Cowman, A.F.
Mol. Biochem. Parasitol. 74, 129-142, 1995
A;Title: Molecular cloning of a gene from Plasmodium falciparum that codes for a protein
A;Reference number: Z18926; MUID:96360471; PMID:8719155
A;Accession: T18397
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-2098 <PRO>
A;Cross-references: UNIPROT:Q25757; EMBL:U34363; NID:gl098897; PID:gl098898; PIDN:AA469

Query Match 87.5%; Score 28; DB 2; Length 2098;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
| | | | |
Db 293 CQGGD 297

RESULT 48
T18995
hypothetical protein C06B8.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18995
R;Steward, C.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19057
A;Accession: T18995
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-3036 <WIL>
A;Cross-references: UNIPROT:O17575; EMBL:Z81463; PIDN:CA803852.1; GSPDB:GN00023; CESP:CO6
A;Experimental source: clone C06B8
C;Genetics:
A;Gene: CESP:CO6B8.7
A;Map position: 5
A;Introns: 102/3; 157/2; 288/2; 439/3; 542/1; 591/3; 798/3; 835/3; 1139/1; 1204/3; 1325/1

Query Match 87.5%; Score 28; DB 2; Length 3036;
Best Local Similarity 80.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
| | | | |
Db 2068 CRGDE 2072

RESULT 49
T19FBP
proteinase inhibitor - flesh fly (Sarcophaga bullata)
C;Species: Sarcophaga bullata
C;Date: 07-Feb-1992 #sequence_revision 22-Jul-1994 #text_change 09-Jul-2004
C;Accession: A37294
R;Papayannopoulos, I.A.; Blemann, K.
Protein Sci. 1, 278-288, 1992
A;Title: Amino acid sequence of a protease inhibitor isolated from Sarcophaga bullata det
A;Reference number: A37294; MUID:93284121; PMID:1304909
A;Accession: A37294
A;Molecule type: protein
A;Residues: 1-57 <PAP>
A;Cross-references: UNIPROT:P26228
A;Experimental source: hemolymph
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolc
C;Keywords: serine proteinase inhibitor
F;6-56/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;6-56,15-39,31-52/Disulfide bonds: #status predicted
F;16/Inhibitory site: Arg (chymotrypsin) #status predicted

Query Match 84.4%; Score 27; DB 1; Length 57;
Best Local Similarity 80.0%; Pred. No. 79;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
| | | | |
Db 39 CRGND 43

RESULT 50
AI3045
hypothetical protein Atu3981 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AI3045
R;Wood, D.W.; Secubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E
ster, E.W.

A>Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AF3045

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-130 <KUR>

A;Cross-references: UNIPROT:Q8UBV7; GB:AE008689; PIDN:AAL44783.1; PID:gl7742422; GSPDB:C

A;Experimental source: strain C58 (Dupont)

C;Genetics:

A;Gene: Atu3981

A;Map position: linear chromosome

Query Match 84.4%; Score 27; DB 2; Length 130;

Best Local Similarity 80.0%; Pred. No. 1.6e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRGDD 5

Db 60 CEGDD 64

RESULT 51

HmrR heavy metal dependent transcription regulator [imported] - *Sinorhizobium meliloti* C

C;Species: *Sinorhizobium meliloti*

C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C;Accession: E95330

R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows

; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A>Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti*

A;Reference number: A95262; MUID:21396509; PMID:11481432

A;Accession: E95330

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-138 <KUR>

A;Cross-references: GB:AE006469; PIDN:AAK65207.1; PID:gl4523654; GSPDB:GN00165

A;Experimental source: strain 1021, megaplasmid pSymA

R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,

pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,

hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.

A>Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.

A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation

C;Genetics:

A;Gene: hmrR

A;Genome: plasmid

C;Superfamily: transcription repressor glnR

Query Match 84.4%; Score 27; DB 2; Length 138;

Best Local Similarity 80.0%; Pred. No. 1.7e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRGDD 5

Db 104 CEGDD 108

RESULT 52

C95369

probable transcription regulator, merR family protein [imported] - *Sinorhizobium meliloti*

C;Species: *Sinorhizobium meliloti*

C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C;Accession: C95969

R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A>Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo

A;Reference number: A95842; MUID:21396508; PMID:11481431

A;Accession: C95969

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-147 <KUR>

A;Cross-references: UNIPROT:P58379; GB:AL591985; PIDN:CAC49419.1; PID:gl5140905; GSPDB:G

A;Experimental source: strain 1021, megaplasmid pSymB

R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,

pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,

hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.

A>Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.

A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation

C;Genetics:

A;Gene: hmrR2; SMB21579

A;Genome: plasmid

C;Superfamily: transcription repressor glnR

Query Match 84.4%; Score 27; DB 2; Length 147;

Best Local Similarity 80.0%; Pred. No. 1.8e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRGDD 5

Db 112 CEGDD 116

RESULT 53

A60585

thyroglobulin - slider turtle (fragments)

C;Species: *Pseudemys scripta* (slider)

C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004

C;Accession: A60585

R;Roe, M.T.; Anderson, P.C.; Dunn, A.D.; Dunn, J.T.

Endocrinology 124, 1327-1332, 1989

A>Title: The homonogenic sites of turtle thyroglobulin and their homology with those of

A;Reference number: A60585; MUID:89136909; PMID:2917515

A;Accession: A60585

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-153 <PROE>

A;Cross-references: UNIPROT:Q7LZC7

C;Superfamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat homolc

Query Match 84.4%; Score 27; DB 2; Length 153;

Best Local Similarity 80.0%; Pred. No. 1.9e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRGDD 5

Db 68 CEGDD 72

RESULT 54

H64803

ybfp protein - *Escherichia coli* (strain K-12)

N;Alternate names: protein b0689

C;Species: *Escherichia coli*

C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004

C;Accession: H64803

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col

.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A>Title: The complete genome sequence of *Escherichia coli* K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: H64803

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-164 <BLAT>

A;Cross-references: UNIPROT:P75737; GB:AE000172; GB:U000096; NID:gl786896; PIDN:AAC73783.1

A;Experimental source: strain K-12, substrain MG1655

C;Genetics:

A;Gene: ybfp

C;Keywords: transmembrane protein

F;7-23/Domain: transmembrane #status predicted <TMM>

Query Match 84.4%; Score 27; DB 2; Length 164;
 Best Local Similarity 80.0%; Pred. No. 2e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 |||||
 Db 63 CRGDN 67

RESULT 55

A70734

Probable cutinase precursor - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C;Accession: A70734

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, M.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Sgares, R.; Sultston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: A70734

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-219 <COL>

A;Cross-references: GB:277163; GB:AL123456; NID:g3261610; PIDN:CAB00997.1; PID:g1449318

A;Experimental source: strain H37RV

C;Genetics:

A;Gene: Rv2301

C;Superfamily: cutinase

Query Match 84.4%; Score 27; DB 2; Length 219;
 Best Local Similarity 80.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRGDD 5
 |||||
 Db 174 CHGDD 178

RESULT 56

A44805

eggshell protein precursor - fluke (Schistosoma haematobium)

C;Species: Schistosoma haematobium

C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 09-Jul-2004

C;Accession: A44805

R;Bobek, L.A.; LeVerde, P.T.; Rekosh, D.M.

Exp. Parasitol. 68, 17-30, 1989

A;Title: Schistosoma haematobium: analysis of eggshell protein genes and their expression

A;Reference number: A44805; MUID:89137380; PMID:2917627

A;Accession: A44805

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-220 <BOB>

A;Cross-references: UNIPROT:O96853; GB:M27659

A;Status: preliminary

A;Accession: C44805

A;Molecule type: DNA

A;Cross-references: GB:M27658; NID:g160978; PID:g150979

C;Superfamily: fluke eggshell protein

C;Keywords: egg shell

F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-220/Product: eggshell protein #status predicted <MAT>

Query Match 84.4%; Score 27; DB 2; Length 220;
 Best Local Similarity 80.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRGDD 5
 |||||
 Db 118 CHGDD 122

RESULT 57

F64859

Putative lambdaoid prophage e14 repressor protein C2 - Escherichia coli (strain K-12) cryI

C;Species: Escherichia coli

C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004

C;Accession: F64859

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col

.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: F64859

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-224 <BLAT>

A;Cross-references: UNIPROT:P75974; GB:AE000214; GB:U000096; NID:g1787382; PIDN:AAC74229.1

A;Experimental source: strain K-12, substrain MG1655

C;Genetics:

A;Genome: cryptic prophage e14

C;Superfamily: repressor protein cI

Query Match 84.4%; Score 27; DB 2; Length 224;
 Best Local Similarity 80.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRGDD 5
 |||||
 Db 158 CHGDD 162

RESULT 58

T15553

hypothetical protein C18B2.2 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C;Accession: T15553

R;Stellies, L.

submitted to the EMBL Data Library, November 1995

A;Description: The sequence of C. elegans cosmid C18B2.

A;Reference number: Z18368

A;Accession: T15553

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-255 <STE>

A;Cross-references: EMBL:U40413; NID:g1065467; PID:g1065472; PIDN:AAA81402.1; CESP:C18B2.

C;Genetics:

A;Gene: CESP.C18B2.2

A;Introns: 75/3; 108/3; 157/2; 206/2

Query Match 84.4%; Score 27; DB 2; Length 255;
 Best Local Similarity 80.0%; Pred. No. 3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 |||||
 Db 159 CRGDN 163

RESULT 59

C56084

interleukin-beta converting enzyme delta isozyme - human

C;Species: Homo sapiens (man)

C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004

C;Accession: C56084

R;Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.

J. Biol. Chem. 270, 4312-4317, 1995

A;Title: Cloning and expression of four novel isoforms of human interleukin-beta convert

A;Reference number: A56084; MUID:95181414; PMID:7876192

A;Accession: C56084
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-263 <ALN>
A;Cross-references: UNIPROT:P29466; GB:U13699; NID:g717043; PIDN:AAC50109.1; PID:g717044
C;Genetics:
A;Gene: IL1BCE
C;Keywords: alternative splicing

Query Match 84.4%; Score 27; DB 2; Length 263;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 192 CRGDN 196

RESULT 60
AF0402
transketolase (EC 2.2.1.1) [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AF0402
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
ell, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AF0402
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-276 <KUR>
A;Cross-references: UNIPROT:Q82BT1; GB:AL590842; PIDN:CAC92546.1; PID:gl5981244; GSPDB:G
C;Genetics:
A;Gene: YPO3314
C;Superfamily: transketolase, N-terminal subunit; ferredoxin 2[4fe-4s] homology
C;Keywords: transferase

Query Match 84.4%; Score 27; DB 2; Length 276;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
Db 213 CRGND 217

RESULT 61
F85835
hypothetical protein Z3252 [imported] - Escherichia coli (strain O157:H7, substrain EDL935)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: F85835
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: AB5480; MUID:21074935; PMID:11206551
A;Accession: F85835
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-299 <STO>
A;Cross-references: UNIPROT:Q8X7H7; GB:AB005174; NID:gl2516292; PIDN:AGS7146.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z3252

Query Match 84.4%; Score 27; DB 2; Length 299;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

A;Molecule type: DNA
A;Residues: 1-323 <SPT>
A;Cross-references: UNIPROT:Q9KBI4; GB:AP001513; GB:BA000004; NID:g10174345; PIDN:BA0566
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH1943

Query Match 84.4%; Score 27; DB 2; Length 323;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRGDD 5
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|
|
Db 248 CRGDD 252

RESULT 65
GV2ML
T2 protein - myxoma virus (strain Lausanne)
C;Species: myxoma virus
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A40566
R;Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.
Virolgy 184, 370-382, 1991
A;Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis factor- α receptor
A;Reference number: A40566; MUID:91335768; PMID:1651597
A;Accession: A40566
A;Molecule type: DNA
A;Residues: 1-326 <UPT>
A;Cross-references: UNIPROT:P29825; GB:M95181; GB:M37976; NID:g332309; PIDN:AAA46632.1;
C;Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology
C;Keywords: glycoprotein
F;64-105/Domain: NGF receptor repeat homology <NG2>
F;106-147/Domain: NGF receptor repeat homology <NG3>
F;66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 84.4%; Score 27; DB 1; Length 326;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
|
|
|
|
Db 28 CRGDD 32

RESULT 66
B42476
hypothetical protein 14.1 - Salmonella typhi (strain Ty2)
C;Species: Salmonella typhi
C;Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 09-Jul-2004
C;Accession: B42476
R;Liu, D.; Verna, N.K.; Romana, L.K.; Reeves, P.R.
J. Bacteriol. 173, 4814-4819, 1991
A;Title: Relationships among the rfb regions of Salmonella serovars A, B, and D.
A;Reference number: A42476; MUID:91310590; PMID:1856174
A;Accession: B42476
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-333 <LIU>
A;Cross-references: UNIPROT:Q99192; GB:M65054; NID:g154334; PIDN:AAB49395.1; PID:g154336

Query Match 84.4%; Score 27; DB 2; Length 333;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
|
|
|
|
Db 221 CRGDD 225

RESULT 67
S15309
hypothetical protein 14.1 - Salmonella typhimurium

C;Species: Salmonella typhimurium
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S15309
R;Jiang, X.M.; Neal, B.; Santiago, F.; Lee, S.J.; Romana, L.K.; Reeves, P.R.
Mol. Microbiol. 5, 695-713, 1991
A;Title: Structure and sequence of the rfb (O antigen) gene cluster of Salmonella serovar
A;Reference number: S15296; MUID:91260454; PMID:1710759
A;Accession: S15309
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-333 <MOL>
A;Cross-references: UNIPROT:P26401

Query Match 84.4%; Score 27; DB 2; Length 333;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
|
|
|
|
Db 221 CRGDD 225

RESULT 68
AC0766
probable glycosyltransferase rfbV [imported] - Salmonella enterica subsp. enterica serovar
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC0766
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AC0766
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-333 <PAR>
A;Cross-references: UNIPROT:Q99192; GB:AL513382; PIDN:CAD02449.1; PID:g16503316; GSPDB:GN
C;Genetics:
A;Gene: rfbV

Query Match 84.4%; Score 27; DB 2; Length 333;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
|
|
|
|
Db 221 CRGDD 225

RESULT 69
H70517
probable lppD protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: H70517
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sgares, R.; Sultston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: H70517
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-343 <COL>
A;Cross-references: GB:Z97193; GB:AL123456; NID:g3261816; PIDN:CAB10035.1; PID:g324870; I
A;Experimental source: strain H37RV
C;Genetics:

A;Gene: lppD

Query Match 84.4%; Score 27; DB 2; Length 343;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
|
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|
|
Db 166 CRGDN 170

RESULT 70

H70722

Probable transferase - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: H70722
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Ruter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: H70722

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-346 <COL>

A;Cross-references: UNIPROT:Q50587; GB:277826; GB:AL123456; NID:g3261623; PIDN:CAB01396.
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv1520

Query Match

Best Local Similarity 84.4%; Score 27; DB 2; Length 346;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRGDD 5
|
|
|
|
Db 88 CRGDD 92

RESULT 71

F84550

hypothetical protein At2g17310 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: F84550
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: F84550

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-370 <STO>

A;Cross-references: UNIPROT:Q8LL17; GB:AE002093; NID:g2262162; PIDN:AAB86508.1; GSPDB:GN
C;Genetics:
A;Gene: At2g17310
A;Map position: 2

C;Superfamily: Arabidopsis thaliana hypothetical protein F2AM12.210

Query Match 84.4%; Score 27; DB 2; Length 370;
Best Local Similarity 80.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRGDD 5
|
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|
|
Db 322 CRGDD 326

RESULT 72

A84972

nicotinate phosphoribosyltransferase (EC 2.4.2.11) [imported] - Buchnera sp. (strain APS)

C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: A84972

R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.

Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. At
A;Reference number: A84930; MUID:20445173; PMID:10993077

A;Accession: A84972

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-399 <STO>

A;Cross-references: GB:AP000398; GSPDB:GN00144

A;Experimental source: strain APS

C;Genetics:

A;Gene: pncB; BU361

C;Superfamily: nicotinate phosphoribosyltransferase

C;Keywords: glycosyltransferase; pentosyltransferase

Query Match 84.4%; Score 27; DB 2; Length 399;
Best Local Similarity 80.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
|
|
|
|
Db 41 CRGDN 45

RESULT 73

C64398

hypothetical protein homolog MJ0787 - Methanococcus jannaschii

C;Species: Methanococcus jannaschii

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C;Accession: C64398

R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, C.; Reisch, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996

A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.

A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.

A;Reference number: A64300; MUID:96337999; PMID:8688087

A;Accession: C64398

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-504 <BUL>

A;Cross-references: UNIPROT:Q58197; GB:U67523; GB:L77117; NID:g2826319; PIDN:AAB98783.1;

C;Genetics:

A;Map position: FOR710775-712289

Query Match 84.4%; Score 27; DB 2; Length 504;
Best Local Similarity 80.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRGDD 5
|
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|
|
Db 465 CRGDD 469

RESULT 74

AD3382

ABC transporter-associated protein BME1042 [imported] - Brucella melitensis (strain 16M)

C;Species: Brucella melitensis

C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C;Accession: AD3382

R;DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltsman, E.; Selkov, E.; Elizer, P.H.; Hagius, S.; O'Callaghan, D.; Letesee
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A;Reference number: AD3252; PMID:11756688

A;Accession: AD3382

A;Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-507 <KUR>
 A:Cross-references: UNIPROT:Q8YGM3; GB:AE008917; PIDN:AAL52223.1; PID:gl7983006; GSPDB:C
 A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BME11042
 A:Map position: 1
 C:Superfamily: conserved hypothetical protein b1693

Query Match 84.4%; Score 27; DB 2; Length 507;
 Best Local Similarity 80.0%; Pred. No. 5.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 |||||
 Db 319 CRGDN 323

RESULT 75
 E27793
 methyl coenzyme M reductase (EC 1.8.-.-) alpha chain - Methanococcus vannielii
 C:Species: Methanococcus vannielii
 C>Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
 C:Accession: E27793
 R:Cram, D.S.; Sherf, B.A.; Libby, R.T.; Mattaliano, R.J.; Ramachandran, K.L.; Reeve, J.N.
 Proc. Natl. Acad. Sci. U.S.A. 84, 3992-3996, 1987
 A>Title: Structure and expression of the genes, mcrBDCGA, which encode the subunits of c
 A:Reference number: A94157
 A:Accession: E27793
 A:Molecule type: DNA
 A:Residues: 1-553 <CRA>
 A:Cross-references: UNIPROT:P07961
 A>Note: the authors translated the codon GAA for residue 396 as Asp
 C:Genetics:
 A:Gene: mcrA
 C:Superfamily: methyl coenzyme M reductase alpha chain
 C:Keywords: metalloprotein; methanogenesis; oxidoreductase
 F:151/Binding site: coenzyme F430 nickel (gln) (axial ligand) #status predicted
 F:336/Active site: Tyr #status predicted
 F:447/Binding site: coenzyme M (Tyr) #status predicted
 F:484/Binding site: coenzyme B (Asn) #status predicted
 Query Match 84.4%; Score 27; DB 2; Length 553;
 Best Local Similarity 80.0%; Pred. No. 5.8e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRGDD 5
 |||||
 Db 85 CRGDD 89

Search completed: September 7, 2005, 20:10:10
 Job time : 54 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 7, 2005, 19:55:25 ; Search time 167 Seconds
(without alignments)
15.332 Million cell updates/sec

Title: US-10-812-238B-41
Perfect score: 32
Sequence: 1 CRGDD 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Uniprot_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	100.0	140	2	Q822Y9 chlamydomophi
2	32	100.0	174	2	Q6ZHH9 oryza sativ
3	32	100.0	187	2	Q9LECI lycopersico
4	32	100.0	199	2	O45047 scirpophaga
5	32	100.0	215	2	Q9MCC2 bacterioph
6	32	100.0	220	2	Q9LEGI lycopersico
7	32	100.0	230	2	Q6D9R3 erwinia car
8	32	100.0	255	1	Y166 METJA
9	32	100.0	280	2	Q9ZMQ4
10	32	100.0	289	2	Q9X6W2
11	32	100.0	304	1	HEM3_XANAC
12	32	100.0	304	1	HEM3_XANCP
13	32	100.0	321	1	LP93_HUMAN
14	32	100.0	321	2	Q6NSI1
15	32	100.0	357	2	Q8ZOU7
16	32	100.0	357	2	Q8ZJW2
17	32	100.0	363	2	Q92VE0
18	32	100.0	372	2	Q98IE7
19	32	100.0	390	2	Q8S9A8
20	32	100.0	393	2	Q8LMH4
21	32	100.0	399	1	PNCB_ECO57
22	32	100.0	399	1	PNCB_ECOLI
23	32	100.0	399	1	PNCB_SALTI
24	32	100.0	399	1	PNCB_SALTY
25	32	100.0	400	2	Q7UDZ7
26	32	100.0	416	2	Q83LN3
27	32	100.0	416	2	Q8FJ98
28	32	100.0	428	2	Q7XF76 oryza sativ
29	32	100.0	430	1	SYS_SYNY3
30	32	100.0	442	1	Q804X1
31	32	100.0	446	2	Q886K3 oryza sativ

32	100.0	446	2	Q8H4V4	Q8H4V4 oryza sativ
33	100.0	448	2	Q8VUB7	Q8VUB7 bradyrhizob
34	100.0	469	2	Q6Z4U6	Q6Z4U6 oryza sativ
35	100.0	491	2	Q7PPD6	Q7PPD6 anopheles g
36	100.0	497	2	Q859H6	Q859H6 bacterioph
37	100.0	497	2	Q9MCC5	Q9MCC5 bacterioph
38	100.0	497	2	Q9KGQ6	Q9KGQ6 vibrio para
39	100.0	640	2	Q8Q861	Q8Q861 pongine her
40	100.0	776	2	Q73RY0	Q73RY0 mycobacteri
41	100.0	934	2	Q8SZX4	Q8SZX4 drosophila
42	100.0	1116	1	MKH1_SCHPO	Q10407 schizosacch
43	100.0	1145	2	Q8JKT0	Q8JKT0 heliothis z
44	100.0	1504	2	Q7PSM9	Q7PSM9 anopheles g
45	100.0	1837	2	Q9VCZ9	Q9VCZ9 drosophila
46	90.6	73	2	Q7QP19	Q7QP19 giardia lam
47	90.6	112	2	Q69T89	Q69T89 oryza sativ
48	90.6	126	2	Q726G7	Q726G7 desulfovibr
49	90.6	168	2	Q8XNS3	Q8XNS3 clostridium
50	90.6	225	2	Q8T399	Q8T399 ciona intes
51	90.6	264	2	Q9NSJ7	Q9NSJ7 homo sapien
52	90.6	276	2	Q8CUR7	Q8CUR7 oceanobacil
53	90.6	296	2	Q92XS2	Q92XS2 rhizobium m
54	90.6	302	2	Q8BJG3	Q8BJG3 mus musculu
55	90.6	319	2	Q7MX77	Q7MX77 porphyromon
56	90.6	324	2	Q940P2	Q940P2 arabidopsis
57	90.6	360	2	Q9LKY3	Q9LKY3 glycine max
58	90.6	360	2	Q9LKY4	Q9LKY4 glycine max
59	90.6	366	2	Q72MX9	Q72MX9 leptospira
60	90.6	366	2	Q8F8R3	Q8F8R3 leptospira
61	90.6	386	2	Q6F1V5	Q6F1V5 candida gla
62	90.6	403	2	Q6EV52	Q6EV52 ciona savi
63	90.6	412	2	Q84M24	Q84M24 arabidopsis
64	90.6	413	2	Q9C7G8	Q9C7G8 arabidopsis
65	90.6	419	2	Q6MK81	Q6MK81 bdellovibri
66	90.6	434	2	Q7YZS7	Q7YZS7 ciona intes
67	90.6	453	2	Q6MZV4	Q6MZV4 homo sapien
68	90.6	519	2	Q8CEG8	Q8CEG8 mus musculu
69	90.6	523	2	Q6GN16	Q6GN16 xenopus lae
70	90.6	525	2	Q66JV8	Q66JV8 mus musculu
71	90.6	525	2	Q9JIG5	Q9JIG5 mus musculu
72	90.6	540	2	Q8BSW2	Q8BSW2 mus musculu
73	90.6	549	2	Q98UH5	Q98UH5 cyprinus ca
74	90.6	553	2	Q69KU3	Q69KU3 oryza sativ
75	90.6	572	2	Q6DCJ1	Q6DCJ1 xenopus lae
76	90.6	593	1	UB22_HUMAN	Q9UPT9 homo sapien
77	90.6	633	2	Q88KQ2	Q88KQ2 pseudomonas
78	90.6	672	2	Q8A4E1	Q8A4E1 bacteroides
79	90.6	737	2	Q654P9	Q654P9 oryza sativ
80	90.6	761	2	Q9RPE0	Q9RPE0 vibrio chol
81	90.6	770	2	Q654V4	Q654V4 oryza sativ
82	90.6	813	2	Q8LLI3	Q8LLI3 oryza sativ
83	90.6	834	2	Q6K2T2	Q6K2T2 oryza sativ
84	90.6	839	2	Q9LIE5	Q9LIE5 arabidopsis
85	90.6	1086	2	Q76C42	Q76C42 arthroderma
86	90.6	1087	2	Q8U2R8	Q8U2R8 microsporium
87	90.6	1089	2	Q76C30	Q76C30 arthroderma
88	90.6	1089	2	Q76C31	Q76C31 arthroderma
89	90.6	1089	2	Q76C32	Q76C32 arthroderma
90	90.6	1089	2	Q76C33	Q76C33 trichophyto
91	90.6	1089	2	Q76C34	Q76C34 trichophyto
92	90.6	1089	2	Q76C35	Q76C35 arthroderma
93	90.6	1089	2	Q76C37	Q76C37 trichophyto
94	90.6	1089	2	Q76C38	Q76C38 arthroderma
95	90.6	1089	2	Q76C44	Q76C44 arthroderma
96	90.6	1093	2	Q8J2S0	Q8J2S0 trichophyto
97	90.6	1094	2	Q8J2R9	Q8J2R9 trichophyto
98	90.6	1097	2	Q8J2S1	Q8J2S1 trichophyto
99	90.6	1696	1	PKK5_BRACL	Q9NJJ5 brachiosteo
100	87.5	39	1	DECO_MACDE	P17350 macrobellia
101	87.5	62	2	Q6GMH9	Q6GMH9 polyomaviru
102	87.5	66	1	DNBI_POVBK	P03085 polyomaviru
103	87.5	66	2	Q656I4	Q656I4 polyomaviru
104	87.5	66	2	Q6GWN3	Q6GWN3 polyomaviru

105	28	87.5	66	2	Q6GWQ7	Q6gwq7 polyomavirus	178	28	87.5	289	2	Q6R7B9	Q6r7b9 ostreid her
106	28	87.5	66	2	Q89856	Q89856 polyomavirus	179	28	87.5	298	2	Q6MJY9	Q6mjy9 bdellovibri
107	28	87.5	74	1	DNBI_POVBA	P14998 polyomavirus	180	28	87.5	301	2	Q87S43	Q87s43 vibrio para
108	28	87.5	82	2	Q8MVZ2	Q8mvz2 ornithodoro	181	28	87.5	307	2	Q6ZLA2	Q6zla2 oryza sativ
109	28	87.5	82	2	Q8MVZ3	Q8mvz3 ornithodoro	182	28	87.5	309	2	Q7IT76	Q7it76 bacterioph
110	28	87.5	98	2	Q7XHM2	Q7xhm2 oryza sativ	183	28	87.5	309	2	Q6INT6	Q6int6 xenopus lae
111	28	87.5	105	2	Q9RJJB5	Q9rjbs streptomyce	184	28	87.5	312	1	ICE2_RAT	P55215 rattus norv
112	28	87.5	106	2	Q69KP7	Q69kp7 oryza sativ	185	28	87.5	312	1	LPP3_MOUSE	Q991y8 mus musculu
113	28	87.5	121	2	Q8V163	Q8v163 reovirus sp	186	28	87.5	312	1	LPP3_RAT	P97544 rattus norv
114	28	87.5	121	2	Q8V164	Q8v164 reovirus sp	187	28	87.5	312	2	Q6IMX4	Q6imx4 rattus norv
115	28	87.5	121	2	Q8V165	Q8v165 reovirus sp	188	28	87.5	325	2	Q7FI67	Q7fi67 oryza sativ
116	28	87.5	121	2	Q8V166	Q8v166 reovirus sp	189	28	87.5	336	2	Q64V52	Q64v52 bacteroides
117	28	87.5	121	2	Q8V167	Q8v167 reovirus sp	190	28	87.5	358	2	Q7Q8Q0	Q7q8q0 anopheles g
118	28	87.5	121	2	Q8V168	Q8v168 reovirus sp	191	28	87.5	362	1	CN29_HUMAN	Q725m8 homo sapien
119	28	87.5	121	2	Q8V169	Q8v169 reovirus sp	192	28	87.5	363	2	Q8TU00	Q8tuc0 methanosarc
120	28	87.5	121	2	Q8V170	Q8v170 reovirus sp	193	28	87.5	372	2	Q98375	Q98375 measles vir
121	28	87.5	121	2	Q8V171	Q8v171 reovirus sp	194	28	87.5	389	2	Q9HIN9	Q9hin9 thermoplas
122	28	87.5	121	2	Q8V172	Q8v172 reovirus sp	195	28	87.5	390	2	Q8N1I7	Q8n1i7 homo sapien
123	28	87.5	121	2	Q8V173	Q8v173 reovirus sp	196	28	87.5	399	2	Q7PYN9	Q7py9 anopheles g
124	28	87.5	121	2	Q8V174	Q8v174 reovirus sp	197	28	87.5	401	2	Q6D454	Q6d454 erwinia car
125	28	87.5	121	2	Q8V175	Q8v175 reovirus sp	198	28	87.5	404	2	Q7N621	Q7n621 photorhabd
126	28	87.5	121	2	Q8V176	Q8v176 reovirus sp	199	28	87.5	404	2	Q6MB08	Q6mb08 parachlamy
127	28	87.5	121	2	Q8V177	Q8v177 reovirus sp	200	28	87.5	414	2	Q87D72	Q87d72 xyella fas
128	28	87.5	121	2	Q8V178	Q8v178 reovirus sp	201	28	87.5	415	2	P97018	P97018 aeromonas j
129	28	87.5	121	2	Q8V179	Q8v179 reovirus sp	202	28	87.5	416	1	TRAI_HUMAN	Q13077 homo sapien
130	28	87.5	121	2	Q8V180	Q8v180 reovirus sp	203	28	87.5	423	2	Q9PBZ0	Q9pbz0 xyella fas
131	28	87.5	121	2	Q8V181	Q8v181 reovirus sp	204	28	87.5	424	1	ICE2_CHICK	Q98943 gallus gall
132	28	87.5	121	2	Q8V182	Q8v182 reovirus sp	205	28	87.5	427	2	O33751	O33751 synecococc
133	28	87.5	121	2	Q8V183	Q8v183 reovirus sp	206	28	87.5	430	2	Q8VPV7	Q8vpv7 synecococc
134	28	87.5	121	2	Q8V184	Q8v184 reovirus sp	207	28	87.5	431	2	P73393	P73393 synecococ
135	28	87.5	121	2	Q8V185	Q8v185 reovirus sp	208	28	87.5	435	1	ICE2_HUMAN	P42575 homo sapien
136	28	87.5	121	2	Q8V186	Q8v186 reovirus sp	209	28	87.5	435	1	ICE2_MOUSE	P29594 mus musculu
137	28	87.5	121	2	Q8V187	Q8v187 reovirus sp	210	28	87.5	435	2	Q8JTB2	Q8jtb2 golden ide
138	28	87.5	121	2	Q8V188	Q8v188 reovirus sp	211	28	87.5	436	2	Q7UY00	Q7uy00 rhodopirell
139	28	87.5	121	2	Q8V189	Q8v189 reovirus sp	212	28	87.5	437	2	Q8DKF3	Q8dkf3 synecococc
140	28	87.5	121	2	Q8V190	Q8v190 reovirus sp	213	28	87.5	450	2	Q9XYF4	Q9xyf4 drosophila
141	28	87.5	121	2	Q8V191	Q8v191 reovirus sp	214	28	87.5	451	2	Q9FB34	Q9fb34 streptomyce
142	28	87.5	121	2	Q8V192	Q8v192 reovirus sp	215	28	87.5	452	2	Q9BUP7	Q9bup7 homo sapien
143	28	87.5	121	2	Q8V193	Q8v193 reovirus sp	216	28	87.5	452	2	O55194	O55194 rattus norv
144	28	87.5	121	2	Q8V194	Q8v194 reovirus sp	217	28	87.5	452	2	Q8C9H7	Q8c9h7 mus musculu
145	28	87.5	121	2	Q8V195	Q8v195 reovirus sp	218	28	87.5	452	2	Q8K241	Q8k241 mus musculu
146	28	87.5	121	2	Q8V196	Q8v196 reovirus sp	219	28	87.5	456	2	Q96UR5	Q96ur5 thermoascus
147	28	87.5	121	2	Q8V197	Q8v197 reovirus sp	220	28	87.5	456	2	Q8S0Y3	Q8s0y3 oryza sativ
148	28	87.5	121	2	Q8V198	Q8v198 reovirus sp	221	28	87.5	457	2	Q8TG37	Q8tg37 thermoascus
149	28	87.5	121	2	Q8V199	Q8v199 reovirus sp	222	28	87.5	466	2	Q9S5X4	Q9s5x4 thermotoga
150	28	87.5	121	2	Q8V1A0	Q8v1a0 reovirus sp	223	28	87.5	469	1	SA50_HUMAN	Q94512 homo sapien
151	28	87.5	121	2	Q8V1A1	Q8v1a1 reovirus sp	224	28	87.5	470	2	Q9WYR5	Q9wyr5 thermotoga
152	28	87.5	121	2	Q8V1A2	Q8v1a2 reovirus sp	225	28	87.5	475	2	Q95PW2	Q95pw2 caenothabdi
153	28	87.5	121	2	Q8V1A3	Q8v1a3 reovirus sp	226	28	87.5	480	2	Q688D5	Q688d5 oryza sativ
154	28	87.5	121	2	Q6RJU0	Q6rju0 reovirus sp	227	28	87.5	490	2	Q22200	Q22200 caenothabdi
155	28	87.5	131	2	Q96CB2	Q96cb2 homo sapien	228	28	87.5	495	2	Q64ZB9	Q64zb9 bacteroides
156	28	87.5	136	2	Q8Q0A9	Q8q0a9 pseudomonas	229	28	87.5	505	2	Q96I80	Q96i80 homo sapien
157	28	87.5	137	2	Q69N67	Q69n67 oryza sativ	230	28	87.5	510	2	Q9MAB8	Q9mab8 arabidopsis
158	28	87.5	151	2	Q7QRP2	Q7qrp2 giardia lam	231	28	87.5	532	2	Q8GWT1	Q8gwt1 arabidopsis
159	28	87.5	154	2	Q8BUS2	Q8bus2 mus musculu	232	28	87.5	535	2	Q9FPH36	Q9fph36 arabidopsis
160	28	87.5	160	2	Q89D66	Q89d66 bradyrhizob	233	28	87.5	540	2	O76771	O76771 dictyosteli
161	28	87.5	165	2	Q684H5	Q684h5 drosophila	234	28	87.5	543	2	O17900	O17900 caenothabdi
162	28	87.5	168	2	Q8GVK1	Q8gvk1 oryza sativ	235	28	87.5	548	2	Q20367	Q20367 caenothabdi
163	28	87.5	177	2	Q7TV51	Q7tv51 prochloroco	236	28	87.5	572	2	Q9LFF35	Q9lff35 arabidopsis
164	28	87.5	177	2	Q8V6L9	Q8v6l9 halovirus h	237	28	87.5	575	2	Q97BA5	Q97ba5 thermoplas
165	28	87.5	177	2	Q7TDD3	Q7tdg3 halovirus h	238	28	87.5	580	2	Q8NMP7	Q8nmp7 corynebacte
166	28	87.5	185	2	Q68IK5	Q68ik5 helicobacte	239	28	87.5	584	2	Q8EJB2	Q8ejb2 shewanella
167	28	87.5	195	2	Q9VRN5	Q9vrn5 drosophila	240	28	87.5	596	2	Q8RYR5	Q8ryr5 oryza sativ
168	28	87.5	196	2	Q6EP29	Q6ep29 oryza sativ	241	28	87.5	607	2	Q8E9M8	Q8e9m8 shewanella
169	28	87.5	210	2	Q8IR71	Q8ir71 drosophila	242	28	87.5	610	2	Q9XHZ1	Q9xhz1 oryza sativ
170	28	87.5	210	2	Q70QV2	Q70qv2 human immun	243	28	87.5	613	2	Q8S8R7	Q8s8r7 arabidopsis
171	28	87.5	220	2	Q8LI15	Q8li15 oryza sativ	244	28	87.5	616	2	Q8N9M3	Q8n9m3 homo sapien
172	28	87.5	222	2	Q7XZ47	Q7xz47 griffithsia	245	28	87.5	617	2	Q9ARR6	Q9arr6 oryza sativ
173	28	87.5	222	2	Q8BNT6	Q8bnt6 mus musculu	246	28	87.5	625	2	Q6M2V5	Q6m2v5 corynebacte
174	28	87.5	232	2	Q7XXQ1	Q7xxq1 oryza sativ	247	28	87.5	632	1	DXS_CHILMU	O9pk62 chlamydia m
175	28	87.5	234	1	Y014_SINY3	Q57208 synecocyst	248	28	87.5	635	2	O64715	O64715 arabidopsis
176	28	87.5	237	2	Q86HV9	Q86hv9 pseudomonas	249	28	87.5	636	2	O04198	O04198 arabidopsis
177	28	87.5	289	2	Q6MLP5	Q6mlp5 bdellovibri	250	28	87.5	637	2	Q8NIU1	Q8niu1 neurospora

251	28	87.5	640	1	DXS_CHLTR	O84335	chlamydia t	324	27	84.4	164	2	Q6IU23	O6iu23	escherichia
252	28	87.5	643	2	Q9FW93	Q9fw93	oryza sativ	325	27	84.4	171	2	Q9UM08	Q9um08	homo sapien
253	28	87.5	649	2	Q6NFM8	Gentm8	corynebacte	326	27	84.4	179	2	Q7QM08	Q7qgm8	anopheles g
254	28	87.5	661	2	Q8JTB6	O8jtb6	striped bas	327	27	84.4	181	2	Q647Q9	Q647q9	uncultured
255	28	87.5	663	2	Q73X78	Q73x78	mycobacteri	328	27	84.4	194	2	Q96853	O96853	schistosoma
256	28	87.5	664	1	DING_MYCBO	P64315	mycobacteri	329	27	84.4	201	2	Q73PP3	Q73pp3	treponema d
257	28	87.5	664	1	DING_MYCTU	P64314	mycobacteri	330	27	84.4	201	2	Q9Q8T2	Q9q8t2	rabbit fibr
258	28	87.5	700	2	Q8PMT4	Q8fmc4	corynebacte	331	27	84.4	206	2	Q997C2	Q997c2	myxoma viru
259	28	87.5	706	2	Q9VHK5	Q9vkh5	drosophila	332	27	84.4	214	1	RHOJ_HUMAN	Q9h4e5	homo sapien
260	28	87.5	707	2	Q7K5U3	Q7k5u3	drosophila	333	27	84.4	219	2	Q6ZGG6	Q6zgg6	oryza sativ
261	28	87.5	710	2	Q7SBR2	Q26473	schistocerc	334	27	84.4	221	2	Q7O6P0	Q7o6p0	anopheles g
262	28	87.5	730	1	SM1A_SCHAM	O26473	schistocerc	335	27	84.4	224	1	YMFK_ECOLI	P75974	escherichia
263	28	87.5	842	2	Q9HXN5	Q9hxn5	pseudomonas	336	27	84.4	224	2	Q8SBF6	O8sbf6	bacterioph
264	28	87.5	846	2	Q7XVU8	Q7xv8	oryza sativ	337	27	84.4	228	2	Q35530	O35530	rhizobium l
265	28	87.5	846	2	Q7XVU8	P56730	homo sapien	338	27	84.4	228	2	Q9L596	Q9l596	heliobacter
266	28	87.5	884	2	Q7XHV0	Q7xhv0	oryza sativ	339	27	84.4	230	1	CUT2_MYCBO	P63881	mycobacteri
267	28	87.5	897	2	Q93Y95	Q93y95	zea mays (m	340	27	84.4	230	1	CUT2_MYCTU	O621g7	mycobacteri
268	28	87.5	912	2	O8L4S1	O8l4s1	oryza sativ	341	27	84.4	235	2	Q62JQ7	O62j97	burkholderi
269	28	87.5	963	1	LRP8_HUMAN	O14114	homo sapien	342	27	84.4	235	2	Q63UY8	O63uy8	burkholderi
270	28	87.5	1129	2	Q7UKD4	Q7ukd4	rhodospirell	343	27	84.4	254	2	Q9U7I8	Q9u7i8	plasmodium
271	28	87.5	1240	2	Q8VA42	G8va42	chum salmon	344	27	84.4	258	2	Q6GL81	Q6gl81	xenopus tro
272	28	87.5	1267	1	VL3_REOVD	P17378	reovirus ty	345	27	84.4	269	2	Q62A18	Q62a18	burkholderi
273	28	87.5	1267	1	VL3_REOVJ	P17377	reovirus ty	346	27	84.4	269	2	Q63NZ8	Q63nz8	burkholderi
274	28	87.5	1267	1	VL3_REOVL	P17376	reovirus ty	347	27	84.4	270	2	Q9O8Q6	Q9o8q6	myxoma viru
275	28	87.5	1267	2	O8V5E5	O8v5e5	ndelle viru	348	27	84.4	270	2	Q9Q931	Q9q931	rabbit fibr
276	28	87.5	1267	2	O8V5E5	O8v5e5	reovirus ty	349	27	84.4	276	2	Q8TMZ5	Q8tmz5	methanosaer
277	28	87.5	1274	2	Q8JU61	O8ju61	golden shin	350	27	84.4	276	2	Q66E77	Q66e77	yersinia ps
278	28	87.5	1274	2	Q9E168	O9e168	grass carp	351	27	84.4	276	2	Q8ZBT1	Q8zbt1	yersinia pe
279	28	87.5	1274	2	Q9E3V9	O9e3v9	grass carp	352	27	84.4	278	2	Q8UV28	Q8uv28	brachydanio
280	28	87.5	1280	2	O9EPX2	O9epx2	mus musculu	353	27	84.4	278	2	Q6DHF1	O6dhf1	brachydanio
281	28	87.5	1323	2	O13686	O13686	schizosacch	354	27	84.4	279	2	Q8OV15	Q8ovi5	mus musculu
282	28	87.5	1685	2	Q9U4A2	Q9u4a2	plasmodium	355	27	84.4	280	2	Q95698	Q95698	homo sapien
283	28	87.5	1764	2	O45657	O45657	caenorhabdi	356	27	84.4	280	2	Q9H160	Q9hi60	homo sapien
284	28	87.5	1766	2	O6BC22	O6bc22	caenorhabdi	357	27	84.4	280	2	Q8JG42	Q8jg42	fugu rubrip
285	28	87.5	1778	2	O9BPP7	O9bpb7	antheraea y	358	27	84.4	281	2	Q8JGM9	Q8jgm9	fugu rubrip
286	28	87.5	1778	2	O9GUX5	O9gux5	antheraea p	359	27	84.4	281	2	O8BSU8	O8bsu8	m mus muscu
287	28	87.5	2043	2	O96943	O96943	geodia cydo	360	27	84.4	281	2	Q9ESK4	Q9esk4	mus musculu
288	28	87.5	2098	2	Q25757	Q25757	plasmodium	361	27	84.4	283	2	Q9W057	Q9w057	drosophila
289	28	87.5	2114	2	Q97267	Q97267	plasmodium	362	27	84.4	283	2	Q56864	Q56864	yersinia en
290	28	87.5	2173	2	Q9U622	O9u622	drosophila	363	27	84.4	283	2	O42284	O42284	gallus gall
291	28	87.5	2177	2	Q9VL32	O9vl32	drosophila	364	27	84.4	285	2	O7MAK7	Q7mak7	wollinella s
292	28	87.5	2209	2	Q9U324	O9u324	plasmodium	365	27	84.4	286	2	Q9DBD2	Q9dbd2	m mus muscu
293	28	87.5	2209	2	Q9U0G6	O9u0g6	plasmodium	366	27	84.4	287	2	P72287	P72287	rhizobium l
294	28	87.5	2285	2	Q8IAS3	O8ias3	plasmodium	367	27	84.4	288	2	Q89FK1	Q89fk1	brachyrhizob
295	28	87.5	2287	2	Q8I520	O8i520	plasmodium	368	27	84.4	291	2	Q8TC72	Q8tc72	homo sapien
296	28	87.5	2658	2	Q8T5G0	O8t5g0	plasmodium	369	27	84.4	298	2	Q7OSQ0	Q7osq0	limosella a
297	28	87.5	2743	2	Q8IET9	O8iet9	plasmodium	370	27	84.4	299	1	YEGS_ECOLI	P76407	escherichia
298	28	87.5	3115	2	Q9VOV1	Q9vov1	drosophila	371	27	84.4	299	2	Q83V54	Q83vs4	escherichia
299	28	87.5	3118	2	O17575	O17575	caenorhabdi	372	27	84.4	299	2	Q7UCB0	Q7ucb0	shigella fl
300	28	87.5	3954	2	Q6LEB2	O6lev2	plasmodium	373	27	84.4	299	2	Q83K10	Q83ki0	shigella fl
301	28	87.5	5176	2	Q6JHN7	O6jhn7	saccharopol	374	27	84.4	299	2	Q8FFZ2	Q8ffz2	escherichia
302	27	84.4	57	1	SBPI_SARBU	P26228	sarcophaga	375	27	84.4	299	2	Q8X7H7	Q8x7h7	escherichia
303	27	84.4	59	2	Q6ETU2	O6etu2	oryza sativ	376	27	84.4	301	2	Q7OSP9	Q7osp9	limosella m
304	27	84.4	75	2	Q9NU96	Q9nu96	chromobacte	377	27	84.4	302	2	Q64T54	Q64t54	bacterioides
305	27	84.4	76	2	Q968S8	O968s8	galleria me	378	27	84.4	308	1	Y040_BPT4	P39254	bacterioph
306	27	84.4	89	2	Q8FCM0	O8fcm0	escherichia	379	27	84.4	322	2	Q84H43	Q84h43	alcaligenes
307	27	84.4	94	2	Q7PSJ2	O7pjs2	anopheles g	380	27	84.4	323	2	Q9A3S2	Q9a3s2	bacterioides
308	27	84.4	95	2	Q6NQF9	O6nfg9	corynebacte	381	27	84.4	323	2	Q9KB14	Q9kb14	bacillus ha
309	27	84.4	98	2	Q853S7	O853s7	mycobacteri	382	27	84.4	324	2	Q7ZX11	Q7zx11	xenopus lae
310	27	84.4	112	2	Q7USG0	Q7usg0	rhodospirell	383	27	84.4	326	1	VT2_MXKVL	P29825	myxoma viru
311	27	84.4	122	2	Q8TAY2	O8tay2	plasmodium	384	27	84.4	326	2	Q8RLZ0	Q8rlz0	salmonella
312	27	84.4	124	2	Q7PEZ3	O7pez3	anopheles g	385	27	84.4	326	2	Q8A2D3	Q8a2d3	bacterioides
313	27	84.4	129	2	Q9VQU0	O9vqu0	drosophila	386	27	84.4	333	1	RFBV_SALTY	P26401	salmonella
314	27	84.4	130	2	Q8U8V7	O8u8v7	agrobacteri	387	27	84.4	333	2	Q99192	Q99192	salmonella
315	27	84.4	137	2	Q9KYT5	O9kvt5	streptomyce	388	27	84.4	333	2	Q7CAW1	Q7caw1	salmonella
316	27	84.4	140	2	Q8BPD2	O8bpd2	m mus muscu	389	27	84.4	337	2	Q6P603	Q6p603	brachydanio
317	27	84.4	141	2	Q7MUA2	Q7mu2	porphyromon	390	27	84.4	337	2	Q8O4G9	Q8o4g9	brachydanio
318	27	84.4	147	1	HMRI_RHIME	P58378	rhizobium m	391	27	84.4	338	2	Q8QLH5	Q8qlh5	mamestra co
319	27	84.4	147	1	HMR2_RHIME	P58379	rhizobium m	392	27	84.4	340	2	Q72F21	Q72f21	desulfovibr
320	27	84.4	153	2	Q7LZC7	Q7lzc7	trachemys s	393	27	84.4	341	2	Q71AF3	Q71af3	mamestra co
321	27	84.4	158	2	O8LRG3	O8lrg3	oryza sativ	394	27	84.4	345	2	Q6K410	Q6k410	oryza sativ
322	27	84.4	159	2	O8XU46	O8xu46	raistonia s	395	27	84.4	345	2	Q9CST5	Q9cst5	mus musculu
323	27	84.4	164	1	YBFP_ECOLI	P75737	escherichia	396	27	84.4	346	1	YF20_MYCTU	P64863	mycobacteri

397	27	84.4	346	1	YF47_MYCBO	P64864 mycobacteri	470	27	84.4	507	2	Q8QHV1	Q8qhv1 spartina mo
398	27	84.4	351	2	Q6AZT18	Q6axt8 xenopus lae	471	27	84.4	513	2	Q83869	Q83869 narcissus l
399	27	84.4	351	2	Q801F1	Q801f1 xenopus lae	472	27	84.4	513	2	Q9DIC4	Q9dic4 bromo strea
400	27	84.4	352	2	Q9WRO6	Q9wrg6 macaca mula	473	27	84.4	514	2	Q8OBV2	Q8obv2 alpinia mos
401	27	84.4	353	2	Q9J2K2	Q9j2k2 rheus monk	474	27	84.4	517	2	Q8BLK4	Q8blk4 debaryomyce
402	27	84.4	355	2	Q8GE93	Q8ge93 mycobacteri	475	27	84.4	524	2	Q7PKK6	Q7pkk6 anopheles g
403	27	84.4	356	1	YXT2_CAEL	Q18078 caenorhabdi	476	27	84.4	527	2	Q8VIX7	Q8vix7 oat necroti
404	27	84.4	358	2	Q7T2B9	Q7t2b9 mycobacteri	477	27	84.4	527	2	Q8VIX8	Q8vix8 oat necroti
405	27	84.4	359	1	Y199_MYCTU	Q07733 mycobacteri	478	27	84.4	528	2	Q6JOM7	Q6jom7 indian card
406	27	84.4	366	2	Q90163	Q90163 choristoneu	479	27	84.4	528	2	Q9QD49	Q9qd49 cardamom mo
407	27	84.4	370	2	Q8LL17	Q8ll17 arabidopsis	480	27	84.4	538	2	Q8VIX9	Q8vix9 wheat strea
408	27	84.4	371	2	Q6VTS9	Q6vts9 choristoneu	481	27	84.4	538	2	Q8VIX2	Q8vix2 wheat strea
409	27	84.4	388	2	Q6DED2	Q6ded2 xenopus lae	482	27	84.4	538	2	Q8VIX0	Q8vix0 wheat strea
410	27	84.4	395	2	Q9R115	Q9r115 mus musculu	483	27	84.4	539	2	Q8VIX1	Q8vix1 wheat strea
411	27	84.4	396	2	Q8BGQ0	Q8bgq0 m mus musculu	484	27	84.4	539	2	Q7T813	Q7t813 wheat strea
412	27	84.4	397	2	Q9BP90	Q9bp90 mus musculu	485	27	84.4	540	2	Q9I7L5	Q9i7l5 drosophila
413	27	84.4	397	2	Q8BG60	Q8bg60 m mus musculu	486	27	84.4	542	2	Q7T809	Q7t809 wheat strea
414	27	84.4	397	2	Q9DC00	Q9dc00 mus musculu	487	27	84.4	543	2	Q7T811	Q7t811 wheat strea
415	27	84.4	397	2	Q8K2B2	Q8k2b2 mus musculu	488	27	84.4	543	2	Q7T812	Q7t812 wheat strea
416	27	84.4	399	1	PNCB_BUCAI	P57442 buchnera ap	489	27	84.4	543	2	Q7T814	Q7t814 wheat strea
417	27	84.4	399	2	Q9QBG5	Q9qbg5 wheat yello	490	27	84.4	543	2	Q7T815	Q7t815 wheat strea
418	27	84.4	400	2	Q91X82	Q91x82 mus musculu	491	27	84.4	543	2	Q7T816	Q7t816 wheat strea
419	27	84.4	402	2	Q93YD4	Q93yd4 nicotiana t	492	27	84.4	544	2	Q63Q00	Q63qq0 burkholderi
420	27	84.4	402	2	Q93YE5	Q93ye5 nicotiana t	493	27	84.4	544	2	Q7T810	Q7t810 wheat strea
421	27	84.4	402	2	Q94BY4	Q94by4 nicotiana t	494	27	84.4	545	2	Q7SEP2	Q7sep2 neurospora
422	27	84.4	406	2	Q9XG74	Q9xg74 nicotiana t	495	27	84.4	549	2	Q24204	Q24204 drosophila
423	27	84.4	406	2	Q93YC1	Q93yc1 nicotiana t	496	27	84.4	553	1	MCRA_METVA	P07961 methanococc
424	27	84.4	406	2	Q6AK56	Q6ak56 desulfotale	497	27	84.4	553	2	Q6LWZ5	Q6lwz5 methanococc
425	27	84.4	417	2	Q748R7	Q748r7 geobacter s	498	27	84.4	554	2	Q9VIB0	Q9vib0 drosophila
426	27	84.4	421	2	Q41898	Q41898 rice necros	499	27	84.4	554	2	Q7TF98	Q7tf98 cucumber ve
427	27	84.4	431	2	Q8TCW7	Q8tcw7 homo sapien	500	27	84.4	555	2	Q9QBG3	Q9qbg3 wheat yello
428	27	84.4	434	2	Q8VMP8	Q8vmp8 gossypium h	501	27	84.4	557	2	Q91DH6	Q91dh6 chinese yam
429	27	84.4	436	2	Q9NE69	Q9ne69 leishmania	502	27	84.4	558	2	Q6DFH2	Q6dfh2 xenopus lae
430	27	84.4	442	2	Q89265	Q89265 wheat strea	503	27	84.4	559	1	PPO2_MOUSE	O88554 mus musculu
431	27	84.4	448	2	Q91BP9	Q91bp9 oat mosaic	504	27	84.4	559	2	Q9E7C0	Q9e7c0 cucumber ve
432	27	84.4	458	2	Q986T2	Q986t2 onion yello	505	27	84.4	561	2	Q7Y0G4	Q7y0g4 oryza sativ
433	27	84.4	469	2	Q8QXP1	Q8qxp1 onion yello	506	27	84.4	562	2	Q7TH69	Q7th69 lycoris pot
434	27	84.4	469	2	Q8QXP2	Q8qxp2 onion yello	507	27	84.4	568	2	Q6NVM1	Q6nvm1 xenopus tro
435	27	84.4	469	2	Q8QXP3	Q8qxp3 onion yello	508	27	84.4	571	2	Q9BPQ2	Q9bpq2 drosophila
436	27	84.4	469	2	Q8U220	Q8uz20 onion yello	509	27	84.4	571	2	Q62GY2	Q62gy2 burkholderi
437	27	84.4	469	2	Q8U221	Q8uz21 onion yello	510	27	84.4	572	2	Q34203	Q34203 drosophila
438	27	84.4	469	2	Q8U222	Q8uz22 onion yello	511	27	84.4	572	2	Q9VIB1	Q9vib1 drosophila
439	27	84.4	469	2	Q8U223	Q8uz23 onion yello	512	27	84.4	573	2	Q7RZQ5	Q7rzq5 neurospora
440	27	84.4	469	2	Q8U224	Q8uz24 onion yello	513	27	84.4	575	2	Q8NAG6	Q8nag6 homo sapien
441	27	84.4	469	2	Q8U225	Q8uz25 onion yello	514	27	84.4	581	2	Q65660	Q65660 barley mild
442	27	84.4	470	2	Q8UYU1	Q8uyu1 shallot yel	515	27	84.4	582	2	Q911I2	Q911i2 cardamom mo
443	27	84.4	470	2	Q7TGA8	Q7tga8 shallot yel	516	27	84.4	585	2	Q65603	Q65603 bovine immu
444	27	84.4	472	2	Q80P32	Q80p32 chinese nar	517	27	84.4	587	1	C08B_ONCMY	Q90x85 oncorhynchu
445	27	84.4	472	2	Q80P33	Q80p33 chinese nar	518	27	84.4	588	2	Q70681	Q70681 sugarcane s
446	27	84.4	476	2	Q6AS69	Q6as69 desulfotale	519	27	84.4	591	2	Q6NP04	Q6np04 drosophila
447	27	84.4	488	2	Q91QR6	Q91qr6 wheat yello	520	27	84.4	591	2	Q7Q6N2	Q7q6n2 anopheles g
448	27	84.4	489	2	Q8RVB6	Q8rvb6 oryza sativ	521	27	84.4	602	1	YH02_YEAST	P38887 saccharomyc
449	27	84.4	494	2	Q92012	Q92012 wheat spind	522	27	84.4	603	1	ALS_MOUSE	P70389 mus musculu
450	27	84.4	495	2	P89683	P89683 wheat strea	523	27	84.4	603	1	ALS_RAT	P35859 rattus norv
451	27	84.4	500	2	Q6AZL3	Q6azl3 limosella a	524	27	84.4	603	2	Q70211	Q70211 rattus norv
452	27	84.4	501	2	Q6KB68	Q6kb68 sweet potat	525	27	84.4	605	1	ALS_HUMAN	P35858 homo sapien
453	27	84.4	501	2	Q6KB69	Q6kb69 sweet potat	526	27	84.4	605	1	ALS_PAPHA	Q02833 papio hamad
454	27	84.4	501	2	Q6KB70	Q6kb70 sweet potat	527	27	84.4	605	2	Q8TAY0	Q8tay0 homo apien
455	27	84.4	501	2	Q8B323	Q8b323 sweet potat	528	27	84.4	610	2	Q70SP5	Q70sp5 limosella g
456	27	84.4	501	2	Q8B324	Q8b324 sweet potat	529	27	84.4	611	2	P89885	P89885 onion yello
457	27	84.4	501	2	Q8B325	Q8b325 sweet potat	530	27	84.4	617	2	Q8UJG0	Q8ujg0 measles vir
458	27	84.4	501	2	Q8B326	Q8b326 sweet potat	531	27	84.4	617	2	Q8UJ11	Q8uj11 measles vir
459	27	84.4	501	2	Q8B327	Q8b327 sweet potat	532	27	84.4	617	2	Q8JSM4	Q8jism4 measles vir
460	27	84.4	501	2	Q8B328	Q8b328 sweet potat	533	27	84.4	617	2	Q8JSM5	Q8jism5 measles vir
461	27	84.4	501	2	Q8B329	Q8b329 sweet potat	534	27	84.4	617	2	Q8JTA8	Q8jta8 measles vir
462	27	84.4	502	2	Q9VIY9	Q9viy9 drosophila	535	27	84.4	617	2	Q8JTA9	Q8jta9 measles vir
463	27	84.4	502	2	Q8QR17	Q8qr17 spartina mo	536	27	84.4	617	2	Q9W8B0	Q9w8b0 measles vir
464	27	84.4	503	2	Q6FZW1	Q6fzw1 bartonella	537	27	84.4	617	2	Q9WIX1	Q9wix1 measles vir
465	27	84.4	503	2	Q6G3B9	Q6g3b9 bartonella	538	27	84.4	617	2	Q9WIX3	Q9wix3 measles vir
466	27	84.4	504	1	Y787_METJA	Q58197 methanococc	539	27	84.4	617	2	Q9WIX4	Q9wix4 measles vir
467	27	84.4	507	2	Q8YGM3	Q8ygm3 brucella me	540	27	84.4	617	2	Q9WIX6	Q9wix6 measles vir
468	27	84.4	507	2	Q8G100	Q8g100 brucella su	541	27	84.4	617	2	Q9WIX8	Q9wix8 measles vir
469	27	84.4	507	2	Q6MBK1	Q6mbk1 parachlamyid	542	27	84.4	617	2	Q9WIY3	Q9wiy3 measles vir

543	27	84.4	617	2	Q9WIZ0	Q9wiz0 measles vir	616	27	84.4	2258	2	O55459	O55459 barley mild
544	27	84.4	617	2	Q9WIZ7	Q9wiz7 measles vir	617	27	84.4	2258	2	O93128	O93128 barley mild
545	27	84.4	624	2	Q8EET5	Q8eet5 shewanella	618	27	84.4	2258	2	Q65654	Q65654 barley mild
546	27	84.4	637	2	Q6CWIJ1	Q6cwi1 kluyveromyc	619	27	84.4	2258	2	Q68VH7	Q68VH7 barley mild
547	27	84.4	638	2	Q91914	Q91914 brachydanio	620	27	84.4	2258	2	Q68VH8	Q68VH8 barley mild
548	27	84.4	644	1	DXS_PROVM	Q7v7c3 prochloroco	621	27	84.4	2258	2	Q68VH9	Q68VH9 barley mild
549	27	84.4	647	2	Q7Q6N1	Q7q6n1 anophelies g	622	27	84.4	2258	2	Q9WAA3	Q9WAA3 barley mild
550	27	84.4	649	2	Q7RRA2	Q7rra2 plasmodium	623	27	84.4	2261	2	Q71BFP1	Q71BFP1 barley mild
551	27	84.4	666	2	Q7QB38	Q7qb38 anophelies g	624	27	84.4	2240	2	Q8UZZ7	Q8UZZ7 oat mosaic
552	27	84.4	671	1	ANK6_CHICK	PS1901 gallus gall	625	27	84.4	2404	2	Q90733	Q90733 wheat yellow
553	27	84.4	678	2	Q9QB66	Q9qb66 wheat yellow	626	27	84.4	2404	2	Q90BG1	Q90BG1 wheat yellow
554	27	84.4	680	2	Q70SP4	Q70sp4 limosella m	627	27	84.4	2404	2	Q90BG4	Q90BG4 wheat yellow
555	27	84.4	684	2	Q9L2E4	Q9l2e4 arabidopsis	628	27	84.4	2407	2	Q9QMA1	Q9QMA1 wheat yellow
556	27	84.4	686	2	Q8RZZ7	Q8rzz7 oryza sativ	629	27	84.4	2410	1	POL1_BAYMJ	Q01206 b genome po
557	27	84.4	687	2	Q9JIL0	Q9jil0 mus musculu	630	27	84.4	2410	1	Q9YJW3	Q9YJW3 barley yell
558	27	84.4	703	2	Q7Q6S1	Q7q6s1 anophelies g	631	27	84.4	2411	2	Q71BD5	Q71BD5 barley yell
559	27	84.4	704	2	Q9BPQ3	Q9bpq3 drosophila	632	27	84.4	2412	1	POL1_BAYMG	Q04574 b genome po
560	27	84.4	717	2	Q9VPT4	Q9vpt4 drosophila	633	27	84.4	2412	2	Q70WS1	Q70WS1 barley yell
561	27	84.4	719	2	P87541	P87541 barley mild	634	27	84.4	2412	2	Q70WS2	Q70WS2 barley yell
562	27	84.4	721	2	Q9PA43	Q9pa43 xyliella fas	635	27	84.4	2412	2	Q70WS3	Q70WS3 barley yell
563	27	84.4	727	2	Q83387	Q83387 maclura mos	636	27	84.4	2412	2	Q70WS4	Q70WS4 barley yell
564	27	84.4	746	2	Q9VFP00	Q9vf00 drosophila	637	27	84.4	2412	2	Q70WS5	Q70WS5 barley yell
565	27	84.4	754	2	Q9C7M3	Q9c7m3 arabidopsis	638	27	84.4	2412	2	Q70WS6	Q70WS6 barley yell
566	27	84.4	803	2	Q6JP85	Q6jpb5 neodiprion	639	27	84.4	2412	2	Q70WS7	Q70WS7 barley yell
567	27	84.4	824	2	Q6JK76	Q6jkr76 neodiprion	640	27	84.4	2447	2	P90580	P90580 plasmodium
568	27	84.4	828	2	Q6Z469	Q6z469 oryza sativ	641	27	84.4	2772	2	Q9VAV4	Q9VAV4 drosophila
569	27	84.4	832	2	Q9ICV1	Q9icv1 wheat yellow	642	27	84.4	2772	2	Q869A0	Q869A0 drosophila
570	27	84.4	842	2	Q95R71	Q95r71 drosophila	643	27	84.4	2894	2	Q7KRX2	Q7KRX2 drosophila
571	27	84.4	845	2	Q8WPP8	Q8wpp8 trypanosoma	644	27	84.4	2898	2	Q868Z9	Q868Z9 drosophila
572	27	84.4	876	2	Q869X6	Q869x6 dictyosteli	645	27	84.4	2931	2	Q9W2C6	Q9W2C6 drosophila
573	27	84.4	892	2	Q6Y138	Q6y138 lactuca sat	646	27	84.4	2968	2	Q8MLU9	Q8MLU9 drosophila
574	27	84.4	912	2	Q76NT5	Q76nt5 dictyosteli	647	27	84.4	3020	2	Q9E160	Q9E160 wheat strea
575	27	84.4	914	2	Q8C726	Q8c726 arabidopsis	648	27	84.4	3023	2	Q6U6H0	Q6U6H0 oat necroti
576	27	84.4	940	2	Q81502	Q81502 arabidopsis	649	27	84.4	3034	2	Q8V1Y4	Q8V1Y4 wheat strea
577	27	84.4	942	1	POLG_BSTVG	Q65729 b genome po	650	27	84.4	3035	2	Q72347	Q72347 wheat strea
578	27	84.4	959	2	O18359	O18359 drosophila	651	27	84.4	3035	2	O8V1Y3	O8V1Y3 wheat strea
579	27	84.4	985	2	O01470	O01470 caenorhabdi	652	27	84.4	3035	2	O9E161	O9E161 wheat strea
580	27	84.4	996	2	Q8KTE5	Q8kte5 methylobact	653	27	84.4	3093	1	POLG_BSTV1	Q65730 b genome po
581	27	84.4	1011	1	UBAL_HUMAN	P41226 homo sapien	654	27	84.4	3403	2	Q7TSA6	Q7TSA6 onion yello
582	27	84.4	1012	2	Q9BRB2	Q9brb2 homo sapien	655	27	84.4	3456	2	P89201	P89201 sweet potat
583	27	84.4	1041	2	Q02442	Q02442 barley mild	656	27	84.4	5202	2	Q6S362	Q6S362 homo sapien
584	27	84.4	1076	2	Q6VAN9	Q6van9 trichoplusi	657	27	84.4	6739	2	Q7OYB8	Q7OYB8 giardia lam
585	27	84.4	1133	2	O8MR55	O8mr55 drosophila	658	26	81.2	30	2	O83DZ9	O83DZ9 coxiella bu
586	27	84.4	1153	2	Q6NS64	Q6ns64 mus musculu	659	26	81.2	38	2	Q8GP25	Q8GP25 pseudomonas
587	27	84.4	1175	2	Q9VCE7	Q9vce7 drosophila	660	26	81.2	43	2	Q7SEH1	Q7SEH1 neurospora
588	27	84.4	1180	2	Q6A025	Q6a025 mus musculu	661	26	81.2	45	2	O49718	O49718 arabidopsis
589	27	84.4	1182	2	Q9N8H1	Q9n8h1 trypanosoma	662	26	81.2	50	2	Q885V4	Q885V4 pseudomonas
590	27	84.4	1194	2	Q9DUM1	Q9dum1 barley yell	663	26	81.2	52	2	Q92159	Q92159 oncorhynch
591	27	84.4	1195	2	Q6BK97	Q6bk97 debaryomyce	664	26	81.2	57	1	YNE2_RH1ET	P24149 rhizobium e
592	27	84.4	1201	2	Q39510	Q39510 barley mild	665	26	81.2	63	2	Q8VJM8	Q8VJM8 mycobacteri
593	27	84.4	1284	1	NRX4_DROME	Q94887 drosophila	666	26	81.2	63	2	Q7TYV1	Q7TYV1 mycobacteri
594	27	84.4	1284	2	Q6NN26	Q6nn26 drosophila	667	26	81.2	63	2	Q8BTE6	Q8BTE6 mus musculu
595	27	84.4	1365	2	Q7REQ5	Q7req5 plasmodium	668	26	81.2	64	1	V3B_IBVB	P30241 avian infec
596	27	84.4	1366	2	Q8IOH0	Q8ioh0 drosophila	669	26	81.2	64	1	V3B_IBVM	P05138 avian infec
597	27	84.4	1420	2	Q9YNB1	Q9ynb1 sugarcane s	670	26	81.2	64	1	V3B_IBVP3	P30242 avian infec
598	27	84.4	1432	2	Q18647	Q18647 caenorhabdi	671	26	81.2	64	2	Q8S0U9	Q8S0U9 oryza sativ
599	27	84.4	1470	2	Q89255	Q89255 wheat spind	672	26	81.2	64	2	Q6DV53	Q6DV53 avian infec
600	27	84.4	1496	2	Q9NFV5	Q9nfv5 drosophila	673	26	81.2	64	2	Q778R9	Q778R9 avian infec
601	27	84.4	1496	2	Q9VIT9	Q9vit9 drosophila	674	26	81.2	64	2	Q778S4	Q778S4 avian infec
602	27	84.4	1607	2	Q87EK2	Q87ek2 xyliella fas	675	26	81.2	64	2	O9J3Q1	O9J3Q1 avian infec
603	27	84.4	1759	2	Q9XTP8	Q9xtp8 plasmodium	676	26	81.2	64	2	Q9J4A8	Q9J4A8 avian infec
604	27	84.4	1820	2	Q90153	Q90153 ustilago ma	677	26	81.2	65	2	Q6PV93	Q6PV93 infectious
605	27	84.4	1821	2	Q6Y140	Q6y140 lactuca sat	678	26	81.2	66	2	Q95R59	Q95R59 drosophila
606	27	84.4	1847	2	Q9ZTP69	Q9zt69 lactuca sat	679	26	81.2	66	2	Q95VA9	Q95VA9 spirometra
607	27	84.4	1905	2	Q9XTP6	Q9xtp6 plasmodium	680	26	81.2	66	2	Q6DTJ5	Q6dtj5 zea mays (m
608	27	84.4	2042	2	Q25766	Q25766 plasmodium	681	26	81.2	69	2	Q8S8D5	Q8S8D5 arabidopsis
609	27	84.4	2081	2	Q7QK87	Q7qk87 anophelies g	682	26	81.2	69	2	Q7VI45	Q7VI45 helicobacte
610	27	84.4	2117	2	Q7KSW1	Q7ksw1 drosophila	683	26	81.2	70	2	Q8VAV0	Q8VAV0 white spot
611	27	84.4	2165	2	Q9VHM9	Q9vhw9 drosophila	684	26	81.2	71	2	Q18256	Q18256 caenorhabdi
612	27	84.4	2174	2	Q9GQRO	Q9gqro drosophila	685	26	81.2	75	2	Q82RN8	Q82RN8 streptomyce
613	27	84.4	2178	2	Q8I643	Q8i643 plasmodium	686	26	81.2	76	1	LC38_ARATH	P82753 arabidopsis
614	27	84.4	2212	2	Q9A657	Q9a657 plasmodium	687	26	81.2	78	2	Q622D8	Q622D8 oryza sativ
615	27	84.4	2258	1	POL1_BAMMN	P90245 b genome po	688	26	81.2	80	2	Q8VX96	Q8VX96 pinus pinas

689	26	81.2	80	2	Q91TJ0	Q91tj0 tupaiid her	762	26	81.2	143	2	Q6TUZ4	Q6tuz4 yaba monkey
690	26	81.2	81	2	Q71TU1	Q71tu1 plethodon i	763	26	81.2	143	2	Q9DHU5	Q9dhu5 yaba-like d
691	26	81.2	84	2	Q6K1T0	Q6k1t0 oryza sativ	764	26	81.2	145	2	Q7Z024	Q7z024 eunapius fr
692	26	81.2	85	2	Q6Y0V0	Q6y0v0 human immun	765	26	81.2	145	2	Q9KQK7	Q9kqk7 vibrio chol
693	26	81.2	87	2	Q86539	Q86539 human herpe	766	26	81.2	147	1	Y237_TROWT	P67323 tropheryma
694	26	81.2	88	2	Q9HNQ6	Q9hnq6 halobacteri	767	26	81.2	147	1	Y533_TROMB	P67324 tropheryma
695	26	81.2	88	2	Q88801	Q88801 eastern equ	768	26	81.2	147	2	Q01599	Q01599 phanerocha
696	26	81.2	92	2	Q6MPQ6	Q6mpq6 bdellovibri	769	26	81.2	148	2	Q88AB6	Q88ab6 pseudomonas
697	26	81.2	93	2	Q6N8E1	Q6n8e1 rhodopsendo	770	26	81.2	149	2	Q95W28	Q95w28 anthonomus
698	26	81.2	93	2	Q7W7K6	Q7w7k6 bordetella	771	26	81.2	149	2	Q6TGP9	Q6tgp9 lecanora st
699	26	81.2	93	2	Q7WKZ5	Q7wkz5 bordetella	772	26	81.2	150	2	Q6RZ15	Q6rz15 aspergillus
700	26	81.2	96	2	Q89US7	Q89us7 bradyrhizob	773	26	81.2	152	2	Q19349	Q19349 caenorhabdi
701	26	81.2	96	2	Q6Z4N8	Q6z4n8 oryza sativ	774	26	81.2	152	2	Q47026	Q47026 escherichia
702	26	81.2	96	2	Q67MW1	Q67mw1 symbiobacte	775	26	81.2	153	2	Q6IIA9	Q6iia9 drosophila
703	26	81.2	101	2	Q8VJ46	Q8vj46 mycobacteri	776	26	81.2	153	2	Q7V188	Q7v188 prochloroco
704	26	81.2	101	2	Q7TWZ1	Q7twz1 mycobacteri	777	26	81.2	157	2	Q6MWJ3	Q6mwj3 oryza sativ
705	26	81.2	102	2	Q9YA21	Q9ya21 aeropyrum p	778	26	81.2	157	2	Q6Z7A4	Q6z7a4 oryza sativ
706	26	81.2	102	2	Q6W3K5	Q6w3k5 alvinella p	779	26	81.2	158	2	Q8S9W1	Q8s9w1 oryza sativ
707	26	81.2	102	2	Q9RQY8	Q9rqy8 mycobacteri	780	26	81.2	158	2	Q6VZB6	Q6vzb6 canarypox v
708	26	81.2	102	2	Q82YG8	Q82yg8 streptomyce	781	26	81.2	160	1	LY96_HUMAN	Q9v6y9 homo sapien
709	26	81.2	103	1	YGU3_YEAST	P53097 saccharomyc	782	26	81.2	160	1	Q9N9Q8	Q9n9q8 leishmania
710	26	81.2	104	2	Q6SX61	Q6sx61 oryza sativ	783	26	81.2	160	2	Q6TGR2	Q6tgr2 equus cabal
711	26	81.2	104	2	Q84192	Q84192 newcastie d	784	26	81.2	161	2	Q7LH18	Q7lh18 phanerocha
712	26	81.2	104	2	Q9WJ27	Q9wj27 newcastle d	785	26	81.2	161	2	Q8Z3S0	Q8z3s0 salmonella
713	26	81.2	109	2	Q7VVZ3	Q7vvz3 bordetella	786	26	81.2	161	2	Q8ZM26	Q8zm26 salmonella
714	26	81.2	110	2	Q9DWM8	Q9dwm8 hepatitis c	787	26	81.2	162	2	Q8PSU4	Q8psu4 methanosarc
715	26	81.2	112	2	Q992S8	Q992s8 human immun	788	26	81.2	162	2	Q67W90	Q67w90 oryza sativ
716	26	81.2	113	2	Q8H6L0	Q8h6l0 brassica ra	789	26	81.2	162	2	Q69T07	Q69t07 oryza sativ
717	26	81.2	114	2	Q7ZEM7	Q7zem7 human immun	790	26	81.2	162	2	Q6X211	Q6x211 bovine herp
718	26	81.2	115	2	Q6GXU6	Q6gxu6 human immun	791	26	81.2	163	1	TPC_BRALA	P80322 branchiosto
719	26	81.2	115	2	Q6GXW9	Q6gxw9 human immun	792	26	81.2	164	2	Q6TGO0	Q6tgo0 lecanora na
720	26	81.2	115	2	Q7ZEHO	Q7zeho human immun	793	26	81.2	164	2	Q6TGO1	Q6tgo1 lecanora na
721	26	81.2	117	2	Q9LRK1	Q9lrk1 arabisdopsis	794	26	81.2	164	2	Q6TGO2	Q6tgo2 lecanora fl
722	26	81.2	117	2	Q9WNX9	Q9wnx9 human immun	795	26	81.2	164	2	Q6TGO3	Q6tgo3 dermatocarp
723	26	81.2	118	2	Q7VWQ1	Q7vwq1 bordetella	796	26	81.2	164	2	Q6ZVJ9	Q6zvj9 homo sapien
724	26	81.2	118	2	Q7WAP4	Q7wap4 bordetella	797	26	81.2	164	2	P90687	P90687 branchiosto
725	26	81.2	118	2	Q7WJU8	Q7wjy8 bordetella	798	26	81.2	164	2	P92198	P92198 branchiosto
726	26	81.2	118	2	Q92517	Q92517 beet virus	799	26	81.2	164	2	Q75NJ6	Q75nj6 branchiosto
727	26	81.2	118	2	Q9YPH2	Q9ypb2 broad bean	800	26	81.2	165	2	Q6VTR5	Q6vtr5 oryza sativ
728	26	81.2	119	2	Q6V2D2	Q6v2d2 potato mop-	801	26	81.2	165	2	Q75LG3	Q75lg3 oryza sativ
729	26	81.2	119	2	Q80QA2	Q80qa2 potato mop-	802	26	81.2	165	2	Q89TW2	Q89tw2 bradyrhizob
730	26	81.2	119	2	Q85292	Q85292 potato mop-	803	26	81.2	166	2	Q77024	Q77024 ephydratia m
731	26	81.2	119	2	Q91V53	Q91v53 potato mop-	804	26	81.2	168	2	Q25231	Q25231 lucilia cup
732	26	81.2	121	2	Q81NN4	Q81nn4 drosophila	805	26	81.2	168	2	Q9RXQ5	Q9rxq5 deinococcus
733	26	81.2	121	2	Q8CKC2	Q8ckc2 versinia pe	806	26	81.2	170	2	Q95PD2	Q95pd2 anopheles d
734	26	81.2	122	2	Q7OMZ0	Q7omz0 anopheles g	807	26	81.2	170	2	Q8KL61	Q8kl61 rhizobium e
735	26	81.2	123	2	Q814A6	Q814a6 caenorhabdi	808	26	81.2	172	2	Q8L170	Q8l170 caenorhabdi
736	26	81.2	125	2	Q96TV9	Q96tv9 pleurotous o	809	26	81.2	173	2	Q6MXZ8	Q6mxz8 serratia ma
737	26	81.2	125	2	Q8LE17	Q8le17 arabisdopsis	810	26	81.2	174	2	Q6RZ25	Q6rz25 westerdykel
738	26	81.2	125	2	Q7D087	Q7d087 agrobacteri	811	26	81.2	175	2	Q8WU36	Q8wu36 homo sapien
739	26	81.2	126	1	CYTL_DROME	P23779 drosophila	812	26	81.2	175	2	Q7Z2G1	Q7z2g1 homo sapien
740	26	81.2	126	2	Q9VMU0	Q9vmu0 drosophila	813	26	81.2	176	2	Q8THI6	Q8thi6 methanosarc
741	26	81.2	127	1	WAP_RABIT	P09412 cryptotagus	814	26	81.2	176	2	Q6RZ19	Q6rz19 pseudoeuroti
742	26	81.2	127	2	Q6WNZ9	Q6wnz9 bdellovibri	815	26	81.2	176	2	Q9SE46	Q9se46 arabisdopsis
743	26	81.2	128	2	Q96MK0	Q96mk0 homo sapien	816	26	81.2	176	2	Q9SBN3	Q9sbn3 arabisdopsis
744	26	81.2	131	2	Q6IHG0	Q6ihg0 drosophila	817	26	81.2	177	2	Q86BA8	Q86ba8 drosophila
745	26	81.2	131	2	Q90817	Q90817 human immun	818	26	81.2	177	2	Q810E7	Q810e7 mus muscucu
746	26	81.2	133	2	Q64564	Q64564 rattus norv	819	26	81.2	178	2	Q95VP9	Q95vp9 leucophaea
747	26	81.2	134	2	Q63NE8	Q63ne8 burkholderi	820	26	81.2	178	2	Q6Z4F8	Q6z4f8 oryza sativ
748	26	81.2	135	2	Q01600	Q01600 phanerocha	821	26	81.2	178	2	Q8PJH1	Q8pjh1 xanthomonas
749	26	81.2	135	2	Q69WT7	Q69wt7 oryza sativ	822	26	81.2	179	2	Q6ZDS3	Q6zds3 burkholderi
750	26	81.2	136	2	Q9DHU8	Q9dhu8 yaba-like d	823	26	81.2	179	2	Q8Y1M2	Q8ylm2 raistonia s
751	26	81.2	138	2	Q800C2	Q800c2 crotalus vi	824	26	81.2	179	2	Q6QQ98	Q6qq98 avipoxvirus
752	26	81.2	138	2	Q800C4	Q800c4 crotalus vi	825	26	81.2	180	2	Q7V167	Q7v167 prochloroco
753	26	81.2	139	2	Q46306	Q46306 drosophila	826	26	81.2	182	2	Q27267	Q27267 methanobact
754	26	81.2	139	2	Q52854	Q52854 rhizobium l	827	26	81.2	182	2	Q19136	Q19136 caenorhabdi
755	26	81.2	140	2	Q8S1C2	Q8s1c2 oryza sativ	828	26	81.2	182	2	Q67UW2	Q67uw2 oryza sativ
756	26	81.2	140	2	Q8KJW3	Q8kjlw3 proteus vul	829	26	81.2	184	2	Q6BZM0	Q6bzm0 debaryomyce
757	26	81.2	140	2	Q6JLB3	Q6jlb3 francisella	830	26	81.2	184	2	Q69K83	Q69k83 oryza sativ
758	26	81.2	140	2	Q70K60	Q70k60 gordonia we	831	26	81.2	185	2	Q84X17	Q84xi7 arabisdopsis
759	26	81.2	141	2	Q8CDG0	Q8cdg0 mus muscucu	832	26	81.2	186	2	Q6SV38	Q6sv38 metarhizium
760	26	81.2	142	2	Q47031	Q47031 escherichia	833	26	81.2	186	2	Q7Q829	Q7qe29 giardia lam
761	26	81.2	142	2	Q8UGR3	Q8ugr3 agrobacteri	834	26	81.2	186	2	Q9FST4	Q9fst4 gnetum gnem

835	26	81.2	187	2	Q653A3	Q653a3 oryza sativ	908	26	81.2	222	2	Q8S0Q2	Q8S0q2 oryza sativ
836	26	81.2	187	2	Q9ZF59	Q9zf59 mycobacteri	909	26	81.2	222	2	Q7VGJ2	Q7vgj2 helicobacte
837	26	81.2	187	2	Q87FA9	Q87fa9 xylella fas	910	26	81.2	223	1	Y863_METTH	Q26951 methanobact
838	26	81.2	187	2	Q9PHB6	Q9phb6 xylella fas	911	26	81.2	223	2	Q6DMR2	Q6dmr2 crassostrea
839	26	81.2	188	1	KLK3_RAT	Pl5950 rattus norv	912	26	81.2	223	2	Q9NSA3	Q9nsa3 caenorhabdi
840	26	81.2	188	2	Q805I9	O80519 arabidopsis	913	26	81.2	223	2	Q6ZJC8	Q6zjc8 oryza sativ
841	26	81.2	188	2	Q9LRL9	Q9lrl9 arabidopsis	914	26	81.2	223	2	Q9LRK5	Q9lrk5 arabidopsis
842	26	81.2	188	2	Q63XE8	Q63xe8 burkholderi	915	26	81.2	224	2	Q47J91	Q47j91 escherichia
843	26	81.2	188	2	Q7U723	Q7u723 synecococc	916	26	81.2	224	2	Q8XAJ2	Q8xaj2 escherichia
844	26	81.2	189	2	Q8HAB3	Q8hab3 salmonella	917	26	81.2	225	1	CLD8_MOUSE	Q8x260 mus musculu
845	26	81.2	189	2	Q89EC3	Q89ec3 burkholderi	918	26	81.2	225	1	RPE_RHOU	P51013 rhodospiril
846	26	81.2	189	2	Q8BMZ3	Q8bmz3 mus musculu	919	26	81.2	226	2	Q9HR90	Q9hr90 halobacteri
847	26	81.2	190	2	Q6CC46	Q6cc46 yarrowia li	920	26	81.2	227	2	Q00786	Q00786 emericella
848	26	81.2	190	2	Q8S8D8	Q8s8d8 arabidopsis	921	26	81.2	228	1	LPRH_MYCBO	P65317 mycobacteri
849	26	81.2	190	2	Q6VMQ2	Q6vmq2 gossypium b	922	26	81.2	228	1	LPRH_MYCTU	P65316 mycobacteri
850	26	81.2	190	2	Q7UIK2	Q7uik2 rhodopirell	923	26	81.2	228	1	NA61_ARATH	Q9m290 arabidopsis
851	26	81.2	191	2	Q6IV75	Q6iv75 saimiri sci	924	26	81.2	228	2	Q75QL7	Q75ql7 bacterioph
852	26	81.2	191	2	Q8JJK3	Q8jjk3 virus phich	925	26	81.2	229	2	Q729J8	Q729j8 fungal endo
853	26	81.2	193	2	Q63IC9	Q63ic9 burkholderi	926	26	81.2	229	2	Q729J9	Q729j9 fungal endo
854	26	81.2	193	2	Q92J63	Q92j63 rhizobium m	927	26	81.2	229	2	Q729K3	Q729k3 fungal endo
855	26	81.2	195	2	Q819P3	Q819p3 aurelia aur	928	26	81.2	229	2	Q6E5T1	Q6est1 fugu rubrip
856	26	81.2	196	2	Q97CB6	Q97cb6 thermoplas	929	26	81.2	230	2	Q63P62	Q63p62 burkholderi
857	26	81.2	196	2	Q23633	Q23633 caenorhabdi	930	26	81.2	231	2	Q9CJX9	Q9cix9 pasteurella
858	26	81.2	196	2	Q8S1B1	Q8s1b1 oryza sativ	931	26	81.2	232	2	Q6IKH5	Q6ikh5 drosophila
859	26	81.2	196	2	Q8L240	Q8l240 salmonella	932	26	81.2	232	2	Q8FIF8	Q8fif8 escherichia
860	26	81.2	196	2	Q7WTH7	Q7wth7 escherichia	933	26	81.2	233	2	Q9PT51	Q9pt51 agkistrodon
861	26	81.2	198	2	Q8K282	Q8k282 mus musculu	934	26	81.2	235	1	NA50_ARATH	Q9fmr3 arabidopsis
862	26	81.2	199	2	Q6CQ07	Q6cq07 yarrowia li	935	26	81.2	236	2	Q9U7H7	Q9u7h7 plasmodium
863	26	81.2	199	2	Q6IJAB	Q6ijab drosophila	936	26	81.2	236	2	Q6ZF66	Q6zfe6 oryza sativ
864	26	81.2	199	2	Q8FRZ4	Q8frz4 corynebacte	937	26	81.2	237	2	Q7P0S9	Q7p0s9 chromobacte
865	26	81.2	200	2	Q6E5F6	Q6e5f6 noseema locu	938	26	81.2	237	2	Q7V4N4	Q7v4n4 prochloroco
866	26	81.2	200	2	Q84J93	Q84j93 arabidopsis	939	26	81.2	237	2	Q6AME6	Q6ame6 desulfotale
867	26	81.2	200	2	Q84JX6	Q84jx6 arabidopsis	940	26	81.2	238	1	VSP1_AGKHA	P81176 agkistrodon
868	26	81.2	200	2	Q84JX5	Q84jx5 arabidopsis	941	26	81.2	238	2	Q67W67	Q67w67 oryza sativ
869	26	81.2	200	2	Q84UG5	Q84ug5 arabidopsis	942	26	81.2	238	2	Q9LRM3	Q9lrm3 arabidopsis
870	26	81.2	201	2	Q9LRSK0	Q9lrsk0 arabidopsis	943	26	81.2	238	2	Q810E6	Q810e6 mus musculu
871	26	81.2	201	2	Q810E8	Q810e8 mus musculu	944	26	81.2	239	2	Q96UV6	Q96uv6 ophiostoma
872	26	81.2	202	2	Q6J9V1	Q6j9v1 zea mays (m	945	26	81.2	239	2	Q7P0A4	Q7p0a4 anopheles g
873	26	81.2	202	2	Q6ZFH8	Q6zfh8 oryza sativ	946	26	81.2	239	2	Q7D6T1	Q7d6t1 mycobacteri
874	26	81.2	202	2	Q9LRLO	Q9lrl0 arabidopsis	947	26	81.2	239	2	Q63275	Q63275 rattus norv
875	26	81.2	202	2	Q8RK24	Q8rk24 pseudomonas	948	26	81.2	239	2	Q6T5L0	Q6t5l0 gloydus sh
876	26	81.2	203	2	Q7SHI7	Q7shi7 neurospora	949	26	81.2	239	2	Q8AVC1	Q8avc1 xenopus lae
877	26	81.2	205	1	CN7A_SCHPO	Q9uu77 schizosacch	950	26	81.2	240	2	Q6BZV7	Q6bzv7 yarrowia li
878	26	81.2	205	1	Q8ZM06	Q8zm06 salmonella	951	26	81.2	240	2	Q7PYJ1	Q7pyj1 anopheles g
879	26	81.2	206	2	Q7S676	Q7s676 neurospora	952	26	81.2	240	2	Q9GV76	Q9gv76 lumbricus t
880	26	81.2	206	2	Q8LCQ1	Q8lcq1 arabidopsis	953	26	81.2	241	2	Q7ZXM1	Q7zxm1 xenopus lae
881	26	81.2	206	2	Q9LIW6	Q9liw6 streptomyce	954	26	81.2	242	2	Q6PIU7	Q6piu7 xenopus tro
882	26	81.2	207	2	Q6MWB3	Q6mwb3 oryza sativ	955	26	81.2	243	2	Q9CZY6	Q9czy6 homo sapien
883	26	81.2	207	2	Q66NL2	Q66nl2 human immun	956	26	81.2	243	2	Q16206	Q16206 caenorhabdi
884	26	81.2	208	2	Q9S214	Q9s214 arabidopsis	957	26	81.2	244	2	Q9A3W7	Q9a3w7 caulobacter
885	26	81.2	208	2	Q93515	Q93515 salmonella	958	26	81.2	244	2	Q93WH5	Q93wh5 oryza sativ
886	26	81.2	209	1	DR1F_ARATH	Q9lm86 arabidopsis	959	26	81.2	244	2	Q7W3G3	Q7w3g3 bordetella
887	26	81.2	209	2	Q6YWN0	Q6ywn0 oryza sativ	960	26	81.2	244	2	Q7WET3	Q7wet3 bordetella
888	26	81.2	211	2	Q94CW9	Q94cw9 oryza sativ	961	26	81.2	246	2	Q95ZC7	Q95zc7 leishmania
889	26	81.2	212	2	Q94SF9	Q94sf9 oryza sativ	962	26	81.2	247	2	Q52201	Q52201 pseudomonas
890	26	81.2	213	2	Q29521	Q29521 oryctolagus	963	26	81.2	247	2	Q88RE6	Q88re6 pseudomonas
891	26	81.2	213	2	Q29522	Q29522 oryctolagus	964	26	81.2	247	2	Q6H9T4	Q6h9t4 phage phi 4
892	26	81.2	213	2	Q82IM9	Q82im9 streptomyce	965	26	81.2	249	2	Q94I62	Q94i62 oryza sativ
893	26	81.2	214	1	ST14_SOLITU	Q41495 solanum tub	966	26	81.2	249	2	Q6H7Z8	Q6h7z8 oryza sativ
894	26	81.2	214	2	Q7QGN9	Q7qgn9 anopheles g	967	26	81.2	250	2	Q6CD23	Q6cd23 yarrowia li
895	26	81.2	214	2	Q7QGN0	Q7qgn0 anopheles g	968	26	81.2	251	2	Q7PF50	Q7pf50 anopheles g
896	26	81.2	214	2	Q6H3Y0	Q6h3y0 oryza sativ	969	26	81.2	251	2	Q9U7H5	Q9u7h5 plasmodium
897	26	81.2	216	2	Q9FBJ8	Q9fbj8 streptomyce	970	26	81.2	252	2	Q9LRJ9	Q9lrj9 arabidopsis
898	26	81.2	217	2	Q6ZKN8	Q6zkn8 homo sapien	971	26	81.2	254	2	Q95UP4	Q95up4 stomoxys ca
899	26	81.2	217	2	Q9LSJ7	Q9lsj7 arabidopsis	972	26	81.2	254	2	Q94IU1	Q94iu1 oryza sativ
900	26	81.2	218	2	Q6ZSC6	Q6zsc6 homo sapien	973	26	81.2	254	2	Q7N741	Q7n741 photorhabdu
901	26	81.2	218	2	Q85LN3	Q85ln3 oryza sativ	974	26	81.2	254	2	Q6IQY4	Q6iqy4 mus musculu
902	26	81.2	218	2	Q9LKR4	Q9lkr4 arabidopsis	975	26	81.2	255	2	Q9LJW2	Q9ljw2 arabidopsis
903	26	81.2	220	2	Q08332	Q08332 lycopersico	976	26	81.2	255	2	Q9SIP6	Q9sip6 arabidopsis
904	26	81.2	220	2	Q9LVZ8	Q9lvz8 arabidopsis	977	26	81.2	256	2	Q9LRK8	Q9lrk8 arabidopsis
905	26	81.2	220	2	Q8FO54	Q8fo54 corynebacte	978	26	81.2	256	2	Q7ML06	Q7ml06 vibrio vuln
906	26	81.2	221	2	Q9FZ32	Q9fz32 arabidopsis	979	26	81.2	256	2	Q7U9S0	Q7u9s0 synecococc
907	26	81.2	221	2	Q9ALZ8	Q9alz8 fremyella d	980	26	81.2	257	2	Q7Q2X4	Q7q2x4 anopheles g

981 26 81.2 257 2 Q9LRK3 Q9lrk3 arabidopsis
 982 26 81.2 257 2 Q9LRK6 Q9lr16 arabidopsis
 983 26 81.2 258 2 Q83P3 Q8s3p3 oryza sativ
 984 26 81.2 258 2 Q6ZDF4 Q6zdf4 oryza sativ
 985 26 81.2 258 2 Q7XN1 Q7x8n1 oryza sativ
 986 26 81.2 258 2 Q9LRK2 Q9lrk2 arabidopsis
 987 26 81.2 258 2 Q9W215 Q9m215 arabidopsis
 988 26 81.2 258 2 P71968 P71968 m possible
 989 26 81.2 258 2 Q7TY53 Q7ty53 mus musculus
 990 26 81.2 259 1 CFAD_MOUSE P03953 schistosoma
 991 26 81.2 259 1 MK16_SCHMA P46435 schistosoma
 992 26 81.2 259 1 RNS2_ARATH P42814 arabidopsis
 993 26 81.2 259 2 Q9V7E5 Q9v7e5 drosophila
 994 26 81.2 259 2 Q6NPE1 Q6npe1 arabidopsis
 995 26 81.2 259 2 Q697D7 Q697d7 escherichia
 996 26 81.2 260 2 Q6VPU6 Q6vp6 sarcoptes s
 997 26 81.2 260 2 Q6FNC8 Q6fnc8 arabidopsis
 998 26 81.2 260 2 Q7SZC3 Q7szc3 gallus gall
 999 26 81.2 261 2 Q7PZP7 Q7pzp7 anopheles g
 1000 26 81.2 261 2 Q9VXC7 Q9vxc7 drosophila

ALIGNMENTS

RESULT 1
 Q822Y9 ID Q822Y9 PRELIMINARY; PRT; 140 AA.
 AC Q822Y9;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=CCA00537;
 OS Chlamydomophila caviae.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomophila.
 OX NCBI_TaxID=83557;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GPIC;
 RX MEDLINE=22569155; PubMed=12682364; DOI=10.1093/nar/gkg321;
 RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
 RA Heidelberg J.F., Holtzaple E.K., Khouri H.M., Federova N.B.,
 RA Carty H.A., Unayam L.A., Haft D.H., Peterson J.D., Beanan M.J.,
 RA White O., Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G.,
 RA Bavoil P.M., Fraser C.M.;
 RT "Genome sequence of Chlamydomophila caviae (Chlamydia psittaci GPIC):
 RT examining the role of niche-specific genes in the evolution of the
 RT Chlamydiaceae.";
 RL Nucleic Acids Res. 31:2134-2147(2003).
 DR EMBL; AB016996; AAP05280.1; -;
 DR TIGR; CCA00537; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 140 AA; 15466 MW; 45345ECBD1EB644 CRC64;

Query Match 100.0%; Score 32; DB 2; Length 140;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 Db 66 CRGDD 70

RESULT 2
 Q8ZHJ9 ID Q8ZHJ9 PRELIMINARY; PRT; 174 AA.
 AC Q6ZHZ9;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Putative Vacuolar ATP synthase subunit G 1.
 GN Name=OU1218_D07.1-1; Synonyms=OU111_E07.26-1;

OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; AP004052; RAD07544.1; -;
 DR EMBL; AP003994; RAD07530.1; -;
 DR InterPro; IPR009019; KH_prok.
 DR InterPro; IPR005124; V-ATPase_G.
 DR Pfam; PF03179; V-ATPase_G; 1.
 SQ SEQUENCE 174 AA; 19423 MW; D8EAD87DC7369580 CRC64;
 Query Match 100.0%; Score 32; DB 2; Length 174;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 Db 21 CRGDD 25

RESULT 3
 Q9LEC1 ID Q9LEC1 PRELIMINARY; PRT; 187 AA.
 AC Q9LEC1;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Inhibitor of yeast proteinase A (Fragment).
 OS Lycopersicon esculentum (Tomato)
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA Cater S.A.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; AJ289776; CAB94854.1; -;
 DR GO; GO:0004866; F:endopeptidase inhibitor activity; IEA.
 DR InterPro; IPR011065; Kunitz like.
 DR InterPro; IPR002160; Prot_inh_Kunz-1g.
 DR Pfam; PF00197; Kunitz_legume; 1.
 DR PRINTS; PR00291; KUNITZINHSTR.
 DR ProDom; PD000891; Prot_inh_Kunz-1g; 1.
 DR SMART; SM00452; STI; 1.
 DR PROSITE; PS00283; SOYBEAN_KUNITZ; 1.
 FT NON_TER 1
 SQ SEQUENCE 187 AA; 20525 MW; 3229395B366D1B2A CRC64;

Query Match 100.0%; Score 32; DB 2; Length 187;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 Db 152 CRGDD 156

RESULT 4
 Q45047 ID Q45047 PRELIMINARY; PRT; 199 AA.
 AC Q45047;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative trypsin-like protein (Fragment).
 GN Name=TL3;

OS Scirpophaga incertulas.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;
 OC Pyralidae; Schoenobiinae; Scirpophaga.
 OX NCBI_TaxID=72366;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=IRRI; TISSUE=Midgut;
 RX MEDLINE=20110891; PubMed=10646971; DOI=10.1016/S0965-1748(99)00097-1;
 RA Mazumdar-Leighton S., Babu C.R., Bennett J.;
 RT "Identification of novel serine proteinase gene transcripts in the
 RT midguts of two tropical insect pests, Scirpophaga incertulas (Wk.) and
 RT Helicoverpa armigera";
 RL Insect Biochem. Mol. Biol. 30:57-68(2000).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=IRRI; TISSUE=Midgut;
 RA Mazumdar S.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF045142; AAC02220.1; -;
 DR HSSP; P00760; 3BTH.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR Pfam; PF00089; Trypsin; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 KW Hydrolase; Protease; Serine protease.
 FT NON_TER 1
 SQ SEQUENCE 199 AA; 21089 MW; 72E0DC50C0BB1968 CRC64;

Query Match 100.0%; Score 32; DB 2; Length 199;
 Best Local Similarity 100.0%; Pred. No. 79;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 |||||
 Db 151 CRGDD 155

RESULT 5
 Q9MCC2 ID Q9MCC2 PRELIMINARY; PRT; 215 AA.
 AC Q9MCC2;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Vpf215.
 GN Names=vpf215;
 OS Bacteriophage vFO4K68.
 OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
 OX NCBI_TaxID=127508;
 RN [1]
 RC SEQUENCE FROM N.A.
 RA Chang B., Miyamoto H., Taniguchi H., Yoshida S.;
 RT "Isolation and Genetic Characterization of a Novel Filamentous
 RT Bacteriophage, a Deleted Form of Phage f237, from a Pandemic Vibrio
 RT parahaemolyticus O4: K68 Strain."
 RL Microbiol. Immunol. 46:565-569(2002).
 DR EMBL; AB043679; BAA96438.1; -;
 SQ SEQUENCE 215 AA; 24626 MW; FF0839A0657EAD1B CRC64;

Query Match 100.0%; Score 32; DB 2; Length 215;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 |||||
 Db 97 CRGDD 101

RESULT 6
 Q9LEG1 ID Q9LEG1 PRELIMINARY; PRT; 220 AA.
 AC Q9LEG1;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cathespin D inhibitor precursor.
 GN Name=cathDinh;
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asteride;
 OC Lamids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA Lison P., Rodrigo I., Conejero V.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ295638; CAC00536.1; -;
 DR GO; GO:0004866; F:endopeptidase inhibitor activity; IEA.
 DR InterPro; IPR011065; Kunitz like.
 DR InterPro; IPR002160; Prot_inh_Kunz-lg.
 DR Pfam; PF00197; Kunitz_legume; 1.
 DR PRINTS; PR00291; KUNITZINHBR.
 DR ProDom; PD000891; Prot_inh_Kunz-lg; 1.
 DR SMART; SM00452; STI; 1.
 DR PROSITE; PS00283; SOYBEAN_KUNITZ; 1.
 KW Signal.
 FT SIGNAL 1 20 Potential.
 SQ SEQUENCE 220 AA; 24188 MW; 5DFFC488938D1F6A CRC64;

Query Match 100.0%; Score 32; DB 2; Length 220;
 Best Local Similarity 100.0%; Pred. No. 87;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 |||||
 Db 185 CRGDD 189

RESULT 7
 Q6D9R3 ID Q6D9R3 PRELIMINARY; PRT; 230 AA.
 AC Q6D9R3;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=ECA0552;
 OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Pectobacterium.
 OX NCBI_TaxID=29471;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=SCRI 1043 / ATCC BAA-672;
 RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
 RA Bell K.S., Sebahia M., Pritchard L., Holden M.T.G., Hyman L.J.,
 RA Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
 RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
 RA Fraser A., Hance Z., Hauser H., Moule S., Norbertczak H.,
 RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
 RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
 RT "Genome sequence of the enterobacterial phytopathogen Erwinia
 RT carotovora subsp. atroseptica and characterization of virulence
 RT factors."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
 DR EMBL; BX950851; CAG73467.1; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 230 AA; 26285 MW; 7E8007B2AADB73F CRC64;

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Query Match      100.0%; Score 32; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRGDD 5
DB      197 CRGDD 201

RESULT 8
Y166_METJA
ID Y166_METJA STANDARD; PRT; 255 AA.
AC Q57630;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypochemical UPF0204 protein MJ0166.
GN OrderedLocusNames=MJ0166;
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OX Methanocaldococcaceae; Methanocaldococcus.
RN [1]_TaxID=2190;
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervilave A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073 (1996).
CC -!- SIMILARITY: Belongs to the UPF0204 family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U67473; AAB98148.1; -.
DR F1R; G64320; G64320.
DR TIGR; MJ0166; -.
DR HAMAP; MF 00562; -; 1.
DR InterPro; IPR011007; B12 binding.
DR InterPro; IPR007508; DUF516.
DR Pfam; PF04414; DUF516; 1.
KW Complete proteome; Hypochemical protein.
SQ SEQUENCE 255 AA; 29072 MW; 6428DF/AEC802CE4 CRC64;

Query Match      100.0%; Score 32; DB 1; Length 255;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRGDD 5
DB      233 CRGDD 237

RESULT 9
Q9ZWQ4
ID Q9ZWQ4 PRELIMINARY; PRT; 280 AA.
AC Q9ZWQ4;
DT 01-MAY-1999 (TEMBLrel. 10, Created)
DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)

UDP-glycose:flavonoid glycosyltransferase (Fragment).
GN Name=UG1YT;
OS Vigna mungo (Rice bean) (Black gram).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCBI_TaxID=3915;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=NIAS no. R-29; TISSUE=First simple leaf;
RX MEDLINE=99108563; PubMed=9891414;
RA Mato M., Ozeki Y., Itoh Y., Higeta D., Yoshitama K., Teramoto S.,
RA Aida R., Ishikura N., Shibata M.;
RT "Isolation and characterization of a cDNA clone of UDP-galactose:
RT flavonoid 3-O-galactosyltransferase (UF3GaT) expressed in Vigna mungo
RT seedlings.";
RL Plant Cell Physiol. 39:1145-1155 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NIAS no. R-29; TISSUE=First simple leaf;
RA Matou M., Sibata M., Ozeki Y.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
DR EMBL; AB012115; BAA36411.1; -.
DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002213; UDP_glucos_trans.
DR Pfam; PF00201; UDPGT; 1.
DR PROSITE; PS00375; UDPGT; 1.
KW Glycosyltransferase; Transferase.
FT NON_TER 1
SQ SEQUENCE 280 AA; 30582 MW; 0A4A3705550B55A0 CRC64;

Query Match      100.0%; Score 32; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRGDD 5
DB      66 CRGDD 70

RESULT 10
Q9X6W2
ID Q9X6W2 PRELIMINARY; PRT; 289 AA.
AC Q9X6W2;
DT 01-NOV-1999 (TEMBLrel. 12, Created)
DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Oligopeptide transport system permease protein (Fragment).
GN Name=OppC;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Plasmid megaplasmid 2.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=CM1-188;
RA Krol E.A., Soberon M., Yurgel S.N., Miranda Rios J., Simarov B.V.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Part of a binding-protein-dependent transport system.
CC Probably responsible for the translocation of the substrate across
CC the membrane (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the binding-protein-dependent transport
CC system permease family.
DR EMBL; AF148072; AAD33993.1; -.
DR F1R; T44599; T44599.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000515; BPD_transp.

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DR InterPro: IPR011028; Cyclin-like.
DR Pfam: PF00528; BPD_transp_1; 1.
DR PROSITE: PS00928; ABC_TM1; 1.
KW Plasmid; Transmembrane; Transport.
FT NON TER 1
SQ SEQUENCE 289 AA; 31798 MW; F49623B724700D58 CRC64;

Query Match 100.0%; Score 32; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
Db 36 CRGDD 40

RESULT 11
HEM3_XANAC
ID HEM3_XANAC STANDARD; PRT; 304 AA.
AC Q8PPE3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Porphobilinogen deaminase (EC 2.5.1.61) (PBG) (Hydroxymethylbilane
synthase) (HMB) (Pre-uroporphyrinogen synthase).
GN Name-hemC; OrderedLocusNames=XAC0622;
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINES=2022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chamberg F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RA "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463 (2002).
CC -!- FUNCTION: Tetrapolymerization of the monopyrrole PBG into the
CC hydroxymethylbilane preuroporphyrinogen in several discrete steps.
CC -!- CATALYTIC ACTIVITY: 4 porphobilinogen + H(2)O =
CC hydroxymethylbilane + 4 NH(3).
CC -!- COFACTOR: Covalently binds a dipyrromethane cofactor to which the
CC porphobilinogen subunits are added (By similarity).
CC -!- PATHWAY: Porphyrin biosynthesis by the C5 pathway; fourth step.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the HMB family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: A5011690; AAC35511.1; -.
CC DR HSSP; P06983; LYPN.
CC DR HAMAP; MF_00260; -. 1.

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DR InterPro: IPR000860; Porphobil_deam.
DR Pfam: PF01379; Porphobil_deam_1.
DR PROSITE: PS03900; Porphobil_deamC; 1.
DR PRINTS: PR00151; PORPHBDMWASE.
DR ProDom: PD002745; Porphobil_deam; 1.
DR TIGRFAMs: TIGR00212; hemC; 1.
DR PROSITE: PS00533; PORPHOBILINOGEN_DEAM; 1.
KW Complete proteome; Porphyrin biosynthesis; Transferase.
FT BINDING 240 240 Pyrromethane cofactor (By similarity).
SQ SEQUENCE 304 AA; 32505 MW; E62CA6440DDA5DE8 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
Db 203 CRGDD 207

RESULT 12
HEM3_XANCP
ID HEM3_XANCP STANDARD; PRT; 304 AA.
AC Q8P536;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Porphobilinogen deaminase (EC 2.5.1.61) (PBG) (Hydroxymethylbilane
synthase) (HMB) (Pre-uroporphyrinogen synthase).
GN Name-hemC; OrderedLocusNames=XCC3511;
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=NTCC 33913 / NCPPB 528;
RX MEDLINES=2022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chamberg F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RA "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463 (2002).
CC -!- FUNCTION: Tetrapolymerization of the monopyrrole PBG into the
CC hydroxymethylbilane preuroporphyrinogen in several discrete steps.
CC -!- CATALYTIC ACTIVITY: 4 porphobilinogen + H(2)O =
CC hydroxymethylbilane + 4 NH(3).
CC -!- COFACTOR: Covalently binds a dipyrromethane cofactor to which the
CC porphobilinogen subunits are added (By similarity).
CC -!- PATHWAY: Porphyrin biosynthesis by the C5 pathway; fourth step.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the HMB family.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: A5011690; AAC35511.1; -.
CC DR HSSP; P06983; LYPN.
CC DR HAMAP; MF_00260; -. 1.

```

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CC -----
DR EMBL; AB012470; AAM42781.1; -.
DR HSP; P06983; 1YPN.
DR HAMAP; MF 00260; -: 1.
DR InterPro; IPR000860; Porphobil_deam.
DR Pfam; PF01379; Porphobil_deam; 1.
DR Pfam; PF03900; Porphobil_deamC; 1.
DR PRINTS; PR00151; PORPHBDNASE.
DR ProDom; PD002745; Porphobil_deam; 1.
DR TIGRFAMs; TIGR00212; hemC; 1.
DR PROSITE; PS00533; PORPHOBILINOGEN_DEAM; 1.
KW Complete proteome; Porphyrin biosynthesis; Transferase.
FT BINDING 240 240 Pyromethane cofactor (By similarity).
SQ SEQUENCE 304 AA; 32460 MW; F77A49FB1932FF02 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
Db 203 CRGDD 207

RESULT 13
LPP3 HUMAN STANDARD; PRT; 311 AA.
ID LPP3 HUMAN STANDARD; Q99782;
AC O14495; O96GW0; Q99782;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Lipid phosphate phosphohydrolase 3 (EC 3.1.3.4) (Phosphatidic acid
DE phosphatase 2b) (Phosphatidate phosphohydrolase type 2b) (PAP2b) (PAP-
DE 2b) (PAP2-beta) (Vascular endothelial growth factor and type I
DE collagen inducible protein) (VCIP).
GN Name=PPAP2B; Synonyms=LPP3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A., CHARACTERIZATION, AND INDUCTION.
RX MEDLINE=97450990; PubMed=9305923; DOI=10.1074/jbc.273.39.24572;
RA Kai M., Wada I., Imai S.-I., Sakane F., Kanoh H.;
RT "Cloning and characterization of two human isozymes of Mg2+-
RT independent phosphatidic acid phosphatase.";
RL J. Biol. Chem. 272:24572-24578(1997).
[2]
SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=98371049; PubMed=9705349; DOI=10.1074/jbc.273.34.22059;
RA Roberts R., Sciorra V.A., Morris A.J.;
RT "Human type 2 phosphatidic acid phosphohydrolases. Substrate
RT specificity of the type 2a, 2b, and 2c enzymes and cell surface
RT activity of the 2a isoform.";
RL J. Biol. Chem. 273:22059-22067(1998).
[3]
SEQUENCE FROM N.A.
RX PubMed=12660161; DOI=10.1093/emboj/cdg165;
RA Humceoe J.O., Feng S., Thakker G.D., Yang J., Hong J., Wary K.K.;
RT "Regulation of cell-cell interactions by phosphatidic acid phosphatase
RT 2b/VCIP.";
RL EMBO J. 22:1539-1554(2003).
[4]
SEQUENCE FROM N.A.
RX Leung D.W., Tompkins C.K.;
RT "Molecular cloning and expression of an isoform of human
RT phosphatidic acid phosphatase cDNA.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
[5]
SEQUENCE FROM N.A.
RX MEDLINE=97264341; PubMed=9110174;
RA Yu W., Anderson B., Worley K.C., Muzny D.M., Ding Y., Liu W.,
RA Ricafrente J.Y., Wentland M.C., Lennon G., Gibbs R.A.;
```

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RT "Large-scale concatenation cDNA sequencing.";
RL Genome Res. 7:353-358(1997).
RN [6]
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[7]
RP SUBUNIT.
PubMed=14725715; DOI=10.1186/1471-2091-5-2;
RA Burnett C., Makridou P., Hewlett L., Howard K.;
RT "Lipid phosphate phosphatases dimerise, but this interaction is not
RT required for in vivo activity.";
RL BMC Biochem. 5:2-2(2004).
CC -!- FUNCTION: Catalyzes the conversion of phosphatidic acid (PA) to
CC diacylglycerol (DG). In addition it hydrolyzes lysophosphatidic
CC acid (LPA), ceramide-1-phosphate (C-1-P) and sphingosine-1-
CC phosphate (S-1-P). The relative catalytic efficiency is LPA = PA >
CC C-1-P > S-1-P. May be involved in cell adhesion and in cell-cell
CC interactions.
CC -!- CATALYTIC ACTIVITY: A 3-sn-phosphatidate + H(2)O = 1,2-diacyl-
CC sn-glycerol + phosphate.
CC -!- ENZYME REGULATION: Inhibited by sphingosine, zinc ions and
CC propanolol. Not inhibited by N-ethylmaleimide treatment.
CC -!- SUBUNIT: Homodimer. This complex seems not to be involved in
CC substrate recognition, it may confer only structural or functional
CC stability.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Post-Golgi and
CC plasma membrane localization.
CC -!- TISSUE SPECIFICITY: Ubiquitously expressed. Highly expressed in
CC heart and placenta.
CC -!- INDUCTION: By epidermal growth factor (EGF), vascular endothelial
CC growth factor (VEGF), basic fibroblast growth factor (bFGF) and
CC phorbol myristate acetate (PMA).
CC -!- PTM: N-glycosylated. Contains high-mannose oligosaccharides.
CC -!- SIMILARITY: Belongs to the PA-phosphatase related phosphoesterase
CC family.
CC -!- CAUTION: Ref 5 sequence differs from that shown due to a
CC frameshift in position 225.
-----
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DR EMBL; AB000889; BAA22594.1; -.
DR EMBL; AF017786; AAC63433.1; -.
DR EMBL; AF480883; AAO84481.1; -.
DR EMBL; AF043329; AAO2271.1; -.
DR EMBL; U79294; AAB50222.1; ALT_FRAME.
DR EMBL; BC009196; AAB09196.1; -.
DR
```

Genew: HGNC:9229; PPAP2B.
 H-InvdB; HIX000628; -.
 Reactome; O14495; -.
 MIM; 607125; -.
 GO; GO:0016020; C:membrane; TAS.
 GO; GO:0004721; F:phosphoprotein phosphatase activity; TAS.
 GO; GO:0008151; P:cell growth and/or maintenance; TAS.
 GO; GO:0008354; P:germ-cell migration; TAS.
 InterPro; IPR008934; AcPase_Vanferase.
 InterPro; IPR000326; Pestase_PA_PTP.
 Pfam; PF01569; PAP2; 1.
 SMART; SM00014; acidPPC; 1.
 Glycoprotein; Hydrolase; Transmembrane.
 DOMAIN 1 33 Cytoplasmic (Potential).
 TRANSMEM 34 54 Potential.
 DOMAIN 55 85 Luminal (Potential).
 TRANSMEM 86 106 Potential.
 DOMAIN 107 122 Cytoplasmic (Potential).
 TRANSMEM 123 143 Potential.
 DOMAIN 144 193 Luminal (Potential).
 TRANSMEM 194 214 Potential.
 DOMAIN 215 227 Cytoplasmic (Potential).
 TRANSMEM 228 248 Potential.
 DOMAIN 249 257 Luminal (Potential).
 TRANSMEM 258 278 Potential.
 DOMAIN 279 311 Cytoplasmic (Potential).
 CARBOHYD 170 170 N-linked (GlcNAc...) (Potential).
 CONFLICT 282 282 T -> M (in Ref. 6).
 SQ SEQUENCE 311 AA; 35116 MW; CB3F60189044DA31 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 311;
 Best Local Similarity 100.0%; Pred. NO. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 |||||
 Db 181 CRGDD 185

RESULT 14
 Q6NS11 PRELIMINARY; PRT; 321 AA.
 AC Q6NS11;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE FLJ43980 protein.
 GN Names=FLJ43980;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RX [1]
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 enterica serovar Typhi CT18.";
 Nature 413:848-852 (2001).
 RC TISSUE=Testis;
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J.J., Heiton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 Krzywicki M.I., Skalek A., Smaluk U., Smaluk D.E., Schnerch A., Schein J.E.,
 Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Director MGC Project;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC070117; AAH70117.1; -.
 DR InterPro; IPR002110; ANK.
 DR Pfam; PF00023; ANK; 4.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 4.
 DR PROSITE; PS00088; ANK_REPEAT; 3.
 DR PROSITE; PS0297; ANK_REPEAT; 1.
 KW ANK repeat.
 SQ SEQUENCE 321 AA; 35410 MW; 60C46EFC62716EB4 CRC64;

Query Match 100.0%; Score 32; DB 2; Length 321;
 Best Local Similarity 100.0%; Pred. NO. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 |||||
 Db 25 CRGDD 29

RESULT 15
 Q8Z0U7 PRELIMINARY; PRT; 357 AA.
 ID Q8Z0U7; Q7C4T9;
 AC Q8Z0U7; Q7C4T9; 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein STV4914.
 GN OrderedLocNames=STV4914, t4606;
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 ON NCBI_TaxID=601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
 Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
 Whitehead S., Barrrell B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 enterica serovar Typhi CT18.";
 Nature 413:848-852 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ty2 / ATCC 700931;
 RX MEDLINE=22531367; PubMed=12644504;
 DOI=10.1128/JB.185.7.2330-2337.2003;
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
 Burland V., Kodoyanni V., Schwartz D.C., Blattner F.R.;
 RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
 and CT18.";
 J. Bacteriol. 185:2330-2337 (2003).
 RL J. Bacteriol. 185:2330-2337 (2003).
 DR EMBL; AL627284; CAD03398.1; -.
 DR EMBL; AE016849; AAO72038.1; -.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
 DR Pfam; PF01734; Patatin; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 357 AA; 39633 MW; A3432EC13D097E6B CRC64;

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Query Match      100.0%; Score 32; DB 2; Length 357;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRGDD 5
DB      139 CRGDD 143

RESULT 16
Q8ZJW2
ID Q8ZJW2 PRELIMINARY; PRT; 357 AA.
AC Q8ZJW2;
DT 01-NAR-2002 (TrEMBLrel. 20, Created)
DT 01-NAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative phosphoesterase.
GN Name=yjjj; OrderedLocusNames=STM4563;
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856 (2001).
DR EMBL; AB008914; AAL23378.1; -.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR Pfam; PF01734; Patatin; 1.
KW Complete proteome.
SQ SEQUENCE 357 AA; 39650 MW; 945E297E5DB3394E CRC64;

Query Match      100.0%; Score 32; DB 2; Length 357;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRGDD 5
DB      139 CRGDD 143

RESULT 17
Q92VE0
ID Q92VE0 PRELIMINARY; PRT; 363 AA.
AC Q92VE0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative mureinpeptideoligopeptide ABC transporter permease
DE protein.
GN ORFNames=SWB21263;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OG Plasmid pSymB.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396508; PubMed=11481431; DOI=10.1073/pnas.161294698;
RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
RA Vorhoelzer F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
RA Golding B., Puehler A.;
RT "The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-
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RT fixing endosymbiont Sinorhizobium meliloti.";
Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894 (2001).
CC -|- FUNCTION: Part of a binding-protein-dependent transport system.
CC Probably responsible for the translocation of the substrate across
CC the membrane (By similarity).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -|- SIMILARITY: Belongs to the binding-protein-dependent transport
CC system permease family.
DR EMBL; AL591985; CAC49167.1; -.
DR PIR; G95937; G95937.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR00515; BPD transp.
DR InterPro; IPR011028; Cyclin like.
DR Pfam; PF00528; BPD transp. 1.
DR PROSITE; PS50928; ABC_TWI_1.
KW Complete proteome; Plasmid; Transmembrane; Transport.
SQ SEQUENCE 363 AA; 40408 MW; 45718411C8821F24 CRC64;

Query Match      100.0%; Score 32; DB 2; Length 363;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRGDD 5
DB      110 CRGDD 114

RESULT 18
Q98IE7
ID Q98IE7 PRELIMINARY; PRT; 372 AA.
AC Q98IE7;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE NADH-dependent dyhydrogenase.
GN OrderedLocusNames=mlr2436;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338 (2000).
DR EMBL; AP002999; BAB49569.1; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000683; GFO/IDH/MocA_N.
DR Pfam; PF01408; GFO_IDH_MocA; 1.
KW Complete proteome.
SQ SEQUENCE 372 AA; 40635 MW; 1A1A307A237B8CCD CRC64;

Query Match      100.0%; Score 32; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRGDD 5
DB      167 CRGDD 171

RESULT 19
Q8S9A8
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ID Q8S9A8 PRELIMINARY; PRT; 390 AA.
AC Q8S9A8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Glucosyltransferase-1 (Fragment).
GN Name=AdGT-1;
OS Phaseolus angularis (Adzuki bean) (Vigna angularis).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCBI_TaxID=3914;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hypocotyl;
RA Xu Z.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
DR EMBL; AB070743; BAB86919.1; -.
DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002213; UDP-glucos_trans.
DR Pfam; PF00201; UDPGT; 1.
DR PROSITE; PS00375; UDPGT; 1.
KW Glycosyltransferase; Transferase.
FT NON_TER 1 1
SQ SEQUENCE 390 AA; 43122 MW; AABDE97E71A8D009 CRC64;

Query Match 100.0%; Score 32; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
Db 176 CRGDD 180

RESULT 20
Q8LMH4 PRELIMINARY; PRT; 393 AA.
ID Q8LMH4;
AC Q8LMH4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein OSJNBa0032N04.16;
GN Name=OSJNBa0032N04.16;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA McCombie W.R., de la Bastide M., Spiegel L., Preston R., Ferraro K.,
RA Kuit K., Nascimento L., Zutavern T., Ballia V., Bell M., Baker J.,
RA Santos L., Miller B., Katzenberger F., Muller S., King L., Yang C.,
RA Dike S., O'Shaughnessy A., Palmer L., Dedhia N.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC114474; AAM74325.2; -.
DR Gramene; Q8LMH4; -.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00846; F-box; 1.
DR SMART; SM00256; FBOX; 1.
KW Hypothetical protein.
SQ SEQUENCE 393 AA; 45232 MW; 7C85AB25EFOA70C2 CRC64;

Query Match 100.0%; Score 32; DB 2; Length 393;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
Db 175 CRGDD 179

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RESULT 21
PNCB_ECO57 STANDARD; PRT; 399 AA.
ID PNCB_ECO57
AC Q8XD58;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Nicotinate phosphoribosyltransferase (EC 2.4.2.11) (NAPRTase).
GN Name=pncB; OrderedLocNames=z1279, EGS1014;
OS Escherichia coli O157:H7;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.P., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22(2001).
CC -!- CATALYTIC ACTIVITY: Nicotinate D-ribonucleotide + diphosphate =
CC nicotinate + 5-phospho-alpha-D-ribose 1-diphosphate.
CC -!- PATHWAY: NAD biosynthesis; nicotinamide to NAMN; second step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the NAPRTase family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; AB005283; AAG55416.1; -.
CC EMBL; AP002553; BAB34437.1; -.
CC PIR; D85619; D85619.
CC PIR; F90755; F90755.
CC HAMAP; MF_00570; -.
CC InterPro; IPR007229; NAPRTase.
CC InterPro; IPR006406; Nic Prtrans.
CC InterPro; IPR008967; P53_like_DNA_bnd.
CC Pfam; PF04095; NAPRTase; 1.
CC PIRSF; PIRSF000484; Nicot_phos_ribo; 1.
CC TIGRFAMs; TIGR01514; NAPRTase; 1.
KW Complete proteome; Glycosyltransferase;
KW Pyridine nucleotide biosynthesis; Transferase.
FT INIT_MET 0 0 By similarity
SQ SEQUENCE 399 AA; 45838 MW; 47DAC387A0EC6926 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5

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Db          40 CRGDD 44

RESULT 22
PNCB_ECOLI
ID PNCB_ECOLI STANDARD; PRT; 399 AA.
AC P18133;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Nicotinate phosphoribosyltransferase (EC 2.4.2.11) (NAPRTase).
GN Name=pncB; OrderedLocusNames=b0931;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
RC STRAIN=GEC70;
RX MEDLINE=91009224; PubMed=2211655;
RA Rubolts M.G., Terpstra P., van Beilen J.B., Kingma J.,
RA Meesters H.A.R., Witholt B.;
RT "Variation of cofactor levels in Escherichia coli. Sequence analysis
RT and expression of the pncB gene encoding nicotinic acid
RT phosphoribosyltransferase."
RL J. Biol. Chem. 265:17665-17672(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-Kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map."
RL DNA Res. 3:137-155(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TY2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RX DOI=10.1128/JB.185.7.2330-2337.2003;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodyanni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18."
RL J. Bacteriol. 185:2330-2337(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TY2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RX DOI=10.1128/JB.185.7.2330-2337.2003;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodyanni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18."
RL J. Bacteriol. 185:2330-2337(2003).
RN [2]
RP SEQUENCE FROM N.A.
CC -!- CATALYTIC ACTIVITY: Nicotinate D-ribonucleotide + diphosphate =
CC nicotinate + 5-phospho-alpha-D-ribose 1-diphosphate.
CC -!- PATHWAY: NAD biosynthesis; nicotinamide to NADH; second step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the NAPRTase family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC -----
CC EMBL; J05568; AAA24400.1; -.
CC EMBL; U00096; AAC74017.1; -.
CC EMBL; D90731; BAA35683.1; -.
CC PIR; JQ0756; JQ0756.
CC ECHOBASE; EB0735; -.
CC EcoGene; EG10742; pncB.
CC HAMAP; MF_00570; -; 1.
CC

```


DR	InterPro: IPR007229; NAPRTase.
DR	InterPro: IPR006406; Nic_Prtans.
DR	InterPro: IPR008967; P53_like_DNA_bnd.
DR	Pfam: PF040095; NAPRTase; 1.
DR	PIRSE: PIRSF000484; Nicot_phos_ribo; 1.
DR	TIGRFAMs: TIGR01514; NAPRTase; 1.
DR	Complete proteome; Glycosyltransferase;
KW	Pyridine nucleotide biosynthesis; Transferase.
FT	INIT MET 0
SQ	SEQUENCE 399 AA; 45530 MW; 90D9C3EDD8C092A6 CRC64;
Query Match 100.0%; Score 32; DB 1; Length 399;	
Best Local Similarity 100.0%; Pred. No. 1.6e+02;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 CRGDD 5
DB	
	40 CRGDD 44
RESULT 25	
Q7UD27	PRELIMINARY; PRT; 400 AA.
ID	Q7UD27
AC	Q7UD27;
DT	01-OCT-2003 (TEMBLrel. 25, Created)
DT	01-OCT-2003 (TEMBLrel. 25, Last sequence update)
DT	01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE	Nicotinate phosphoribosyltransferase.
GN	Name=pncB; OrderedLocusNames=S0992;
OS	Shigella flexneri.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC	Enterobacteriaceae; Shigella.
NCBI_TaxID=623;	
LN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=2457T;
RC	MEDLINE=22590274; PubMed=12704152;
RX	DOI=10.1128/IAI.71.5.2775-2786.2003;
RA	Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA	Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA	Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA	Schwartz D.C., Blattner F.R.;
RT	"Complete genome sequence and comparative genomics of Shigella
RT	flexneri serotype 2a strain 2457T.";
RL	Infect. Immun. 71:2775-2786(2003).
DR	EMBL: AE015981; AAP16443.1; -
DR	GO: GO:0004516; F:nicotinate phosphoribosyltransferase activity; IEA.
DR	GO: GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR	GO: GO:0019357; P:nicotinate nucleotide biosynthesis; IEA.
GO	GO: GO:0019363; P:pyridine nucleotide biosynthesis; IEA.
DR	InterPro: IPR007229; NAPRTase.
DR	InterPro: IPR006406; Nic_Prtans.
DR	InterPro: IPR008967; P53_like_DNA_bnd.
DR	Pfam: PF040095; NAPRTase; 1.
DR	PIRSE: PIRSF000484; Nicot_phos_ribo; 1.
DR	TIGRFAMs: TIGR01514; NAPRTase; 1.
KW	Glycosyltransferase; Transferase.
SQ	SEQUENCE 400 AA; 45911 MW; 5385BCB1A8703095 CRC64;
Query Match 100.0%; Score 32; DB 2; Length 400;	
Best Local Similarity 100.0%; Pred. No. 1.6e+02;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 CRGDD 5
DB	
	41 CRGDD 45
RESULT 26	
Q83LN3	PRELIMINARY; PRT; 416 AA.
ID	Q83LN3
AC	Q83LN3;
DT	01-JUN-2003 (TEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Nicotinate phosphoribosyltransferase.
 GN Name=pncB; OrderedLocusNames=SF0928;
 OS Shigella flexneri.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Shigella.
 OX NCBI_TaxID=623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=301 / Serotype 2a;
 RX MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
 RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
 RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
 RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
 RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
 RA Yu J.;
 RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
 through comparison with genomes of Escherichia coli K12 and O157.";
 RL Nucleic Acids Res. 30:4432-4441(2002).
 DR EMBL; AE015122; AAN42557.1; -;
 DR GO; GO:0004516; F:nicotinate phosphoribosyltransferase activity; IEA.
 DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
 DR GO; GO:0019357; P:nicotinate nucleotide biosynthesis; IEA.
 DR GO; GO:0019363; P:pyridine nucleotide biosynthesis; IEA.
 DR InterPro; IPR007229; NAPRTase.
 DR InterPro; IPR006406; Nic_Prtans.
 DR InterPro; IPR008967; P53_like_DNA_bnd.
 DR Pfam; PF04095; NAPRTase; 1.
 DR PIRSF; PIRSF000484; Nicot_phos_ribo; 1.
 DR TIGRFAMs; TIGR01514; NAPRTase; 1.
 DR Complete proteome; Glycosyltransferase; Transferase.
 KW Complete proteome; Glycosyltransferase; Transferase.
 SQ SEQUENCE 416 AA; 47700 MW; E43D723542AF2DD5 CRC64;

 Query Match 100.0%; Score 32; DB 2; Length 416;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 CRGDD 5
 Db |||||
 57 CRGDD 61

 RESULT 27
 ID Q8FJ98 PRELIMINARY; PRT; 416 AA.
 AC Q8FJ98;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Nicotinate phosphoribosyltransferase (EC 2.4.2.11).
 GN Name=pncB; OrderedLocusNames=c1073;
 OS Escherichia coli O6.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=217992;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O6:H1 / CFT073 / ATCC 700928 / UPEC;
 RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
 RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
 RT "Extensive mosaic structure revealed by the complete genome sequence
 of uropathogenic Escherichia coli.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
 RL EMBL; AE016758; AAN79541.1; -;
 DR GO; GO:0004516; F:nicotinate phosphoribosyltransferase activity; IEA.
 DR GO; GO:0019357; P:nicotinate nucleotide biosynthesis; IEA.
 DR GO; GO:0019363; P:pyridine nucleotide biosynthesis; IEA.
 DR InterPro; IPR007229; NAPRTase.
 DR InterPro; IPR006406; Nic_Prtans.

DR InterPro; IPR008967; P53_like_DNA_bnd.
 DR Pfam; PF04095; NAPRTase; 1.
 DR PIRSF; PIRSF000484; Nicot_phos_ribo; 1.
 DR TIGRFAMs; TIGR01514; NAPRTase; 1.
 KW Complete proteome.
 SQ SEQUENCE 416 AA; 47722 MW; F00AFC07B04B1E23 CRC64;

 Query Match 100.0%; Score 32; DB 2; Length 416;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 CRGDD 5
 Db |||||
 57 CRGDD 61

 RESULT 28
 ID Q7XF76 PRELIMINARY; PRT; 428 AA.
 AC Q7XF76;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=OSJNB0032N04.17;
 DE ORFNames=OSJNB0032N04.17;
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA The Rice Chromosome 10 Sequencing Consortium;
 RT "In-depth view of structure, activity, and evolution of rice
 chromosome 10.";
 RL Science 300:1566-1569 (2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE017087; AAP53454.1; -;
 DR Gramene; Q7XF76; -;
 DR InterPro; IPR001810; F-box.
 DR Pfam; PF00646; F-box; 1.
 DR SMART; SM00256; FBOX; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 428 AA; 49415 MW; B2A9D80D969D2C1F CRC64;

 Query Match 100.0%; Score 32; DB 2; Length 428;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 CRGDD 5
 Db |||||
 175 CRGDD 179

 RESULT 29
 ID SYS_SYNY3 STANDARD; PRT; 430 AA.
 AC P73201;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Seryl-tRNA synthetase (EC 6.1.1.11) (Serine--tRNA ligase) (SerRS).
 GN Name=serS; OrderedLocusNames=srl1703;
 OC Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,

RA Miyajima N., Hirose M., Sugiura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -1- CATALYTIC ACTIVITY: ATP + L-serine + tRNA(Ser) = AMP + diphosphate
CC + L-seryl-tRNA(Ser).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the class-II aminoacyl-tRNA synthetase
CC family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D90904; BAA17227.1; -.
CC PIR: S75313; S75313.
CC HSP: P34945; I5ER.
CC HAMAP: MF_00176; -; 1.
CC InterPro: IPR002314; tRNA-synt 2b.
CC InterPro: IPR002317; tRNA-synt ser.
CC InterPro: IPR010978; tRNA binding arm.
CC InterPro: IPR006195; tRNA_ligase_II.
CC Pfam: PF02403; Seryl_tRNA_N; 1.
CC Pfam: PF00587; tRNA-synt 2b; 1.
CC PRINTS: PR00981; TRNASYNTHSER.
CC TIGRFAMs: TIGR00414; serS; 1.
CC PROSITE: PS50862; AA tRNA LIGASE II; 1.
KW Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Ligase;
KW Protein biosynthesis.
SQ SEQUENCE 430 AA; 48038 MW; 0E6A54434DB355E4 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 430;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
Db 228 CRGDD 232

RESULT 30
Q804X1 PRELIMINARY; PRT; 442 AA.
AC Q804X1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Coagulation factor VIIb (EC 3.4.21.21).
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorphia; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA Davidson C.J., Hirt R.P., Lal K., Snell P., Elgar G.,
RA Tuddenham E.G.D., McVey J.H.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family S1.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
DR EMBL: AF465274; AAO33369.1; -.
DR HSP: P00740; 1CFH.
DR GO: GO:0005576; C:extracellular; IEA.

DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0004263; F:chymotrypsin activity; IEA.
DR GO: GO:0003802; F:coagulation factor VIIa activity; IEA.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0004295; F:trypsin activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR002383; GLA blood.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR001254; Peptidase S1.
DR InterPro: IPR001314; Peptidase_S1A.
DR InterPro: IPR009003; Pst_Ser_Cys.
DR InterPro: IPR000294; VICK_dep_GLA.
DR Pfam: PF00008; EGF; 2.
DR Pfam: PF00594; Gla; 1.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF; 2.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; Tryp_SPC; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS50026; EGF_3; 1.
DR PROSITE: PS00011; GLA_1; 1.
DR PROSITE: PS0240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 442 AA; 48787 MW; 810A561A127F0CF7 CRC64;

Query Match 100.0%; Score 32; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
Db 383 CRGDD 387

RESULT 31
Q8S6K3 PRELIMINARY; PRT; 446 AA.
ID Q8S6K3;
AC Q8S6K3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein OSJNBa0019N10.23.
GN Name=OSJNBa0019N10.23;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nipponbare;
RA McCombie W.R., de la Bastide M., Spiegel L., Preston R., Kirchoff K.,
RA Kuit K., Nascimento L., Zucavern T., Balija V., Bell M., Baker J.,
RA Santos L., Miller B., Katzenberger F., Muller S., King L., Yang C.,
RA O'Shaughnessy A., Palmer L., Dedhia N.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC092748; AAM01085.1; -.
DR Gramene; Q8S6K3; -.
DR InterPro: IPR001810; F-box.
DR Pfam: PF00646; F-box; 1.
DR SMART: SM00256; FBOX; 1.
KW Hypothetical protein.
SQ SEQUENCE 446 AA; 51647 MW; 361F9047C4CCA649 CRC64;

Query Match 100.0%; Score 32; DB 2; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 CRGDD 5
Db      175 CRGDD 179

RESULT 32
Q8H4V4
ID      Q8H4V4      PRELIMINARY;      PRT;      446 AA.
AC      Q8H4V4;
DT      01-MAR-2003 (TrEMBLrel. 23, Created)
DT      01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Putative wall-associated kinase.
GN      Name=OJ1484.G09.127;
OS      Oryza sativa (japonica cultivar-group).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC      Ehrhartoideae; Oryzeae; Oryza.
OX      NCBI_TaxID=39947;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Sasaki T., Matsumoto T., Yamamoto K.;
RL      Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF003913; BAC24910.1; -.
DR      Gramene; Q8H4V4; -.
DR      GO; GO:0016301; F:kinase activity; IEA.
DR      InterPro; IPR006210; IEGF.
DR      SMART; SM00181; EGF; 1.
KW      Kinase.
SQ      SEQUENCE 446 AA; 47726 MW; 7BE3D91AD2ABC49C CRC64;

Query Match      100.0%; Score 32; DB 2; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRGDD 5
Db      232 CRGDD 236

RESULT 33
Q8VUB7
ID      Q8VUB7      PRELIMINARY;      PRT;      448 AA.
AC      Q8VUB7;
DT      01-MAR-2002 (TrEMBLrel. 20, Created)
DT      01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Hypothetical protein orf448.
GN      Name=orf448;
OS      Bradyrhizobium sp. ORS278.
OC      Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC      Bradyrhizobiaceae; Bradyrhizobium.
OX      NCBI_TaxID=114615;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      STRAIN=ORS278;
RX      MEDLINE=20570559; PubMed=11114184; DOI=10.1073/pnas.250484097;
RA      Giraud E., Hannibal L., Fardoux J., Jaubert M., Jourand P.,
RT      "Effect of Bradyrhizobium photosynthesis on stem nodulation of
RT      Aeschynomene sensitiva.";
RL      Proc. Natl. Acad. Sci. U.S.A. 97:14795-14800 (2000).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=ORS278;
RX      PubMed=14734565; DOI=10.1074/jbc.M312113200;
RA      Giraud E., Hannibal L., Fardoux J., Jaubert M., Jourand P.,
RA      Dreyfus B., Sturgis J.N., Vermeglio A.;
RT      "Two distinct crt gene clusters for two different functional classes
RT      of carotenoid in bradyrhizobium.";
RL      J. Biol. Chem. 279:15076-15083 (2004).
RN      [3]
RP      SEQUENCE FROM N.A.

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RC      STRAIN=ORS278;
RA      Giraud E., Hannibal L., Fardoux J., Jaubert M., Vermeglio A.,
RA      Pignol D.;
RT      "Light and redox control of photosynthesis gene expression in
RT      Bradyrhizobium: Dual roles of two Ppsk.";
RL      Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF182374; AAL68699.1; -.
DR      GO; GO:0003677; F:DNA binding; IEA.
DR      GO; GO:0004803; F:transposase activity; IEA.
DR      GO; GO:0006313; P:DNA transposition; IEA.
DR      Pfam; PF01609; Transposase_11; 1.
SQ      SEQUENCE 448 AA; 50151 MW; 9387B4BB95BAA0FE CRC64;

Query Match      100.0%; Score 32; DB 2; Length 448;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRGDD 5
Db      337 CRGDD 341

RESULT 34
Q6Z4U6
ID      Q6Z4U6      PRELIMINARY;      PRT;      469 AA.
AC      Q6Z4U6;
DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DT      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE      Putative Anthocyanin 5-aromatic acyltransferase.
GN      Name=OSJNBa0054L03.25;
OS      Oryza sativa (japonica cultivar-group).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC      Ehrhartoideae; Oryzeae; Oryza.
OX      NCBI_TaxID=39947;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Sasaki T., Matsumoto T., Katayose Y.;
RT      "Oryza sativa nipponbare (GAL) genomic DNA, chromosome 8, BAC
RT      clone:OSJNBa0054L03.";
RL      Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AP005164; BAD05543.1; -.
DR      GO; GO:0008415; F:acyltransferase activity; IEA.
DR      GO; GO:0016740; F:transferase activity; IEA.
DR      InterPro; IPR003480; Transferase.
DR      Pfam; PF02458; Transferase; 1.
KW      Acyltransferase; Transferase.
SQ      SEQUENCE 469 AA; 48770 MW; 08C7B6076576A39C CRC64;

Query Match      100.0%; Score 32; DB 2; Length 469;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRGDD 5
Db      201 CRGDD 205

RESULT 35
Q7PPD6
ID      Q7PPD6      PRELIMINARY;      PRT;      491 AA.
AC      Q7PPD6;
DT      01-MAR-2004 (TrEMBLrel. 26, Created)
DT      01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      ENSANGP0000021570 (Fragment).
GN      Name=ENSANGG00000019081;
OS      Anopheles gambiae str. PEST.
OC      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC      Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX      NCBI_TaxID=180454;

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RP SEQUENCE FROM N.A.
RA STRAIN=PEST;
RL Anopheles Genome Sequencing Consortium;
RM Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
SQ SEQUENCE 497 AA; 55709 MW; 13EB96600D557B74 CRC64;
Query Match 100.0%; Score 32; DB 2; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRGDD 5
DB 252 CRGDD 256

RESULT 36
Q859H6 PRELIMINARY; PRT; 497 AA.
AC Q859H6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
OS Bacteriophage f237.
OC Viruses.
ON NCBI_TaxID=221993;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22562669; PubMed=12676700;
RX DOI=10.1128/AEM.69.4.2194-2200.2003;
RA Myers M.L., Panicker G., Bej A.K.;
RT PCR detection of a newly emerged pandemic Vibrio parahaemolyticus
RT O3:k6 pathogen in pure cultures and seeded waters from the Gulf of
RT Mexico.";
RL Appl. Environ. Microbiol. 69:2194-2200(2003).
DR EMBL: AY196594; AAO46790.1; -.
KW Hypothetical protein.
SQ SEQUENCE 497 AA; 55709 MW; 13EB96600D557B74 CRC64;
Query Match 100.0%; Score 32; DB 2; Length 497;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRGDD 5
DB 97 CRGDD 101

RESULT 37
Q9MCC5 PRELIMINARY; PRT; 497 AA.
AC Q9MCC5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Vpf497.
GN Names=vpf497;
OS Bacteriophage VFO3K6.
OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
ON NCBI_TaxID=127507;
RN [1]

RP SEQUENCE FROM N.A.
RA Chang B., Miyamoto H., Ogawa M., Yoshida S., Taniguchi H.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB043678; BAA96428.1; -.
SQ SEQUENCE 497 AA; 55788 MW; 274E868DEB6E8B19 CRC64;
Query Match 100.0%; Score 32; DB 2; Length 497;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRGDD 5
DB 97 CRGDD 101

RESULT 38
Q9KGQ6 PRELIMINARY; PRT; 497 AA.
AC Q9KGQ6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein orf8 (Bacteriophage f237 ORF8).
GN Name=orf8; OrderedLocustNames=VP1561;
OS Vibrio parahaemolyticus.
OG Plasmid pO3K6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KKV237; PLASMID=PO3K6;
RX MEDLINE=20295086; PubMed=10834969;
RA Nasu H., Iida T., Sugahara T., Yamaichi Y., Park K., Yokoyama K.,
RA Makino K., Shinagawa H., Honda T.;
RT "A filamentous phage associated with recent pandemic Vibrio
RT parahaemolyticus O3:k6 strains.";
RL J. Clin. Microbiol. 38:2156-2161(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:k6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
DR EMBL: AP005078; BAA97266.1; -.
DR EMBL: AP005078; BAC59824.1; -.
KW Complete proteome; Hypothetical protein; Plasmid.
SQ SEQUENCE 497 AA; 55788 MW; 274E868DEB6E8B19 CRC64;
Query Match 100.0%; Score 32; DB 2; Length 497;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRGDD 5
DB 97 CRGDD 101

RESULT 39
Q8QS61 PRELIMINARY; PRT; 640 AA.
AC Q8QS61;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE UL27.
OS Pongine herpesvirus 4.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.

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OX NCBI_TaxID=188763;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22421467; PubMed=12533697; DOI=10.1099/vir.0.18606-0;
RA Davison A.J., Dolan A., Akter P., Addison C., Dargan D.J.,
RA Alexander D.J., McGeoch D.J., Hayward G.S.;
RT "The human cytomegalovirus genome revisited: comparison with the
RL chimpanzee cytomegalovirus genome.";
RL J. Gen. Virol. 84:17-28(2003).
DR EMBL; AF480884; RAM00678.1; -
DR InterPro; IPR010302; Herpes_US.
DR Pfam; PF05999; Herpes_U5; 1.
SQ SEQUENCE 640 AA; 73457 MW; E4969DFC8EF4F34F CRC64;

Query Match 100.0%; Score 32; DB 2; Length 640;
Best Local Similarity 100.0%; Pred. No. 2.5e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 CRGDD 5
DB 46 CRGDD 50

RESULT 40
Q73RY0
ID Q73RY0 PRELIMINARY; PRT; 776 AA.
AC Q73RY0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=MAP4298c;
OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1770;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=k10;
RA Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AS017242; AA506848.1; -
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR003673; CAIB BAIF.
DR Pfam; PF02515; CoA_transf_3; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 776 AA; 82189 MW; 38A4528FC5B0B4BB CRC64;

Query Match 100.0%; Score 32; DB 2; Length 776;
Best Local Similarity 100.0%; Pred. No. 3.1e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 CRGDD 5
DB 617 CRGDD 621

RESULT 41
Q8SZX4
ID Q8SZX4 PRELIMINARY; PRT; 934 AA.
AC Q8SZX4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE LP03809P.
GN Name=Nrx-1;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephyroidae; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Paclet J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV069731; AAL39876.1; -
DR HSSP; O63373; 1C4R.
DR FlyBase; FBgn0038975; Nrx-1.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008985; CoxA_like_lec_gl.
DR InterPro; IPR00742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR003129; TSP_N.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF02210; Laminin_G_2.
DR SMART; SM00282; LamG; 2.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS50025; Lam_G_DOMAIN; 2.
SQ SEQUENCE 934 AA; 99518 MW; BC805CB3522A2EF8 CRC64;

Query Match 100.0%; Score 32; DB 2; Length 934;
Best Local Similarity 100.0%; Pred. No. 3.7e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 CRGDD 5
DB 510 CRGDD 514

RESULT 42
MKH1_SCHPO
ID MKH1_SCHPO STANDARD; PRT; 1116 AA.
AC Q10407;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE MAP kinase kinase kinase mkhl (EC 2.7.1.-).
GN Name=mkhl; ORFNames=SPAC1F3.02c;
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP66;
RX MEDLINE=97342589; PubMed=9199286;
RA Sengar A.S., Markley N.A., Marini N.J., Young D.;
RT "Mkhl, a MEK kinase required for cell wall integrity and proper
RT response to osmotic and temperature stress in Schizosaccharomyces
RT pombe.";
RL Mol. Cell. Biol. 17:3508-3519(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

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RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Leck A., Beck A., Lechach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,
RA Cerutti L., Lowe T., McCombe W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of *Schizosaccharomyces pombe*."
RL Nature 415:871-880(2002).
CC -!- FUNCTION: May regulate cell morphology, cell wall integrity, salt
CC resistance, cell cycle reentry from stationary-phase arrest, and
CC filamentous growth in response to stress. Activates the MAP kinase
CC kinase skh1/peki by phosphorylation.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. MAP
CC kinase kinase subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U53872; AAB62319.1; -;
CC EMBL; 270690; CAA94620.1; -;
CC FIR; T38073; T38073.
CC HSP; Q16539; 1KVI.
CC GeneDB:SPombe; SPAC1F3.02c; -;
CC InterPro; IPR011009; Kinase like.
CC InterPro; IPR007119; Prot_kinase.
CC InterPro; IPR001650; SAM_kinase.
CC InterPro; IPR010993; SAM_homology.
CC InterPro; IPR008271; Ser_thr_pkin_AS.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; Pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00220; S_TKc; 1.
CC SMART; SM00454; SAM; 1.
CC PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
CC PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN KINASE_ST; 1.
CC ATP-binding; Serine/threonine-protein kinase; Transferase.
KW DOMAIN 825 1094 Protein kinase.
FT NP_BIND 831 839 ATP (By similarity).
FT BINDING 854 854 ATP (By similarity).
FT ACT_SITE 955 955 Proton acceptor (By similarity).
SQ SEQUENCE 1116 AA; 125132 MW; 7AFDB3EC62EED47B CRC64;
Query Match 100.0%; Score 32; DB 1; Length 1116;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRGDD 5
Db 677 CRGDD 681
RESULT 43
Q8JKT0 PRELIMINARY; PRT; 1145 AA.
AC Q8JKT0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Orf31.
GN Name=orf31;
OS Heliothis zea virus 1.
OC Viruses; dsDNA viruses, no RNA stage; unclassified dsDNA viruses.

OX NCBI_TaxID=29250;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22174892; PubMed=12186886;
RX DOI=10.1128/JVI.76.18.9024-9034.2002;
RA Cheng C.H., Liu S.M., Chow T.Y., Hsiao Y.Y., Wang D.P., Huang J.J.,
RA Chen H.H.;
RT "Analysis of the complete genome sequence of the Hs-1 virus suggests
RT that it is related to members of the Baculoviridae.";
RL J. Virol. 76:9024-9034(2002).
RN [2]
RP SEQUENCE FROM N.A.
RP Cheng C.H., Liu H.M., Hsiao Y.Y., Chow T.Y., Chen H.H.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Chao Y.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Chen H.H., Yeh W.B., Tso D.J.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Cheng C.H., Hsiao Y.Y., Liu S.M., Chow T.Y., Chen H.H.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF451898; AAN04326.1; -;
SQ SEQUENCE 1145 AA; 125435 MW; B0DCB3BDCDC7DC42 CRC64;
Query Match 100.0%; Score 32; DB 2; Length 1145;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRGDD 5
Db 17 CRGDD 21
RESULT 44
Q7PSM9 PRELIMINARY; PRT; 1504 AA.
AC Q7PSM9;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000010133 (Fragment).
GN Name=ENSANGP0000007644;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAB801008817; EAA05336.2; -;
CC HSP; Q63373; 1C4R.
CC GO; GO:0005198; F:structural molecule activity; IEA.
CC GO; GO:0007155; P:cell adhesion; IEA.
CC InterPro; IPR008985; Cona like_lec_gl.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR006209; EGF-like.
CC InterPro; IPR001791; Laminin_G.
CC InterPro; IPR003129; TSP_N.
CC Pfam; PF02210; Laminin_G_2; 5.
CC Pfam; PF02008; EGF_3.
CC PROSITE; PS50026; EGF_3_3.
CC PROSITE; PS50025; LAM_G_DOMAIN; 4.
FT NON_TER 1

[illegible]

OX NCBI_TaxID=184922;
 RN SEQUENCE FROM N.A.
 RC STRAIN=WB CG;
 RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
 RA Olsen G.J., Sogin M.L.;
 RT "Draft sequence of the Giardia lamblia genome."
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AACB0100181; EAA36741.1; -;
 SQ SEQUENCE 73 AA; 8125 MW; 4F866C8AEF254DDE CRC64;

Query Match 90.6%; Score 29; DB 2; Length 73;
 Best Local Similarity 80.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
 Db 30 CRGDD 34

RESULT 47
 Q69T89 ID Q69T89 PRELIMINARY; PRT; 112 AA.
 AC Q69T89;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein P0652D10.11.
 GN Name=P0652D10.11;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC
 RT clone:P0652D10."
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP004757; BAD33235.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 112 AA; 12420 MW; 8BEA619585F664F9 CRC64;

Query Match 90.6%; Score 29; DB 2; Length 112;
 Best Local Similarity 80.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
 Db 45 CRGDD 49

RESULT 48
 Q726G7 ID Q726G7 PRELIMINARY; PRT; 126 AA.
 AC Q726G7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Lipoprotein, putative.
 GN OrderedLocNames=DVU3141;
 OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
 OS 8303).
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
 OC Desulfovibrionaceae; Desulfovibrio.
 OX NCBI_TaxID=882;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15077118; DOI=10.1038/nbt959;

RA Heidelberg J.F., Sebadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
 RA Kolonay J.F., Eisen J.A., Ward N.D., Meche B.A., Brinkac L.M.,
 RA Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
 RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
 RA Peterson J.D., Davidson T.M., Zafar N., Zhou L., Radune D.,
 RA Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
 RA Felblyum T.V., Wall J.D., Voordouw G., Frazer C.M.;
 RT "The genome sequence of the anaerobic, sulfate-reducing bacterium
 RT Desulfovibrio vulgaris Hildenborough."
 RL Nat. Biotechnol. 22:554-559(2004).
 DR EMBL; AE017319; AAS97611.1; -;
 DR TIGR; DVU3141; -;
 KW Complete proteome; Lipoprotein.
 SQ SEQUENCE 126 AA; 13270 MW; DB78BD19B539D9EB CRC64;

Query Match 90.6%; Score 29; DB 2; Length 126;
 Best Local Similarity 80.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
 Db 106 CRGDD 110

RESULT 49
 Q8XNS3 ID Q8XNS3 PRELIMINARY; PRT; 168 AA.
 AC Q8XNS3;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Probable transcriptional regulator.
 OS OrderedLocNames=CPE0259;
 OC Clostridium perfringens.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1502;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=13;
 RX MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
 RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
 RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic
 RT flesh-eater."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 DR EMBL; AP003186; BAB79965.1; -;
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR Pfam; PF02559; Card_TRCF; 1.
 KW Complete proteome.
 SQ SEQUENCE 168 AA; 19582 MW; B6AC5EAA335AF717 CRC64;

Query Match 90.6%; Score 29; DB 2; Length 168;
 Best Local Similarity 80.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
 Db 129 CRGDD 133

RESULT 50
 Q8T399 ID Q8T399 PRELIMINARY; PRT; 225 AA.
 AC Q8T399;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative coagulation serine protease.
 GN Name=sp5;
 OS Ciona intestinalis.
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

```
OC Phlebobranchia; Cionidae; Ciona.
OX NCBI_TaxID=7719;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Repatopancreas;
RA Hammond J.A., Nakao M., Yano T., Kemp G.D., Smith V.J.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AJ431687; CAD24310.1; -
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR009003; Pept Ser_Cys.
DR PRINTS; PR00722; CHYMOTRFSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
KW Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 225 AA; 24146 MW; 0EC9AE25D7CB743B CRC64;

Query Match          90.6%; Score 29; DB 2; Length 225;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
Db 193 CRGDD 197
|:|:|

RESULT 51
Q9NSJ7 PRELIMINARY; PRT; 264 AA.
AC Q9NSJ7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Hypothetical protein DKEZp434K1822 (Fragment).
GN Name=DKEZp434K1822;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Blum H., Bauersachs S., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL162082; CAB82415.1; -
DR PIR; T47183; T47183.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0004221; F:ubiquitin thiolesterase activity; IEA.
DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR001394; Peptidase_C19.
DR Pfam; PF00443; UCH; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
DR PROSITE; PS00973; UCH_2_2; 1.
DR PROSITE; PS0235; UCH_2_3; 1.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 264 AA; 29783 MW; 60D25351F7BE8464 CRC64;

Query Match          90.6%; Score 29; DB 2; Length 264;
Best Local Similarity 80.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
Db 17 CRGDD 21
|:|:|

us-10-812-238b-41.rup

RESULT 52
Q8CUR7 PRELIMINARY; PRT; 276 AA.
AC Q8CUR7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phosphomethylpyrimidine kinase.
GN Name=thiD; OrderedLocusNames=OB1040;
OS Oceanobacillus theyensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=HTE831.
RX MEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus theyensis isolated from the Iheya
RT Ridge and its unexpected adaptive capabilities to extreme
RT environments.";
RL Nucleic Acids Res. 30:3927-3935(2002).
DR EMBL; AP004596; BAC12996.1; -.
DR HSP; F55882; IJXH.
DR GO; GO:0008972; F:phosphomethylpyrimidine kinase activity; IEA.
DR GO; GO:0009228; P:thiamin biosynthesis; IEA.
DR InterPro; IPR004399; HMP-P_kinase.
DR TIGRFAMs; TIGR00097; HMP-P_kinase; 1.
KW Complete proteome.
SQ SEQUENCE 276 AA; 29916 MW; 65D5E6A236F216B9 CRC64;

Query Match          90.6%; Score 29; DB 2; Length 276;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
Db 110 CRGDD 114
|:|:|

RESULT 53
Q92XS2 PRELIMINARY; PRT; 296 AA.
AC Q92XS2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Sma2147;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=213396509; PubMed=11481432; DOI=10.1073/pnas.161294798;
RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
RA Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
RT "Nucleotide sequence and predicted functions of the entire
RT Sinorhizobium meliloti pSyma megaplasmid.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
DR EMBL; AE007302; AAK65827.1; -.
DR PIR; A95408; A95408.
DR InterPro; IPR011111; Plasmid_RepB.
DR Pfam; PF07506; RepB; 1.
KW Complete proteome; Hypothetical protein; Plasmid.
SQ SEQUENCE 296 AA; 32439 MW; D7D0AF683E0AE178 CRC64;

Query Match          90.6%; Score 29; DB 2; Length 296;
```

Best Local Similarity 80.0%; Pred. No. 5.1e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
 Db 5 CKGDD 9

RESULT 54
 Q8BJG3 PRELIMINARY; PRT; 302 AA.

AC Q8BJG3
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DE Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length
 DE enriched library, clone: D130076P14 product: similar to UBIQUITIN
 DE SPECIFIC PROTEASE (Fragment).
 GN Name=Usp22;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kishunai T., Tachiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki K.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer."
 RL Genomics Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Kato F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK084022; BAC39100.1; -;
 DR MEROPS; C19_035; -;
 DR MGD; MGI:2144157; Usp22.
 DR GO; GO:0004197; F:peptidase-type endopeptidase activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004221; F:ubiquitin thiolesterase activity; IEA.
 DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; IEA.
 DR InterPro; IPR000345; CytC heme BS.
 DR InterPro; IPR001394; Peptidase_C19.
 DR Pfam; PF00443; UCH; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
 DR PROSITE; PS00973; UCH_2_2; 1.
 DR PROSITE; PS0235; UCH_2_3; 1.
 KW Protease.
 FT NON_TER
 SQ SEQUENCE 302 AA; 34288 MW; 3E0A5CFA7CD8F72C CRC64;
 Query Match 90.6%; Score 29; DB 2; Length 302;
 Best Local Similarity 80.0%; Pred. No. 5.2e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
 Db 55 CKGDD 59

RESULT 55
 Q7MX77 PRELIMINARY; PRT; 319 AA.

AC Q7MX77
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Glycosyl transferase, group 2 family protein.
 DE OrderedLocusNames=PG0334;
 OS Porphyromonas gingivalis (Bacteroides gingivalis).
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Porphyromonadaceae; Porphyromonas.
 OX NCBI_TaxID=837;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=W83;
 RX MEDLINE=22829867; PubMed=12949112;
 RX DOI=10.1128/JB.185.18.5591-5601.2003;
 RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
 RA Eisen J.A., Dougherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
 RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
 RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
 RA Dewhirst F.E., Fraser C.M.;
 RT "Complete genome sequence of the oral pathogenic bacterium
 RT Porphyromonas gingivalis strain W83."
 RL J. Bacteriol. 185:5591-5601(2003).
 DR EMBL; AB017173; AAQ65547.1; -;
 DR TIGR; PG0334; -;
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR InterPro; IPR001173; Glyco_trans_2.
 DR Pfam; PF00535; Glycoe_transf_2; 1.
 KW Complete proteome; Transferase.
 SQ SEQUENCE 319 AA; 36313 MW; 73E349629EEF80CD CRC64;
 Query Match 90.6%; Score 29; DB 2; Length 319;
 Best Local Similarity 80.0%; Pred. No. 5.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 CRGDD 5
DB      63 CRGDD 67

RESULT 56
Q940P2 ID Q940P2 PRELIMINARY; PRT; 324 AA.
AC Q940P2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE At1g72050/F28P5 6.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurooids I; Brassicales; Brassicaceae; Arabidopsie.
NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
RA Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narusaka M., Nguyen T., Onodera C.S., Palm C.J.,
RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,
RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Meyers M.C., Banh J., Bowser L.,
RA Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen T., Onodera C.S.,
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,
RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY054225; AL06885.1; -
DR EMBL; AY066042; AL47409.1; -
DR GO; GO:0003634; Cinnuleus; IEA.
DR GO; GO:0003676; Fnuclleic acid binding; IEA.
DR GO; GO:0008270; Fzinc ion binding; IEA.
DR InterPro; IPR007087; ZnF_C2H2.
DR Pfam; PF00096; zf-C2H2; 5.
DR SMART; SM00355; ZnF_C2H2; 7.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 6.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 4.
SQ SEQUENCE 324 AA; 36527 MW; ED4AB6747A2FCE34 CRC64;

Query Match 90.6%; Score 29; DB 2; Length 324;
Best Local Similarity 80.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRGDD 5
DB      81 CRGDD 85

RESULT 57
Q9LKY3 ID Q9LKY3 PRELIMINARY; PRT; 360 AA.
AC Q9LKY3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ptl1 kinase-like protein.
GN Name=Ptl1b;
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

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OC eurooids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21036115; PubMed=11185558; DOI=10.1006/abbi.2000.2080;
RA Staswick P.;
RT "Two expressed soybean genes with high sequence identity to tomato
RT Ptl1 kinase lack autophosphorylation activity.";
RL Arch. Biochem. Biophys. 383:233-237(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Staswick P.E.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249318; AAF91337.1; -
DR HSSP; P00523; 2PTK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR00719; Prot Kinase.
DR ProDom; PD000001; Prot Kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
ATP-binding; Kinase.
SQ SEQUENCE 360 AA; 39481 MW; 0B54143D695C2B90 CRC64;

Query Match 90.6%; Score 29; DB 2; Length 360;
Best Local Similarity 80.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRGDD 5
DB      7 CRGDD 11

RESULT 58
Q9LKY4 ID Q9LKY4 PRELIMINARY; PRT; 360 AA.
AC Q9LKY4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ptl1 kinase-like protein.
GN Name=Ptl1a;
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurooids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21036115; PubMed=11185558; DOI=10.1006/abbi.2000.2080;
RA Staswick P.;
RT "Two expressed soybean genes with high sequence identity to tomato
RT Ptl1 kinase lack autophosphorylation activity.";
RL Arch. Biochem. Biophys. 383:233-237(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Staswick P.E.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249317; AAF91336.1; -
DR HSSP; P00523; 2PTK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR00719; Prot Kinase.
DR ProDom; PD000001; Prot Kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
ATP-binding; Kinase.
SQ SEQUENCE 360 AA; 39375 MW; E170D95DD20E2D6F CRC64;

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Query Match          90.6%; Score 29; DB 2; Length 360;
Best Local Similarity 80.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
DB 7 CKGDD 11

RESULT 59
Q72MX9 PRELIMINARY; PRT; 366 AA.
AC Q72MX9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE LipL36.
GN Names=lipL36; OrderedLocusNames=LIC13060;
OS Leptospira interrogans (serogroup Icterohaemorrhagiae / serovar Copenhageni);
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OC NCBI_TaxID=44275;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fiocruz L1-130;
RX PubMed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;
RA Nascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B., Ho P.L., Haake D.A., Verjovski-Almeida S., Hartkeel R.A., Marques M.V., Oliveira M.C., Mence C.F.M., Leite L.C.C., Carrer H., Coutinho L.L., Degraeve W.M., Dellagostin O.A., El-Dorry H., Ferro E.S., Ferro M.I.T., Furlan L.R., Gamberini M., Gigliotti E.A., Goes-Neto A., Goldman G.H., Goldman M.H.S., Harakava R., Jeronimo S.M.B., Junqueira-de-Azevedo J.L.M., Kimura E.T., Kuramae E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R., de Oliveira R.C., Pereira G.G., Reis M.S., Schriefer A., Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A., Camargo L.E.A., Kitajima J.P., Setubal J.C., Van Sluys M.A.;
RA "Comparative genomics of two Leptospira interrogans serovars reveals novel insights into physiology and pathogenesis.";
RL J. Bacteriol. 186:2164-2172(2004).
DR EMBL; AB017299; AAS71609.1; -.
KW Complete proteome.
SQ SEQUENCE 366 AA; 37620 MW; 68924462DADA1F73 CRC64;

Query Match          90.6%; Score 29; DB 2; Length 366;
Best Local Similarity 80.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
DB 21 CKGDD 25

RESULT 60
Q8F8R3 PRELIMINARY; PRT; 366 AA.
AC Q8F8R3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE LipL36 protein.
GN Names=lipL36; OrderedLocusNames=LA0492;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OC NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H., Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F., Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-P., Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,

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RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A., Saint Grons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z., Xu J.-G., Zhao G.-P.;
RA "Unique physiological and pathogenic features of Leptospira interrogans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
DR EMBL; AB011235; AAN47691.1; -.
KW Complete proteome.
SQ SEQUENCE 366 AA; 37677 MW; 106A18B837388EC5 CRC64;

Query Match          90.6%; Score 29; DB 2; Length 366;
Best Local Similarity 80.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
DB 21 CKGDD 25

RESULT 61
Q6FIV5 PRELIMINARY; PRT; 386 AA.
AC Q6FIV5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Similar to sp|Q12385 Saccharomyces cerevisiae YLR099c ICT1.
GN ORFNames=CAGL0M11462g;
OC Candida glabrata CBS138.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OC NCBI_TaxID=284593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS138;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E., Goffard N., Frangoul L., Aigle M., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C., Boisarane A., Boyer J., Cattolico L., Confanioli F., de Daruvar A., Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H., Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A., Swenne D., Tekia F., Wesolowski-Louvel M., Westhof E., Wirth B., Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A., Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J., Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
DR EMBL; CR380959; CAG62819.1; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
DR InterPro; IPR000073; A/b hydrolase.
DR InterPro; IPR003089; AB hydrolase.
DR InterPro; IPR003079; Ser esters.
DR Pfam; PF00561; Abhydrolase 1; 1.
DR PRINTS; PR00111; ABHYDROLASE.
SQ SEQUENCE 386 AA; 44552 MW; 1F58363365217E51 CRC64;

Query Match          90.6%; Score 29; DB 2; Length 386;
Best Local Similarity 80.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
DB 3 CKGDD 7

RESULT 62
Q6EV52

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ID Q6EV52 PRELIMINARY; PRT; 403 AA.
AC Q6EV52;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Protein-O-fucosyltransferase 2 (Fragment).
GN Name=fut13;
OS Clona savignyi.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Clonidae; Clona.
OX NCBI_TaxID=51511;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12966037; DOI=10.1093/glycob/cwgl13;
RA Martinez-Duncker I., Mollicone R., Candelieri J.J., Breton C.,
RA Oriol R.;
RT "A new superfamily of protein-O-fucosyltransferases, alpha2-
RT fucosyltransferases and alpha6-fucosyltransferases: phylogeny and
RT identification of conserved peptide motifs.";
RL Glycobiology 13:1C-5C(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Martinez-Duncker I., Oriol R., Mollicone R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ781760; CHA03735.1; -;
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
KW Glycosyltransferase; Transferase.
FT NON_TER 1
SQ SEQUENCE 403 AA; 47347 MW; E930EB3E3A23C416 CRC64;
Query Match 90.6%; Score 29; DB 2; Length 403;
Best Local Similarity 80.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRGDD 5
Db 38 CRGDD 42
RESULT 63
Q84MZ4 PRELIMINARY; PRT; 412 AA.
ID Q84MZ4;
AC Q84MZ4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Transcription factor IIIA (Hypothetical protein) (At1g72050).
GN Name=TFIIIA; ORFNames=At1g72050;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22598218; PubMed=12711688; DOI=10.1093/nar/gkg335;
RA Mathieu O., Yukawa Y., Prieto J.L., Vaillant I., Sugiura M.,
RA Tourmente S.;
RT "Identification and characterization of transcription factor IIIA and
RT ribosomal protein L5 from Arabidopsis thaliana.";
RL Nucleic Acids Res. 31:2424-2433(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Gong W., Shen Y.P., Ma L.G., Du Y.L., Wang D.H., Yang J.Y., Hu L.D.,
RA Liu X.F., Dong C.X., Ma L., Chen Y.H., Yang X.Y., Gao Y., Zhu D.,
RA Tan X., Mu J.Y., Zhang D.B., Liu Y.T., Dinesh-Kumar S.P., Li Y.,
RA Wang X.P., Gu H.Y., Qu L.J., Bai S.N., Lu Y.T., Li J.Y., Zhao J.D.,
RA Zuo J., Huang H., Deng X.W., Zhu Y.X.;
RT "Genome-Wide ORFome Cloning and Analysis of Arabidopsis Transcription
RT Factor Genes.";
RL Plant Physiol. 135:773-782(2004).
RN [3]
RP SEQUENCE FROM N.A.

RA Zhu Y.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Gong W., Pan Y., Du Y.-L., Wang D.-H., Yang J.-Y., Hu L.-D.,
RA Dong C.-X., Ma L., Ma L.-G., Mu J.-Y., Zhang D.-B., Li Y., Wang X.-P.,
RA Gu H.-Y., Qu L.-J., Bai S.-N., Lu Y.-T., Li J.-Y., Zhao J.-D.,
RA Zuo J.-R., Huang H., Deng X.-W., Zhu Y.-X.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY186610; AAO73339.1; -;
DR EMBL; AJ630478; CAG25851.1; -;
DR EMBL; AY568650; AAS79540.1; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR007087; Znf_C2H2;
DR Pfam; PF00096; zf-C2H2; 7.
DR SMART; SM00355; Znf_C2H2; 9.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 5.
KW Hypothetical protein.
SQ SEQUENCE 412 AA; 46653 MW; AC171P610724C09F CRC64;
Query Match 90.6%; Score 29; DB 2; Length 412;
Best Local Similarity 80.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRGDD 5
Db 169 CKGDD 173
RESULT 64
Q9C7G8 PRELIMINARY; PRT; 413 AA.
ID Q9C7G8;
AC Q9C7G8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C2H2-type zinc finger protein, putative.
GN Name=F28PS.6;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
RA Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC069273; AAG51140.1; -;
DR PIR; F96743; F96743.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR007087; Znf_C2H2;
DR Pfam; PF00096; zf-C2H2; 6.
DR SMART; SM00355; Znf_C2H2; 9.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 6.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 5.
SQ SEQUENCE 413 AA; 46592 MW; B9F505F90B4C94FD CRC64;
Query Match 90.6%; Score 29; DB 2; Length 413;
Best Local Similarity 80.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRGDD 5
Db 191 CKGDD 195

RESULT 65

Q6MK81 ID Q6MK81 PRELIMINARY; PRT; 419 AA.
AC Q6MK81; AC
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein precursor.
GN OrderedLocustNames=Bd529;
OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164; DOI=10.1126/science.1093027;
RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
RA Keller H., Lambert C., Evans K.J., Gosemann A., Meyer F.,
RA Sockett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
RT genomic perspective.";
RL Science 303:689-692(2004).
DR EMBL; BX842653; CAE80328.1; -.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR009056; Cytochrome_c.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
KW Complete proteome.
FT SIGNAL 1 10 Potential.
SQ SEQUENCE 419 AA; 44302 MW; B45746CAFAA17E2 CRC64;

Query Match 90.6%; Score 29; DB 2; Length 419;
Best Local Similarity 80.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5

Db 163 CRGDD 167

RESULT 66

Q7YZS7 ID Q7YZS7 PRELIMINARY; PRT; 434 AA.
AC Q7YZS7; AC
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein fut13.
GN Name=fut13;
OS Ciona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Clonidae; Ciona.
OX NCBI_TaxID=7719;
RN [1]
RP SEQUENCE FROM N.A.
RA Martinez-Dunker I., Mollicone R., Candellier J.J., Breton C., Oriol R.;
RT "A new superfamily of protein-O-fucosyltransferases, alpha2-
RT fucosyltransferase, and alpha6-fucosyltransferases: phylogeny and
RT identification of conserved peptide motifs.";
RL Glycobiology 13:1c-5c(2003).
DR EMBL; AJ575656; CAE02609.1; -.
KW Hypothetical protein.
SQ SEQUENCE 434 AA; 50605 MW; D853C746D6E896C CRC64;

Query Match 90.6%; Score 29; DB 2; Length 434;
Best Local Similarity 80.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5

Db 69 CRGDD 73

RESULT 67

Q6MZY4 ID Q6MZY4 PRELIMINARY; PRT; 453 AA.
AC Q6MZY4; AC
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686P16150 (fragment).
GN Name=DKFZp686P16150;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human colon endothel primary cell culture;
RG The German Human CDNA Consortium;
RA Bloecker H., Boecker M., Mewes H.W., Weil B., Amid C., Oeanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640815; CAE45893.1; -.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0004221; F:ubiquitin thioesterase activity; IEA.
DR GO; GO:0006511; F:ubiquitin-dependent protein catabolism; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR001394; Peptidase_C19.
DR Pfam; PF00443; UCH; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
DR PROSITE; PS00972; UCH_2_1; 1.
DR PROSITE; PS00973; UCH_2_2; 1.
DR PROSITE; PS50235; UCH_2_3; 1.
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 453 AA; 51965 MW; 9A513E25242A420C CRC64;

Query Match 90.6%; Score 29; DB 2; Length 453;
Best Local Similarity 80.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5

Db 206 CRGDD 210

RESULT 68

Q8CEG8 ID Q8CEG8 PRELIMINARY; PRT; 519 AA.
AC Q8CEG8; AC
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 12 days embryo head cDNA, RIKEN full-length enriched
DE library, clone:3002003A21 product:ubiquitin specific protease 27, X
DE chromosome, full insert sequence.
GN Name=Usp27x;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).

RN [3] SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RA The FANTOM Consortium.
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayata N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384 format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito K., Saitoh K., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL, AK028249; BAC25840.1; -;
 DR MGD; MGI:1859645; Usp27x.
 DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004221; F:ubiquitin thiolesterase activity; IEA.
 DR GO; GO:0006511; F:ubiquitin-dependent protein catabolism; IEA.
 DR InterPro; IPR000345; CytC heme_BS.
 DR InterPro; IPR001394; Peptidase_C19.
 DR InterPro; IPR001607; Znf_UBP.
 DR Pfam; PF00443; UCH; 1.
 DR Pfam; PF02148; zf-UBP; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
 DR PROSITE; PS00972; UCH_2_1; 1.
 DR PROSITE; PS50235; UCH_2_3; 1.
 KW Protease.
 SQ SEQUENCE 519 AA; 58106 MW; DCC088BEC616AC86 CRC64;

Query Match 90.6%; Score 29; DB 2; Length 519;
 Best Local Similarity 80.0%; Pred. No. 8.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
 Db 301 CKGDD 305

RESULT 69

Q6GNI6
 ID Q6GNI6 PRELIMINARY; PRT; 523 AA.
 AC Q6GNI6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE MGC82781 protein.
 GN Name=MGC82781;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Klein S., Gerhard D.S.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073524; AAH73524.1; -;
 DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
 DR GO; GO:0004221; F:ubiquitin thiolesterase activity; IEA.
 DR GO; GO:0006511; F:ubiquitin-dependent protein catabolism; IEA.
 DR InterPro; IPR000345; CytC heme_BS.
 DR InterPro; IPR001394; Peptidase_C19.
 DR InterPro; IPR001607; Znf_UBP.
 DR Pfam; PF00443; UCH; 1.
 DR Pfam; PF02148; zf-UBP; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
 DR PROSITE; PS00972; UCH_2_1; 1.
 DR PROSITE; PS00973; UCH_2_2; 1.
 DR PROSITE; PS50235; UCH_2_3; 1.
 SQ SEQUENCE 523 AA; 60048 MW; 731A0AE1C2E67D61 CRC64;

Query Match 90.6%; Score 29; DB 2; Length 523;
 Best Local Similarity 80.0%; Pred. No. 9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDD 5
 Db 276 CKGDD 280

RESULT 70

Q66JV8 PRELIMINARY; PRT; 525 AA.
 AC Q66JV8; (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Ubiquitin specific protease 22.
 GN Names=Usp22;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Embryo;
 RC PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RA Director MGC Project;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC080737; AAH80737.1; -.
 DR InterPro; IPR001394; Peptidase_C19.
 DR Pfam; PF00443; UCH_1.
 DR PROSITE; PS00973; UCH_2_2; 1.
 DR PROSITE; PS50235; UCH_2_3; 1.
 KW Protease.
 SQ SEQUENCE 525 AA; 59954 MW; F884EDE9B2PBF988 CRC64;

Query Match 90.6%; Score 29; DB 2; Length 525;
 Best Local Similarity 80.0%; Pred. No. 9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5

Db 278 CXGDD 282
 :|||

RESULT 71

Q9JIG5 PRELIMINARY; PRT; 525 AA.
 AC Q9JIG5;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Ubiquitin specific protease (Fragment).
 GN Names=Usp27x; Synonyms=Uspgx;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20313888; PubMed=10857745; DOI=10.1006/geno.2000.6173;

RA Means G.D., Toy D.Y., Baum P.R., Derry J.M.J.;

RT "A transcript map of a 2-Mb BAC contig in the proximal portion of the

mouse X chromosome and regional mapping of the scurfy mutation.";

RL Genomics 65:213-223(2000).

DR EMBL; AF229643; AAF66953.1; -.

DR MEROPS; C19.075; -.

DR MGD; MGI:1859645; Usp27x.

DR GO; GO:0004197; F-cysteine-type endopeptidase activity; IEA.

DR GO; GO:0008233; F-peptidase activity; IEA.

DR GO; GO:0004221; Fubiquitin thiolesterase activity; IEA.

DR GO; GO:0006511; Fubiquitin-dependent protein catabolism; IEA.

DR InterPro; IPR000345; CytC heme BS.

DR InterPro; IPR001394; Peptidase_C19.

DR InterPro; IPR001607; Znf_UBP.

DR Pfam; PF00443; UCH_1.

DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.

DR PROSITE; PS00972; UCH_2_1; 1.

DR PROSITE; PS00973; UCH_2_2; 1.

DR PROSITE; PS50235; UCH_2_3; 1.

KW Protease.

FT NON_TER 1

SQ SEQUENCE 525 AA; 59670 MW; 71B7F18E25A2720B CRC64;

Query Match 90.6%; Score 29; DB 2; Length 525;

Best Local Similarity 80.0%; Pred. No. 9e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5

Db 267 CXGDD 271
 :|||

RESULT 72

Q8BSW2 PRELIMINARY; PRT; 540 AA.
 AC Q8BSW2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Mus musculus adult male pituitary gland cDNA, RIKEN full-length
 enriched library, clone:530405105 product:ubiquitin specific protease
 27, X chromosome, full insert sequence. (Fragment).
 DE 27, X chromosome, full insert sequence. (Fragment).
 GN Name=Usp27x;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Pituitary gland;
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RX Carninci P., Hayashizaki Y.;
 RA "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Pituitary gland;
 RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Pituitary gland;
 RC The FANTOM Consortium;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";

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RL Nature 420:563-573 (2002).
RN [14]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata K., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [15]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [16]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Kori F., Inotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Hori H., Kawai J., Kojima J., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Nunazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK030383; BAC26935.1; -.
DR MEROPS; C19.075; -.
DR MGD; MGI:1859645; Usp27X.
DR GO; GO:0004197; F:cytosteine-type endopeptidase activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004221; P:ubiquitin thiolesterase activity; IEA.
DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR001394; Peptidase_C19.
DR InterPro; IPR001607; Znf_UBP.
DR Pfam; PF00443; UCH; 1.
DR Pfam; PF02148; zf-UBP; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00972; UCH_2_1; 1.
DR PROSITE; PS00973; UCH_2_2; 1.
DR PROSITE; PS02335; UCH_2_3; 1.
DR Protease.
KW NON_TER
FT
SQ SEQUENCE 540 AA; 61206 MW; E0F4C3E840A0A4A CRC64;

Query Match 90.6%; Score 29; DB 2; Length 540;
Best Local Similarity 80.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
DB 282 CKGDD 286

RESULT 73
Q98UH5 PRELIMINARY; PRT; 549 AA.
AC Q98UH5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
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DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE G protein-coupled receptor kinase 7.
GN Name=GRK7;
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RA Shimauchi Y., Tachibana S., Kawamura S.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. GPRK
CC subfamily.
CC -!- SIMILARITY: Contains 1 RGS domain.
DR EMBL; AB055658; BAB32498.1; -.
DR HSSP; P31751; IGZK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004703; F:G-protein coupled receptor kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006740; F:transferase activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000239; GPCR_Kinase.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR000342; RGS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00615; RGS; 1.
DR PRINTS; PR00717; GPCR_KINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00315; RGS; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00132; RGS; 1.
KW ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
KW Transferase.
SQ SEQUENCE 549 AA; 62423 MW; CB186B8587A0B183 CRC64;

Query Match 90.6%; Score 29; DB 2; Length 549;
Best Local Similarity 80.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
DB 438 CKGDD 442

RESULT 74
Q99KU3 PRELIMINARY; PRT; 553 AA.
AC Q99KU3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein OSUNBA0006G10.30 (Hypothetical protein
DE P0584D02.22).
GN Name=OSUNBA0006G10.30; Synonyms=P0584D02.22;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
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RP SEQUENCE FROM N.A.
 RA Sabaki T., Matsumoto T., Katayose Y.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 9, BAC
 RT clone:OSJNBa006G10."
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Sabaki T., Matsumoto T., Katayose Y.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 9, PAC
 RT clone:P0584D02."
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005909; BAD34163.1; -
 DR EMBL; AP005634; BAD33695.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 553 AA; 60475 MW; 24E5AF1DADA67D4 CRC64;

Query Match 90.6%; Score 29; DB 2; Length 553;
 Best Local Similarity 80.0%; Pred.No. 9.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
 |::||
 Db 289 CKGDD 293

RESULT 75

Q6DCJ1 PRELIMINARY; PRT; 572 AA.
 AC Q6DCJ1;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 ON NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.B., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative."
 RL Dev. Dyn. 225:384-391(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywicki N.I., Skalska U., Smallos D.B., Schmerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC078033; AAH78033.1; -
 DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
 DR GO; GO:0004221; F:ubiquitin thiolesterase activity; IEA.
 DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; IEA.
 DR InterPro; IPR000345; CytC_heme_BS.
 DR InterPro; IPR001394; Peptidase_C19.
 DR Pfam; PF00443; UCH; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
 DR PROSITE; PS00972; UCH_2_1; 1.
 DR PROSITE; PS00973; UCH_2_2; 1.
 DR PROSITE; PS0235; UCH_2_3; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 572 AA; 65376 MW; 2877008E74EB7B6B CRC64;

Query Match 90.6%; Score 29; DB 2; Length 572;
 Best Local Similarity 80.0%; Pred.No. 9.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDD 5
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 Db 325 CKGDD 329

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